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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run
                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on:
                                                                                                                                                                                                                                                                                                   B B
                                                                                                                                                                                                                                                                                                   seq
                                                                                                                                                                                                                                                                                                   length:
length:
                                                                                                        SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
    10:
11:
12:
13:
14:
15:
16:
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-119-209-2_COPY_39_155
666
1 WTYHYSEKPMNWQRARRFCR.....
                                                                                                                                                                                                                                                                                                                                                                  562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                      WTYHYSEKPMNWQRARRFCR.....NKDAGKWNDDACHKLKAALC
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
                                                                                                       sp_phage: *
                                                                                                                   sp_organelle:*
                                                                                                                                              sp_mammal:*
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20000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Search time 61.04 Seconds
(without alignments)
331.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      117
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7654327	Score 666 598 557 445 445	100.0 89.8 83.6 66.8 66.8	Length 385 376 372 616 740 740 484	DB 6 111	Q9U743 Q9U743 Q28629 Q63762 Q95509 Q95507 Q95508	Q9uj43 homo sapien Q28629 oryctolagus Q63762 rattus nor Q95509 homo sapien Q95507 homo sapien Q95192 ovis aries
٢	666	100.0	385	42	Q9UJ43	Q9uj4
N	598	89.8	376	6	Q28629	Q2862
ω	557	83.6	372	11	Q63762	Q63 7
4	445	66.8	616	4	095509	09550
₅	445	66.8	740	4	095507	09550
თ	445	66.8	740	4	095508	09550
7	440	66.1	484	თ	Q95LG2	Q951g
œ	437	65.6	485	σ	Q95LG3	Q951g
ø	434	65.2	754	σ	Q28290	Q2829
_	425	63.8	482	σ	Q28982	Q28982
11	420	63.1	649	6	Q28657	Q28657
	408	61.3	609	σ	Q9GLF0	Q9g1f
_	401	60.2	646	6	Q29097	029097
	392.5	58.9	610	σ	Q95LG1	Q951g
15	177	26.6	328	4	Q9UJ71	Q9uj71
16	166	24.9	359	Ç	Q9VQX3	Q9vqx3

ALIGNMENTS

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Interpro; IPR000436; Sushi_SCR_CCP.
pfam; pF00008; EGF; 1.
pfam; pF00008; Sushi_C; 1.
pfam; pF00084; sushi; 2.
prints; pR0034; sushi; 2.
prints; pR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; pS00018; EGF; 1.
pROSITE; pS00012; CTYPE_LECTIN_1; 1.
pROSITE; pS00012; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UJ43 PRELIMINARY;
Q9UJ43;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-DEC-2001 (TrEMBLrel. 19, L
L-SELECTIN PRECURSOR.
                                                                                                                                     Figer C.B.;
Thesis (1998), Freie Universtiaet Berlin, Fachbereich Chemie.
EMBL; AJ246000; CAB55488.1; -.
HSSP; P14151; 1KJB.
InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin.
InterPro; IPR001396; Selectin.
InterPro; IPR002396; Selectin.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-HEMATOPOIETIC (B LYMPHOCYTE);
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 TISSUE-HEMATOPOIETIC Fieger C.B.;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                           L-SELECTIN
                                                                                                                                                                                                                                                                                                              (B LYMPHOCYTE);
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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                  385
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RESULT RE
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Best Local S
Matches 103
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROCYTEF DECOCTEF TO THE PROCYTEF TO
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EGF-like
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qian J., Marks R.M.;
"cDNA for rabbit L-selectin.";
"bubmitted (MAY-1995) to the EMBL/GenBank/DDBJ
EMBL; U26535; AAA67896.1; -.
HSSP; P14151; 1KJB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS00041; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF_1; UNKNOWN_1. PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=KIDNEY CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Lagomorpha; Leporid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (Tremblrel 01, 01-NOV-1996 (Tremblrel 01, 01-DEC-2001 (Tremblrel 19, L-SELECTIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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                  TWVGTNKSLTAEAENWGEGEPNNKKTKEDCVETYIKRLRDSGKWNDDSCQKRKAALC
                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00008;
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                              domain; Glycoprotein; Lectin;

9 POTENTIAL.

39 376 L-SELECTII

376 AA; 42346 MW; 59F6AD53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01186; EGF_2; 1. domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000561; EGF-like.
IPR001304; lectin_c.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                   89.8%; ilarity 88.0%; Conservative
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                                                                                                                                                                                                                                             Score 598; DB Pred. No. 1.3e 7; Mismatches
                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                              L-SELECTIN.
; 59F6AD530F490947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
L-SELECTIN.
; 1205F691BA638EF1
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Pred. No. 1.8e-59;
Mismatches 0;
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                                                                                                                                                                                                                                                                           598;
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                                                                                                                                                                                                                                          DB 6;
1.3e-52;
--- 7;
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RESULT
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Best Local :
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01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TREMBLrel. 1
01-DEC-2001 (TREMBLREL. 1
DJ780M13.1.3 (SELECTIN P
CD62, GMP140)) (ISOFORM 3
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
         SEQUENCE .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; I
InterPro; IPR001304; I
InterPro; IPR002396; S
InterPro; IPR000436; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sackstein R., Meng L., Xu X.M., C. Evidence of post-transcriptional expression in rat lymphoid cells. Immunology 85:198-204(1995).
EMBL; $79523; AACG0710.2; -. HSSP; P14151; 1KJB.
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS00022; EGF_1; UNKNOWN_1
PROSITE; PS01186; EGF_2; 1.
EGF-11ke domain; Glycoprotein.
SEQUENCE 372 AA; 42471 MW; 7DFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63762
Q63762;
                                                    Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (Tremblrel. 01, 01-NOV-1996 (Tremblrel. 01, 01-DEC-2001 (Tremblrel. 19, LYMPHOCYTE MEMBRANE PROTEIN
 Submitted
                                                                         Homo sapiens
                                                                                                                                                              095509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95369821; PubMed=7543874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                    1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u
                                                                                                                                                                                                               WTYHYSERSMNWENARKFCKHNYTDLVAIQNKREIEYLEKTLPKNPTYYWIGIRKIGKTW
                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                             Similarity
                      FROM
                                                    Eutheria;
(NOV-1998)
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                             PRELIMINARY;
                                                                        (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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; Rodentia;
                                                    Chordata;
Primates;
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lectin_c.
Selectin.
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. 10, Last sequence update)
. 19, Last annotation update)
. 19, Last annotation update)
P (GRANULE MEMBRANE PROTEIN
M 3) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.
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Last sequence update)
Last annotation update)
A.11.
 EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                              Pred.
                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                      7DFD125610DD6E4A CRC64;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chin Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation
                                                                                                                                                                                                                                                                                                           557;
No. 1.
                                                                                                                                                             616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372
                                                                                                                                                                                                                                                                                                             DB 11;
.9e-48;
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                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                        140
                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
                                                                                                        Ğ,
                                                                                                                                                                                                                                                                                                                        372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                   0;
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AL022146; CAA18144.1;

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Best Loc
Matches
Pfam; PF00008; EGF; 1.

Pfam; PF00008; lectin_C; 1.

Pfam; PF00084; Sushi; 8.

PRINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 8.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PR0SITE; PS00615; C_TYPE_LECTIN_2; 1.

PR0SITE; PS00614; C_TYPE_LECTIN_2; 1.

PR0SITE; PS00041; C_TYPE_LECTIN_2; 1.

PR0SITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS001186; EGF_2; 1.

EGF-1ike domain; Glycoprotein.

NON_TER

740

740

SEQUENCE
740
AA; 81095 MW; 3B5F70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pf00008; EGF; 1.
pfam; pf00059; lectin_G; 1.
pfam; pf00084; sushi; 6.
prints; pr00343; selectin.
smart; sm00034; clect; 1.
smart; sm00034; clect; 1.
smart; sm00181; EGF; 1.
smart; sm00181; EGF; 1.
pr0SITE; pS00615; C_TYPE_LECTIN_1; 1.
pr0SITE; pS00615; C_TYPE_LECTIN_2; 1.
pr0SITE; pS00022; EGF 1; UNKNOWN_1.
pr0SITE; pS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O95507 PRELIMINARY; PRT; 740 AA.
O95507;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ780M13.1.1 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140
CD62, GMP140)) (ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1998) to the EMBL; AL022146; CAA18142.1; HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like domain; Glycoprotein NON_TER 616 616 SEQUENCE 616 AA; 67736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561; EGF-like.
InterPro; IPR00396; Selectin.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
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HSSP; P16109;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002395; Selectin
InterPro; IPR000436; Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 65.8
77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 445; DB 4;
Pred. No. 7.8e-37;
l; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae
          3B5F70A45B1A3CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35CD4BFADE61D724 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KD,
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095508
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Best Local S
Matches 77
                                                                                                                                                                                    Matches
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                               Pfam; PF000008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 8.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 8.
SMART; SM00034; CLECT; 1.
SMART; SM00081; EGF; 1.
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Q95LG2 PRELIMINARY;
Q95LG2;
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                               EGF-like domain; Glycoprotein.
NON_TER 740 740
SEQUENCE 740 AA; 81390 MW;
                                                                                                                                                                                                                                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS0061; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF_1; UNKNOWN_1 PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1998) to the EMBL; AL022146; CAA18143.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL022146; CAA
HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Howden P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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nes 77; Conser
                                                                                                                                                                                                 Local
                                                                                                                                                1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                  TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                     TWVGTKKALTNEAENWADNEPNNKRNNEDCVETYTKSPSAPGKWNDEHCLKKKHALC
                                                                                                                                     WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                    Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000561; EGF-like.
IPR001304; lectin_c.
                                                                                                                                                                                    Conservative
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                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                               66.8%;
65.8%;
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                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                 Score 445; DB 4;
Pred. No. 9.7e-37;
1; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 445; DB 4;
Pred. No. 9.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vo
Catarrhini;
                         PRT;
                                                                                                                                                                                                                                                1D2E35E6D93745CE CRC64;
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                         484
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                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
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                                                                                                                                                                                    0;
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19,

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RESULT

1D 295LG3

AC 995LG3

AC 
RESULT
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Best Local S
Matches 76
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Best Loc
Matches
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Q95LG3;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21421234; PubMed=11529941;
MEDLINE=21421234; PubMed=11529941;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              "Characterization of equine E-selectin.";
Immunology 103:498-504(2001).
EMBL; AF307970; AAK48710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odocoileus hemionus (Mule deer) (Black-tailed deer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; (Cetartiodactyla; Ruminantia; Pecora; Cervoidea;

Cervidae; Odocoileinae; Odocoileus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                       Hedges J.F., Demaula MacLachlan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-SELECTIN
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EMBL; AF307971; AAK48711.1; -
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MEDLINE=21421234; PubMed=11529941;
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Ovis aries
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Best Local
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                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; (Mammalia; Eutheria; (NCBI_TaxID=9823;
                                                                                                                                                                                                     Q28982;
01-NOV-1996
01-NOV-1996
01-DEC-2001
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97075911; PubMed-8918234;
Winkler H., Brostjan C., Csizmadi
Bach F.H.;
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EGF-like
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01-DEC-2001
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SMART; SM00032; CCP; 8.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
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Interpro; IPR001304; lectin_c.
Interpro; IPR002396; Selectin.
Interpro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases EMBL; M88170; AAA63789.1; -. HSSP; P16109; 1FSB.
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Rosenbloom C.L., Hawkins H.L., Michael L.H.,
Beaudet A.L., Anderson D.C.;
"Molecular cloning of canine GMP140 and stud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00059; lectin_c; Pfam; PF00084; sushi; 8.
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Mammalia; E
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Eukaryota; Metazoa; Chordata;
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PS50041; C_TYPE_LECTIN_2;
PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
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Sus.
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Best Local S
Matches 74
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Pfam; PP000059; lectin_c; 1.

Pfam; PP00084; sushi; 4.

PRINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 4.

SMART; SM00034; CLECT; 1.

SMART; SM00031; EGF; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS01086; EGF_1; UNKNOWN_1.

PROSITE; PS01086; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.
             InterPro; IPR000561; EGF-11ke.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin
InterPro; IPR002396; Selectin
InterPro; IPR002435; Sushi_SCR_C()
Pfam; PP00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR001343; SELECTIN.
SMART; SM00032; CCP; 6.
SMART; SM00031; EGF; 1.
SMART; SM00031; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28657; PRELIMINARY;
Q28657; O1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
P-SELECTIN.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
Warden C.
                                                                                                                                                                                                                                                                 Submitted (OCT-1995) to the EMBL; U39446; AAA81385.1; -HSSP; P16109; IFSB.
                                                                                                                                                                                                                                                                                                                                                                                                                               Territo M.C., Berliner u.
"Induction of p-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Ve.
Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The intron-exon structure Gene 176:67-72(1996). EMBL; U37521; AAC48680.1; HSSP; P16581; LESL.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vora D.K., Fang Z., Liva
Territo M.C., Berliner J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-1ike.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR
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                                                                                                                                                                                                                                                                                                                                                                                                      (NOV-1995) to
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C_TYPE_LECTIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.8%;
                                                                                                                                                                              Sushi_SCR_CCP
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J.A.;
h by MM-LDL
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                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No. 6:1e-35;
3; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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Best Local S
Matches 69
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Best Local S
Matches 78
                                                                                                                                            Lectin; SEQUENCE
                                                                                                                                                                                    PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 4.
SMART; SM00001; EGF_like; 1.
                                                                                                                                                                                                                                                                                                           TISSUE-ENDOTHELIAL CELLS;
Zheng L., Shi Y., Wu H., Zhang G.;
"Cloning and sequencing of beagle E-selectin g
comparison with other species.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL, AF287257; AAG010039.1; -
HSSP; P16581; IESL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9GLF0
Q9GLF0;
Q1-MAR-2001 (TrEMBLrel. 16,
Q1-MAR-2001 (TrEMBLrel. 16,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
EGF-like
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
NCBI_TaxID=9615;
                                                                                                                                                                                                                                          Pfam; PF00059; lectin_c; 1. Pfam; PF00084; sushi; 6.
                                                                                                                                                      PROSITE; PS50041;
PROSITE; PS00022;
Lectin; Selectin.
                                                                                                                                                                                                                                                                           InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-SELECTIN
                                                                                                                                                                                                                                                                  InterPro;
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  83
                     61
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                                                               WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRK---IG
                                           WSYNASTEAMTFDEASTYCOORYTHLVAIQNQEEIKYLNSMFSYTPTYYWIGIRKVNKKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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                                                                                      69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
edomain; Glycoprotein; Lect
649 AA; 71755 MW; ECCD
                                                                                                                                                                                                                                                                  IPR000436; Sushi_SCR_CCP
                                                                                                                                             609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                             AA;
                                                                                                                                                          C_TYPE_LECTIN_2,
EGF_1; UNKNOWN_1.
                                                                                                                                             66073
                                                                                               61.3%;
59.0%;
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                                                                                       18;
                                                                                     Score 408; DE
Pred. No. 4.3e
L8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred.
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No. 2.
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                                                                                                 DB 6;
.3e-33;
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                                                                                                                                            CRC64;
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Canis.
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 139
                                                                                     Gaps
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RESULT Q29097

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RESULT
Q95LG1
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AC Q9
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Best Local S
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                                                                                               095LG1 PRELIMINARY;
095LG1;
01-DEC-2001 (TremBLrel. 1
01-DEC-2001 (TremBLrel. 1
01-DEC-2001 (TremBLrel. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
SEQUENCE
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Perissodactyla;
NCBI_TaxID=9796;
                                                                                      E-SELECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNO
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
Lectin; PS01186; EGF_2; 1.
Lectin; SIGNAL
42
646
P-SELECTIN
646
P-SELECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=AORTA;
MEDLINE=20171534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF163766; AAF43272.1; -. HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stocker C.J., Sugars Haskard D.O.;
                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "TNF-alpha, IL-4, and IFN-gamma regulate differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                               1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d E-selectin expression by porcine Immunol. 164:3309-3315(2000). BL; L39075; AAA79007.1;
                                                                                                                                                                                                                                                                                                               TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                                                                                        WTYNYSTSAYSWNTSRVFCQRYFTDLVAIQNKKEIAYLNDVIPYYSSYYWIGMRKINNKW
                                                                                                                                                                                                                                                                                            TWVGTKKTLTQEAENWAKNEPNNESNNQDCVEMYIKSPLAPGKWNDEPCVKRKRALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00032; CCP; 6.
SM00034; CLECT; 1.
SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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ars K.L., Harari
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71127
                                       Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.2%;
59.0%;
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to the
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Pred. No. 2.4e-32;
4; Mismatches 34
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Matches 41
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Best Local
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Q9VQX3
Q9VQX3;
01-MAY-2000
                                                                                                                                                                                                                                                                               Valladeau J., Ravel O., Dezutter-Dambuyant C., Moore K Duvert-Frances V., Vincent C., Schmitt D., Davoust J., Lebecque S., Saeland S.;
"Langerin, a new transmembrane C-type lectin specific cells, induces the formation of Birbeck granules.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ database EMBL; AJ242859; CAB62403.1; -.
HSSP; P20693; IHLJ.
                                                                                                                                                                                                                  PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 328 AA; 36697 MW; 83DF5A1B347D1B62
                                                                                                                                                                                                                                                   InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE=21421234; PubMed=11529941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of equine E-
Immunology 103:498-504(2001).
EMBL; AF307972; AAK48712.1; -
                                                                           265
                                                                                                                     207
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                                                                         SWVDDTPFNKVQSARFWIPGEPNNAGNNEHCGNI---KAPSLQAWNDAPCDKTFLFIC
                                                                                             TWV-GTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                  YYFSLIPKTWYSAEQFCVSRNSHLTSVTSESEQEFLYKTA--GGLIYWIGLTKAGMEGDW 264
                                                                                                                                 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW 60
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71; Conservative
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O (TrEMBLrel.
L (TrEMBLrel.
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(TrEMBLrel. 13,
                      PRELIMINARY;
                                                                                                                                                              Conservative
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Primates;
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34.7%;
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60.7%;
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13,
17,
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Pred. No. 5.3e
16; Mismatches
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Last sequence update)
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Pred. No. 1.6e
12; Mismatches
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                      PRT;
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                      359
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SORRER REPORTED DO DE LA COMPTANTA DE LA COMPT
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wz Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Descript M.
                                                                                                                                                                                                                                                                                                                                                                                             Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AE003577; AAF51038.1; -
EMBL; AY061025; AAL28573.1; -
HSSP; P14151; 1KJB.
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P.,
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                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0040102; lectin-24Db
InterPro; IPR001304; lectin_c.
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LECTIN-24DB OR CG2958.
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F; SM00034; CLECT; 1.
ITE; PS50041; C_TYPE_LE
ENCE 359 AA; 41546 M
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    166; DB 5;
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J.,
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Haggarty B.S., Ahmad N., Macfarlan T., Ec
Arnason J., Reinhart T.A., Kimata J.T., I
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Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGR
                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
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      Catano
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      G.,
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6; Mismatches
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Catarrhini; Hominidae
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      Hoefle
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   Α.,
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Edwards T.G., Leslie G.J.,
Littman D.R., Hoxie J.A.,
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Jimenez F., Ahuja S.S., Ahuja S.K.;
"Extensive Repertoire of Membrane-bound an
specific ICAM-3-grabbing Nonintegrin 1 (DC
Isoforms. Inter-individual Variation in Ex
Transcripts.";
J. Biol. Chem. 276:33196-33212(2001).
EMBL; AV04223; AAK91848.1;
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CD209.

Homo sapiens (Human).

'harvota; Metazoa; Chordata; heria; Primates;
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J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042227; AAK91852.1; -.
EMBL; AY042227 AAK91852.1; -.
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"Extensive Repertoire of Membrane-bound and Soluble Dendritic Specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2 ISoforms. Inter-individual Variation in Expression of DC-SIGN
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37; Conservative
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29.6%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 161.5;
Pred. No. 1.5e
L6; Mismatches
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ches 57;
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nes 57;
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Best Local
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01-DEC-2001
01-DEC-2001
01-DEC-2001
SDC-SIGNIA TY
                                  J. Biol. Chem. 276:33196-33212(2001).
J. AAK91851.1; -- **DEPPF
                                                                                                         Mummidi S., Catáno G., Lam L., Hoefle A., Telles V., Begum K., Jimenez F., Ahuja S.S., Ahuja S.K.; "Extensive Repertoire of Membrane-bound and Soluble Dendritic (specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2 Isoforms. Inter-individual Variation in Expression of DC-SIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96QP9;
01-DEC-2001 (TrE
01-DEC-2001 (TrE
01-DEC-2001 (TrE
SDC-SIGN1B TYPE
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. PubMed-11337487;
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                             SEQUENCE
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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"Extensive Repertoire of Membrane-bound and Soluble Dendritic Cell-specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2 ISoforms. Inter-individual Variation in Expression of DC-SIGN
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J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042231; AAK91856.1; -.
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Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'``rvota; Primates;
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Biol. Chem. 2/0...
Biol. Chem. 2/0...
#ABL; AY042226; AAK91851.1; -.
#OTIENCE 360 AA; 41009 MW;
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No sapiens (Human).

No sapiens (Human).

No sapiens (Human).

No sapiens (Human).

No sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
37; Conser
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01 (TrEMBLrel. 19,
01 (TrEMBLrel. 19,
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A TYPE II ISOFORM.
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annotation
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No. 2e-
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Query Match Best Local S Matches 37

Similarity 37; Conserv

24.28; 29.68;

16;

Score 161.5; DB 4; Pred. No. 2.2e-08; 16; Mismatches 57;

Indels Length

Gaps

4.

360; 15;

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01-DEC-2001 (TrEMBLrel. 19, Lr
01-DEC-2001 (TrEMBLrel. 19, Lr
01-DEC-2001 (TrEMBLrel. 19, Lr
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Transcripts.";
J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042225; AAK91850.1; -.
EMBL; AY042225, AAK91850.1; -.
380 AA; 43330 MW; BCF9CC
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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SDC-SIGNIA TYPE I ISOFORM.
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Jimenez F., Ahuja S.S., Ahuja S.K.;
"Extensive Repertoire of Membrane-bound and
specific ICAM-3-grabbing Monintegrin 1 (DC-5
Isoforms. Inter-individual Variation in Expu
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM N.A. PubMed=11337487;
                                                                  NCBI_TaxID=9606; [1]
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Catarrhini; Hominidae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGRIN.
Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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"Extensive Repertoire of Membrane-bound and Soluble Dendritic specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2 Isoforms. Inter-individual Variation in Expression of DC-SIGN2
                                                                                                                                                                                                                                            "Functional and antigenic characterization pigtalled macaque, and murine dc-sign."; J. Virol. 75:10281-10289(2001).
EMBL; AF343727; AAL14428.1; -.
                                                                                                                                                                                                                                                                                                           Baribaud F., Pohlmann S., Sparwasser T., Haggarty B.S., Ahmad N., Macfarlan T., E Arnason J., Reinhart T.A., Kimata J.T.,
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NCBI_TaxID=9545;
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J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042230; AAK91855.1; -.
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37; Conservative
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Pred. No. 2.3e-08;
6; Mismatches 57;
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Expression of DC-SIGN
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Leslie G.J.,
Hoxie J.A.,
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MEDLINE=20432267; PubMed=10975799;
MEDLINE=2043267; PubMed=10975799;
MEDLINE=2043267; PubMed=1097579;
MEDLINE=2043267; PubMed=1097579;
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MEDLINE=2043267; PubMed=1097579;
MEDLINE=2043267; PubMed=10975799;
MEDLINE=2047579; PubMed=1097579; PubMe
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EMBL; AF209479; AAG13814.1; --
EMBL; AF209886; AAK20997.1; --
EMBL; AY042221; AAK91846.1; --
EMBL; AY042231; AAK91846.1; --
HSSP; P20693; 1HLJ;
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"Extensive Repertoire of Membrane-bound and
specific ICAM-3-grabbing Nonintegrin 1 (DC-5
Isoforms. Inter-individual Variation in Expr
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MEDILINE-21157496; PubMed-11257134;

MEDILINE-21157496; PubMed-11257134;

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liver sinusoidal endothelial cells and promotes HIV-1 infection.";

j. Exp. Med. 193:671-678(2001).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE-ASSOCIATED LECTIN TYPE-C (PROBABLE MANNOSE-BINDING
LECTIN DC-SIGN) (MDC-SIGNIA TYPE I ISOFORM).
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19p13.";
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"Sequence and expression of a membrane-associated exhibits CD4-independent binding of human immunode envelope glycoprotein gp 120.";
Proc. Natl. Acad. Sci. U.S.A. 89:8356-8360(1992).
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Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1.
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  KIG--GIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKL
                                                                                                WT - - -
                                                WTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLS
                                                                                                                                                                    Similarity
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                                                                                             --YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIR
                                                                                                                                                Conservative
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                                                                                                                                        Score 161.5;
Pred. No. 2.5e
16; Mismatches
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Catarrhini; Hominidae;
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Q14538;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                       antigen.";
                                                                            Suzuki N., Yamamoto K., Toyoshima "Molecular cloning and expression
                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96108853;
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Eukaryota; Metazoa; (
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                                                           type lectin:
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AY042229; AAK91854.1; -.
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     156:128-135(1996).
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Catarrhini;
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Q95L98;
Q1-DEC-2001 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
01-DEC-2001 (TREMBLrel. 1:
DENDRITIC CELL-SPECIFIC II
DC-SIGN.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Geijtenbeek T.B.H., Koopman G., van Duijnhoven G.C.F., van Vliet van Schijndel A.C., Engering A., Heeney J.L., van Kooyk Y.;

"Identification of Rhesus and Chimpanzee DC-SIGN, both act as HIV gpl20 trans-receptors similar as Human DC-SIGN.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; lectin_c
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 WT-----YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIR 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW 62
                                                                                                                                                                                                       KFWIC
                                                                                                                                                                                                                                                KAALC 117
                                                                                                                                                                                                                                                                                            DLNEEGTWQWVDGSPLLPSFNQYWNRGEPNN-VGEEDCAEF----SGNGWNDDKCNLA
                                                                                                                                                                                                                                                                                                                                     KIG--GIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKL 112
                                                                                                                                                                                                                                                                                                                                                                                 WTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLS
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    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                           PRELIMINARY;
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45885 MW;
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29.6%;
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19, Last sequence update)
19, Last annotation update)
17, Last annotation update)
17, Last annotation update)
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Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.2e
16; Mismatches
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Pred.
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                                                                                           PRT;
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No. 2.1
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nes 57;
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Best Local S
Matches 37
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Best Local
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Lectin.
SEQUENCE 304 AA: 34600
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE GALACTOSE N-ACETYL-GALACTOSAMINE SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LYMPH NODE; Geijtenbeek T.B.H., Koopman G., van Duijnhoven G.C.F., Geijtenbeek T.B.H., Koopman G., van Duijnhoven G.C.F., van Kooyk van Schijndel A.C., Engering A., Heeney J.L., van Kooyk "Identification of Rhesus and Chimpanzee DC-SIGN, both gp120 trans-receptors similar as Human DC-SIGN."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF391086; AAK97459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca múlatta (Rhesus macaque)
Eukaryota; Metazoa; Chordata; Cl
Mammalia; Eutheria; Primates; Ca
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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288
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                                                                                                   WTEHEGSCYWFSESEKSWPEADKYCRLENSHLVVVNSLEEQNFLONRL--ANVVSWIGLT
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CORTFRWIC
                       CHKLKAALC
                                                  DQNGPWRWVDGTD--FEKGFKNWAPLQPDNWFGHGLGGGEDCAHI----TTGGPWNDDV
                                                                          KIGGIWTWV-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDA 108
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                       117
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                                                                                                                                                   Score 153.5;
Pred. No. 1.2e
8; Mismatches
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Pred. No. 3.2e-08;
6; Mismatches 57;
                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae
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Catarrhini;
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i; Cercopithecidae;
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                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                            Muridae;
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SEQUENCE
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SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane.

Lectin; Glycoprotein; Noter (GLCNAC. . .) (BY SIM CARBOHYD 78 N-LINKED (GLCNAC. . .) (BY SIM CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (BY SIM CARBOHYD 146 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . . ) (BY SIM CARBOHYD 146 N-LINKED (GLCNAC. . 
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01-NOV-1996
01-NOV-1996
01-DEC-2001
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-i- SUBUNIT: THE FUNCTIONING LIGAND-BINDING UNIT OF THIS RECEPTOR THOUGHT TO BE AT LEAST A DIMER.

-i- MISCELLANEOUS: THIS PROTEIN IS A VARIANT OF HUMAN HEPATIC LECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
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Hepatology 15:395-402(1992).
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"Differences in the abundance of variably spliced transcripts
second asialoglycoprotein receptor polypeptide, H2, in normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Homo sapiens (Human).

Chordata;
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116
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MISCELLANEOUS: THE UNUSUAL ORIENTATION OF THIS PROTEIN ACROSS MEMBRANE IS POSTULATED TO OCCUR BY RECOGNITION OF AN INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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1. X55283; CAA38997.1; -

1. BC017251; AAH17251.1; -

2. P06734; IHLI.
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       5
                                                                  WVDGTD--YRHNYKNWAVTQPDNWHGHELGGSEDCVEV-----QPDGRWNDDFCLQVYRW
                                                                                                                                         WV-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAA
                                                                                                                                                                                                                   YWFSHSGKAWAEAEKYCQLENAHLYVINSWEEQKFIVQHTNPFNT---WIGLTDSDGSWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AC P07307).
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287 AA;
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(TremBLrel. 01, Last sequence update)
(TremBLrel. 19, Last annotation update)
(IN H2, VARIANT (ASIALOGLYCOPROTEIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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281 N
32550 MW;
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30.3%;
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Pred. No. 2.2e
21; Mismatches
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N-LINKED (GLCNAC. ..) (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (BY SIMILARITY);
E9528ACF7CBB1435 CRC64;
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Matches 37
Q9R0Q8;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spiess M., Lodish H.F.;
Spiess M., Lodish H.F.;
"Sequence of a second human asialoglycoprotein receptor: conservation of two receptor genes during evolution.";
Proc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
                                             Q9R0Q8
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Lee D.G., Lee S.G., Kim K.L.,
"Sequences of cDNAs encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                              second asialoglycoprotein receptor transformed human liver.";
Hepatology 15:395-402(1992).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92184202; PubMed=1371982;
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VC 281
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                                                                                                                                                                                                               YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYL-EKTLPFSRSYYWIGIRKIGGIWT 61
                                                                                                                                                                    WV-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAA 115
                                                                                                                                                                                          YWFSHSGKAWAEAEKYCQLENAHLVVINSWEEQKFIVQHTNPFNT---WIGLTDSDGSWK
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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Primates;
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Last sequence update)
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Last annotation update)
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l; Mismatches
                                                                                                                                                                                                                                                Score 150.5;
Pred. No. 2.
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two subunits
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                                              PRT;
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Submitted (FEB 2001) to the El EMBL; AB024717; BAA83754.1; -
EMBL; BC003218; AAH03218.1; -
HSSP; P20693; 1HLJ.
HSSP; MGI:1861222; Clecsf9.
                                                                                                                                                                                                                                    Q91ZW9;
Q91ZW9;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                      STRAIN-C57BL/6;
PubMed-11581173;
Park C.G., Takahara K., Umemoto E., Yashima Y., Mat
Matsuda Y., Clausen B.E., Inaba K., Steinman R.M.;
"Five mouse homologues of the human dendritic cell
                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=99458965; PubMed=10528209;

Matsumoto M., Silmada T., Kaisho T.,

Copeland N.G., Gilbert D.J., Jenkins
"A novel LPS-inducible C-type lectin
NF-IL6 in macrophages.";
                                                                                                                                                            NCBI_TaxID=10090;
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Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTI

PROSITE; PS50041; C_TYPE_LECTI
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLECSF9 OR MINCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACROPHAGE C-TYPE LECTIN CARBOHYDRATE RECOGNITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                      92
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                                           Immunol. 13:1283-1290(2001).
; AF373410; AAL13236.1; -.
ENCE 178 AA; 21245 MW; 03
                                                                                                                                                                                                                                                                                                                                                       TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                                                                                                                          YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGI--RKIGGIW 60
                                                                                                                                                                                                                                                                                                                                         QWV-DDTPFTESLSFWDAGEPNNIVLVEDCATIRDSSN-SRKNWNDIPCFYSMPWIC
                                                                                                                                                                                                                                                                                                                                                                                     YFFSTTTLTWSSSLKNCSDMGAHLVVIDTQEEQEFLFRTKP-KRKEFYIGLTDQVVEGQW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 32.9
38; Conservative
                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA;
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C_TYPE_LECTIN_1; UNKNOWN_1.
C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24431 MW;
 22
31
 . 28
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                                                                                                                                                                                                                                    Created)
Last seq
Last ann
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 149.5; DB 1
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                             Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                  PRT;
                                            034F94CE02BD9032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2FEF318A69BDAFE3
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (C-TYPE (CALCIUM DEPENDENT, LECTIN, SUPERFAMILY MEMBER
                                                                                                                                                                                                                                    sequence update) annotation updat
 148;
No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanjo H., Tanaka T.,
N.A., Akira S.;
is a transcriptional
                                                                                                                                                                                                                                                                                  178
 N
 DB 11;
.2e-07;
                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 60;
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                                            CRC64;
                                                                                                             Matsubara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
          Length
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                                                                                      C-type
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; Murinae; Mus
                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                               Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target
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Best Local S
Matches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91ZW7
Q91ZW7;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                  Q9UBGO PRELIMINARY; PKT; 14/7 AA.
Q9UBGO;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
UROKINASE RECEPTOR-ASSOCIATED PROTEIN UPARAP.
                                                 JRONALIS
KIAAO709
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGN."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park C.G., Takahara K., Un
Matsuda Y., Clausen B.E.,
"Five mouse homologues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
PubMed=11581173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
    SEQUENCE
                                        NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WT----YHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIR 54
                                                                                                                                                                                                                                                                                                                                                                         KEWIC
                                                                                                                                                                                                                                                                                                                                                                                                                 KAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLNKEGEWYWLDGSPLSDSFEKYWKKGQPNN-VGGQDCVEF----RDNG-WNDAKCEQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIG--GIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTFFNGNCYFFSKSQRDWHDSMTACKEMGAQLVIIKSHEEQSFLQQTSK-KNSYTWMGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 13:1283-1290(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- KIGGIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKL
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  FROM
                                                                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
      Z
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24389 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Umemoto E., E., Inaba K., of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 148; DB
Pred. No. 2.6e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                   Craniata; Vi
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219CF71ED878DEB7 CRC64;
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Steinman R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dendritic
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                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsubara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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; Murinae; Mus
                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGDGWNDAPCTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00615; C_TYPE_LECTIN_1; 3.

PROSITE; PS50041; C_TYPE_LECTIN_2; 8.

PROSITE; PS00023; FIBROWECTIN_2; UNKNOWN_

R PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.

R PROSITE; PS50321; RICIN_B_LECTIN; 1.

Receptor; Kinase.
SEQUENCE 1479 ax
                                                                                                                                                                                                                                                                                            097599;
01-NOV-1999 (TrEMBLrel. 12, C:
01-NOV-1999 (TrEMBLrel. 12, L
01-DEC-2001 (TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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               SEQUENCE FROM N.A.

MEDLIND=20148849; PubMed=10683150;
Sheikh H., Yarwood H., Ashworth A., Isacke C.;
Sheidol80, an endocytic recycling glycoprotein related to macrophage mannose receptor is expressed on fibroblasts, cells and macrophages and functions as a lectin receptor.

J. Cell Sci. 113:1021-1032(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
SMART;
SMART;
  EMBL;
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                               ENDO180.
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y5P9
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Nomura N.
                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000566; Lipocln_cytFABP.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000562; FN_Type_II.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prediction of the coding sequences of The complete sequences of 100 new cDNA code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding properties."
Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Behrendt N., Jensen O.N., Engelha
"A urokinase receptor-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98403880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWSDGSLVSFT----HWHPFEPNNFRDSLEDCVTIW----GPEGRWNDSPCNQSLPSIC
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les 15:169-176(1998).

AF107292; AAF14192.1; -.

AB014609; BAA31684.1; -.

P02751; 2FN2.
      AF134838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00034; CLECT;
SM00059; FN2; 1
SM00458; RICIN;
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36; Conserv
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I., Ohara
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3880; PubMed=9734811;
Nagase T., Suyama M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.;
                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 148; DB Pred. No. 2.8e Pred. Mismatches
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                                                                                                                                                                                                                    Catarrhini;
                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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protein with specific
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.8e-06;
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                                                                                                                                                                                                                    Hominidae;
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Best Local (
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SMART; SM00059; FN2; 1.

SMART; SM00059; RV2; 1.

SMART; SM00059; RCIN; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 3.

PROSITE; PS50041; C_TYPE_LECTIN_2; 8.

PROSITE; PS50023; FIBRONECTIN.2; UNKNOWN_1.

PROSITE; PS00213; LIPCCALIN; UNKNOWN_1.

PROSITE; PS50231; RICIN_B_LECTIN; 1.
                   PRINTS; PRO0013; FNTYPEII.
PRODOM; PD000995; FNTYPEII; 1
SMART; SM00034; CLECT; 8.
SMART; SM00059; FN2; 1.
SMART; SM00058; CYTOCHROME_P4
PROSITE; PS000615; C_TYPE_LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
01-NOV-1996
01-DEC-2001
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InterPro; IPR001304;
InterPro; IPR000566; |
InterPro; IPR000772; |
IPR00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q64449;
Q64449;
                                                                                                                                                                  Pfam; PF00040; fn2; 1. Pfam; PF00059; lectin_c;
                                                                                                                                                                                                    InterPro; IPR001128; Cyt_P450.
InterPro; IPR001562; FN. Type_II.
InterPro; IPR001304; lectin_c.
InterPro; IPR000566; Lipcoln_CytFABP.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 271-21323-21330(1996).
EMBL; U56734; AAC52729.1; -.
HSSP; P02751; 2FN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                            type C lectin family.
J. Biol. Chem. 271:21
                                                                                                                                                                                                                                                                                                                                                                                           Wu K., Yuan J., Lasky L...., "Characterization of a novel member of
                                                                                                                                                                                                                                                                                                               MGD; MGI:107818; Mrc2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96355501; PubMed=8702911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECTIN
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PS00086; CYTOCHROME_P450;
PS00615; C_TYPE_LECTIN_1;
PS50041; C_TYPE_LECTIN_2;
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G (TrEMBLrel.
L (TrEMBLrel.
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Pred.
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Sciurognathi;
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                                        UNKNOWN_1
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No. :
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thi; Muridae;
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.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
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Best Local S
Matches 34
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Best Local S
Matches 36
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C.
Mammalia; Eutheria; Primates; C.
NCBI_TaxID=9606;
[1]
                                                                                                                    0960P5 PRELIMINARY;

0960P5;

01-DEC-2001 (TrEMBLrel. 19, C

01-DEC-2001 (TrEMBLrel. 19, I

01-DEC-2001 (TrEMBLrel. 19, I

SDC-SIGN2 TYPE I ISOFORM.

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Q96QP3;
01-DEC-2001
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PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcripts.";
J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042240; AAK91865.1; -.
SEQUENCE 263 AA; 30102 MW; C611C7
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PS00213; LIPOCALIN; UNKNOWN_1.
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1479 AA; 167112 MW; 62D4561
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24; Mismatches 47
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J. Biol. Chem. 276:33196-33212(2001).
EMBL; AY042238; AAK91863.1; -.
SEQUENCE 332 AA; 37953 MW; C6FDEF
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34; Conserv
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Q95237 pan troglod
Q95235 pongo pygma
Q95198 macaca mula
Q95198 macaca mula
Q28768 papio hamad
P98131 bos taurus
P18337 mus musculu
P30836 rattus norv
P98109 ovis aries
Q01102 mus musculu
P42201 bos taurus
P98107 bos taurus
P98108 rattus norv
P27113 oryctolagus
P98110 sus scrofa
P16581 homo sapien
P98105 rattus norv
P33730 canis famil
Q00690 mus musculu
P28897 homo sapien
P98104 mus musculu
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P70197 gallus gall
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ALIGNMENTS

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SEQUENCE FROM N.A. MEDLINE-90243637; PubMed-1692315; Ord D.C., Ernst T.J., Zhou L.J., Rambaldi A., Spertini O., Griffin J., Tedder T.F.; "Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1, Leu-8) of lymphocytes and neutrophils."; J. Biol. Chem. 265:7760-7767(1990). [6] 3D-STRUCTURE MODELING.	Camerini D., James S.P., Stamenkovic I., Seed B.; "Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor."; Nature 342:78-82(1989). [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDILINE-89308881; PubMed-2663882; BOWEN B.R., Nguyen T., Lasky L.A.; "Characterization of a human homologue of the murine peripheral lymph node homing receptor."; J. Cell Biol. 109:421-427(1989).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Tonsil; MEDLINE-9310330; PubMed-2473156; MEDLINE-9310330; PubMed-2473156; Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A., Disteche C.M.; Disteche C.M.; "Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins."; J. Exp. Med. 170:123-133(1989). J. Exp. Med. 170:123-133(1989). SEQUENCE FROM N.A. MEDLINE-90044046; PubMed-2509939;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. BEDLINE=89315837; PubMed=2664786; Siegelman M.H. Weissman I.L.; "Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains."; Proc. Natl. Acad. Sci. U.S.A. 86:5562-5566(1989).	LT 1 LPMIAN STANDARD; PRT; 372 AA. LPMI_HUMAN STANDARD; PRT; 372 AA. P14151; P15023; 01-JAN-1990 (Rel. 13, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) L-selectin precursor (Lymph node homing receptor) (Leselectin precursor) L-selectin precursor (Lymph node homing receptor) (Leselecule-1) (LAM-1) (Leukocyte surface antigen Leu-8 (Leukocyte-endotheilal cell adhesion molecule 1) (LE SELL OR LYAM1 OR LNHR. Homo saplens (Human).

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RT **R Tatemplate for generation and comparison of three-dimensional RT selectin models.";

RT **Selectin models.";

RI Biochem. Biophys. Res. Commun. 216:1018-1023(1995).

CC -:- FUNCTION: CELL SURFACE ADHESTON PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOT
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RT; SM00034; CCECT; 1.

RT; SM00181; EGF; 1.

SITE; PS00181; EGF; 1.

DSITE; PS00186; EGF=2; 1.

DSITE; PS00186; C_TYPE_LECTIN_1; 1.

OSITE; PS0041; C_TYPE_LECTIN_2; 1.

OSITE; PS50041; C_TYPE_LECTIN_2; 1.
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IPR002396;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
EGF-LIKE.
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SUSHI 2.
BY SIMILARITY.
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Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
(LECAM1) (CD62L).
                                         This
                                                                                                          Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE TH
OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                      VENULES IN PERIPHERAL LYMPH NODES.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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LEM1_PONPY STANDAR 95235; 01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, L-selectin precursor (molecule-1) (LAM-1) (L (LECAM1) (CD62L).
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SMART; SM00181; EGF; 1.

PROSITE; PS000122; EGF_1; 1.

PROSITE; PS001186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

Cc11 adhesion; Transmembrane; Glycoprotein;
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
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IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
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                (Lymph node homing receptor) (Leukocyte adhesion (Leukocyte-endothelial cell adhesion molecule 1)
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SMART; SM00032; CCP; 2.

SMART; SM00032; CCP; 1.

SMART; SM00018; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS001186; EGF=2; 1.

PROSITE; PS001186; EGF=2; 1.

PROSITE; PS001186; EGF=2; 1.

PROSITE; PS00141; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
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Budman J.I., Fu H., Johns
Tsurushita N.;
Submitted (NOV-1996) to t
-!- FUNCTION: CELL SUPPRO
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HSSP; P14151; 1KJB.
InterPro; IPR000561; EGF-like.
InterPro; IPR002396; Selectin.
InterPro; IPR001396; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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PF00059; lectin_c; 1.
PF00084; sushi; 2.
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Best I
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           SMART; SM00032; CCP; 2.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEM1_MACMU
Q95198;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                       Pfam;
Pfam;
                                                                                                                                                                                                                                                               EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                        the
   Selectin;
                                                                                                                                         Pfam; PF00084; SUPRINTS; PR00343;
                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996) to the EMBL/GenBank/DDBJ-I- FUNCTION: CELL SURFACE ADHESION PROTETN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                            entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsurushita N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Budman
                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LECAM1) (CD62L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                             send
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nes 116; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                               PUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADIOF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                       PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U73730; AAB18246.1; -. P14151; 1KJB.
                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                                                                                                                                                                                  IPR000436;
; IPR001304;
)0008; EGF; 1
                                                                                                                                                                                                                                 IPR000561;
IPR002396;
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                                                                                                                                         ; lectin_c; l.; sushi; 2.
43; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., Johnson C.E., Thakur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca
                                                                                                                                                                                                                                                                                                                            license agreement
                                                                                                                                                                                                               Selectin.
Sushi_SCR_CCP.
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 662; DB 1;
Pred. No. 7.3e-61;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6517DD22213FF15E CRC64;
                                                                                                                                                                                                                                                                                                                        moved. Usage by and fo
(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     А.В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
               EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases.
MEDIATE THE
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                 Lectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsurushita N., Fu H., Berg E.L.;
"POR cloning of the cDNA encoding baboon L-selectin. Gene 181:219-220(1996).

-i- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE OF LYMPHCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOY VENUES IN PERIPHERAL LYMPH NODES.

-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SUMILARITY: TO OTHER SELECTINS/LECAMS.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMA:
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local :
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Q28768;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
(LFGTY) (TEGRAM) (TEGRAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                               _PAPHA
                                                                                                                                                                                                                             Cercopithecinae; Papio. NCBI_TaxID=9557;
                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=97128794;
                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                         Papio hamadryas (Hamadryas baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                       (LECAM1) (CD62L).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110;
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                                                                                                                                                                                                                                                       ; Métazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
356
156
1196
2588
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2588
57
1128
160
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226
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                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                              PubMed=8973334;
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94.0%;
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SUSHI 2.

BY SIMILARITY.

BY SIMILAR
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C-TYPE LECTIN (SHORT FO
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-LIKE
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BY SIMILARITY.
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                                                                                                                                                  baboon L-selectin.";
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b (GLCNAC...
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b (GLCNAC...
c (GLCNAC...
b (GLCNAC...
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..1e-57;
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Length

372;

Indels

0,

Gaps

0

155

CRC64;

(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDIATE THE

ADHERENCE

Euteleostomi;

ENDOTHELIAL

DOMAIN

between

SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL

collaboration -

outstation

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RESULT 6
LEM1_BOVIN
ID LEM1_BOVIN
AC P98131;
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Best Local S
Matches 110
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SMART; SM00032; CCE; 2.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS001186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                               TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                          WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                            WTYHYSENPMNWQKARRFCRENYTDLVAIQNKAEIEYLEKTLPFSPSYYWIGIRKIGGIW
                                                                                               TWVGTNKSLTQEAENWGDGEPNNKKNKEDCVEIYIKRKKDAGKWNDDACHKPKAALC
                                                                                                                                                                                                                          110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P14151;
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561; EGF-like.
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59; lectin_c; 1.
84; sushi; 2.
                                                                                                                                                                                                                        Conservative
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                  STANDARD;
                                                                                                                                                                                                                                                                                                  94.78;
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                                                                                                                                                                                                                                                                                                      MW;
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SUSHI 2.
BY SIMILARITY
BY SIMILAR
                                                                                                                                                                                                                     Score 631; DB Pred. No. 1.1e 3; Mismatches
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CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
EGF-LIKE.
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                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                  370
                                                                                                                                                                                                                                       DB 1;
.1e-57;
                  A
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                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                      Length 372;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                        0;
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MEDLINE-94055053; PubMed-7694420;

BOSWORTH B.T., Dowbenko D., Shuster D.E., Harp J.A.;

PROVING L.SELCTION PROTEIN. MEDIATE RECEPTOR. MEDIATE THE ADHERI OF LIGHTEDIATE THE ADHERICAL SOF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.

-I. SUBCELLULAR LOCATION: Type I membrane protein.

-I. SUBCELLULAR LOCATION: Type I membrane protein.

-I. SIMILARITY: CONTAINS 1 C.TYPE LECTIN FAMILY DOMAIN.

-I. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-I. SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00032; CCP; 1.
SMART; SM00031; EGF; 1.
PR0SITE; PS00002; EGF_1; 1.
PR0SITE; PS01186; EGF_2; 1.
PR0SITE; PS01186; EGF_2; 1.
PR0SITE; PS01186; EGF_2; 1.
PR0SITE; PS00187; C_TYPE_LECTIN_1; 1.
PR0SITE; PS00041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-92164727; PubMed=1371468;

Malcheck B., White M., Kurk S., Kishimoto T.K., Jutila Walcheck B., White M., Kurk S., Rishimoto T.K., Jutila Walcheck B., White M., Kurk S., Rishimoto T.K., Jutila Walcheck B., White M., Kurk S., Rishimoto T.K., Jutila Walcheck B., Jutila Walcheck B., William C., Jutila Walcheck B., White M., Jutila Walcheck B., W
    DOMAIN
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DOMAIN
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bovidae; Bovinae; Bos.
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IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                        Signal;
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                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                             Sushi;
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                                                                                                                                                                                                                                                                                          Repeat.
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POTENTIAL.
L-SELECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
ECF-LIKE.
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                      EGF-like domain; Lectin;
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P18337;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAW-1) (LY-22) (Lymphocyte surface MEL-14 antigen)
(Leukocyte endothelial cell adhesion molecule 1) (LECAM1) (CD62L).

SELL OR LNHR OR LY-22.

Mus musculus (Mouse).

Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science [2]
                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=89168433; PubMed=2647302;

Lasky L.A., Singer M.S., Yednock T.A., Dowbenko D., Fennie Rodriguez H., Nguyen T., Stachel S., Rosen S.D.;

"Cloning of a lymphocyte homing receptor reveals a lectin cicell 56:1045-1055(1989).
                                                                                                                                                                                                                                                                                                                               MEDLINE-90263086; PubMed-1693096; Siegelman M.H., Cheng I.C., Weissman I "The mouse lymph node homing receptor lymphocyte cell surface marker Ly-22: endothelial binding."; Cell 61:611-622(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-89162048; PubMed-2646713;

Siegelman M.H., van de Rijn M., Weissman I.L.

"Mouse lymph node homing receptor cDNA clone revealing tandem interaction domains.";

Science 243:1165-1172(1989).
            SEQUENCE OF 1-360 FROM N.A. MEDLINE=91169529; PubMed=2004776; Dowbenko D.J., Diep A., Taylor B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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97; Conservative
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82.9%;
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g receptor is identical with t
ker Ly-22: role of the EGF dom
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.6e-52;
            А.J.,
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               Lasky L.A.;
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InterPro; IPR002396; Sele
InterPro; IPR001212; Somat
DR InterPro; IPR001212; Somat
DR InterPro; IPR001304; Icetin
DR Pfam; PF00008; EGF; 1.
The Pfam; PF00008; EGF; 1.
The Pfam; PF000084; Sushi; 2.
The Pfam; PF00084; Selectin_C; 1.
The Pfam; PF00084; Selectin_C; 1.
The Pfam; PF00034; Selectin_C; 1.
The Pfam; Pf00004; Sel
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SMART; SMO0032; CCC; 2.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

SMART; SM00201; EGF; 1.

SMART; SM00201; EGF; 1.

R PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

R PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
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-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P; P14151; 1K
; MGI:98279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. The by non-profit institutions as long lifted and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VENULES IN PERIPHERAL LYMPH NODES. SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X14772; CAA32880.1;
M36055; AAA39722.1;
M36058; AAA39723.1;
M36058; AAA39431.1;
M25324; AAA39431.1;
M64549; AAA75651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M64440; AAA75651.1;
M64545; AAA75651.1;
M64548; AAA75651.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement (S an email to license@isb-sib.ch).
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      A32375.
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Sushi_SCR_CCP.
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EXTRACELLULAR (POTENTIAL)

POTENTIAL).

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORE
GEF-LIKE.

SUSHI 1.

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BY SIMILARITY.

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Best Local S
Matches 97
          Pfam; PF00008; EGF; 1
Pfam; PF00059; lectin
Pfam; PF00084; sushi;
PRINTS; PR00343; SELE
                                                                                                                                                                                                                                                  MEDLINE-92329548; PubMed-1378303;

Watanabe T., Song Y., Hirayama Y., Tamatani T., Kuida K., Miyasaka "Sequence and expression of a rat cDNA for LECAM-1.";

"Sequence and expression of a rat cDNA for LECAM-1.";

Blochim. Biophys. Acta 1131:321-324(1992).

-I- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDLATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.

-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I- SIMILARITY: CONTAINS 1 SGF-LIKE DOMAIN.
-I- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (LY-22) (Lymphocyte surface MEL-14 antigen) (Leukocyte-endothelial cell adhesion molecule 1) (LECAMI) (CD62L).
SELL OR LNHR OR LY-22.
Rattus norventaments.
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InterPro;
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InterPro;
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CONFLICT
SEQUENCE
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PIR;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30836;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
01-FEB-1996 (Rel. 33, Last annotation
                                                                                                                                                                                                                               This
                                                                                                          HSSP;
                                                                                                                                                                     entities
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                                                                                                                    s23936; s
                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                        P14151;
                                                                                                                                                         an
                                                        4151; 1KJB.

7; IPR000561; EGF-like.

7; IPR002396; Selectin.

7; IPR000436; Sushi_SCR_CCP.

7; IPR001304; lectin_c.
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                                                                                                                                                                   non-profit institutions as long and this statement is not removed requires a license agreement (See
                                                                                                                                                     equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                    S23936.
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                      lectin_c; 1. sushi; 2.
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Sciurognathi; Muridae;
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No. 7
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.1e-51;
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                                                                                                                                                                  http://www.isb-sib.ch/announce/
                                                                                                                                                                              Usage
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; Murinae; Rat
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Best I
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Heart;

BURDS S.A., Neufeld E.J., Donady J.J.;

BURDS S.A., Neufeld E.J., Donady J.J.;

BURDS S.A., Neufeld E.J., Donady J.J.;

Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

THE FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS

THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                           LEM3_SHEEP STANDARD; PRT; 769 AA.
P98109;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
CCD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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DOMAIN
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Mammalia; Eutheria;
Bovidae; Caprinae; (
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DOMAIN
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SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS00615; C_TYPE_LECTIN_2;
CG11 SANGE(10.)
                                                                                                                                                                                             Bovidae; Caprinae; NCBI_TaxID=9940;
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95; Conserv
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                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Eute Cetartiodactyla; Ruminantia; Pecora;
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CYTOPLASMIC (POTENT)
C-TYPE LECTIN (SHOR)
EGG-LIKE.
SUSHI 1.
SUSHI 2.
BY SIMILARITY
BY SIMILARIT
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L-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 557; DB 1;
Pred. No. 4.7e-50;
1; Mismatches 11
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 CTYPE LECTIN FAMILY DO
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS.

DOMAIN

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THE PRESENTATION OF THE PR
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Pram; prionon8; EGF; 1.

Priam; prionon8; EGF; 1.

Priam; prionon4; sushi; 8

PRINTS; prionon4; selectin.

R SMART; SMO0034; CLECT; 1.

R SMART; SMO0034; CLECT; 1.

R SMART; SMO0034; EGF; 1.

R PROSITE; PS00186; EGF_1; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00186; EGF_2; 1.

Cell adhesion; Transmembrane: Clucococci
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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P16109; 1FSB.
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an email to license@isb-sib.ch).
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IPR001304;
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32
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158
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           Selectin.
Sushi_SCR_CCP.
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SUSHI 3.
SUSHI 4.
SUSHI 6.
SUSHI 6.
SUSHI 7.
SUSHI 8.
BY SIMILARITY.
BY SIMILARIT
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C-TYPE LECTIN.
EGF-LIKE.
SUSHI 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92345617; Pt
Sanders W.E. Jr., Wi
"Molecular cloning as
Selectin.";
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
SELP OR GRMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
VARIANT
SEQUENCE
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SITE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                            Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. Expression of and P-selectin is inducible by tumor necrosis factor alpha.
J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92340571; PubMed=1378846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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                                                                                                                                                                                                      ecti., od 80:795-800(1992), od RETION CARROHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE TO CARROHYDRATES ON NEUTROPHILS AND CARROHYDRATES OF PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS STALYL-LEWIS X.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND MEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL CONTINUED OF PLATELETS AND MEIBEL-PALADE BODIES, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 WTYHYSDKPYSWNYSRAFCQKYYTDLVAIQNKNEIAYLNETIPYYNSYYWIGIRKIDNKW
                                                                                          ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSP
THE CELL SURFACE.
INDUCTION: BY TNF-ALPHA.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS;
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                                                                             HUMAN
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Similarity 68.4%;
80; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; PubMed=1379089;
, Wilson R.W., Bal
ng and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
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                                                                             EQUIVALENT.
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Pred. No. 4.le
10; Mismatches
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L -> V.
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Sciurognathi; Muridae
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s of in vivo
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1. No. 4.1e-40;
1. Thes 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
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                                                                                                 MOUSE
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               Beaudet A.L.;
ession of muri
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                                                                                               P-LECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L; M87861;
L; M72332;
; A42755; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:98280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P16109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561; EGF-like.
IPR000742; EGF_2.
 AAA40008.1; -.
AAA37712.1; -.
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BY SIMILARITY.

BY SIMILARIT
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SUSHI 3.
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SUSHI 6.
SUSHI 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
NDOCYTOSIS SIGNAL (PROBABLE).
-> E (IN REF. 2).
E5173074D2F66E68 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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n; Palmitate.
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EMBL; L12041; AAA30743.1; -.
HSSP; P16109; 1FSB.
InterPro; IPR000561; EGF-like.
InterPro; IPR002396; Selectin.
InterPro; IPR001346; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
Pfam; PF00008; EGF; 1.

PRINTS; PR00343;

CCP; 6

PF00008; PF00059; PF00084;

lectin_c; 1. sushi; 6.

SELECTIN

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LEM3_BOVIN

LEM3_BOVIN

AC P42201B

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AC O1-NOV

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DT 15-UIL

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GE EURAF;

OC Mammal

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Capillary endothelium;

X MEDLINE-93249394; PubMed-7633458;

A Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;

A TISOLAtion and characterization of a bovine cDNA encoding a functional homolog of human P-selectin.

Eliochem. Biophys. Res. Commun. 192:338-344(1993).

C -!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS CONTROL TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDLATES THE TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES MEDIATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEM3_BOVIN P42201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE CELL SURFACE.

SIMILARITY: OOTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS; BOVINE

THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
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8.4e-39;
nes 28;
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01-FEB-1996
01-FEB-1996
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                                                                                                                                                                                                                                   TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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                                                                                                                                                                                                              TWVGTKKTLTEEAENWADNEPNNKRNNQDCVEIYIKSLSAPGKWNDEPCWKRKRALC
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                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00181; EGF; 1.
S; PS00022; EGF_1; 1.
S; PS01186; EGF_2; 1.
S; PS00615; C_TYPE_LECTIN_1; 1
S; PS50041; C_TYPE_LECTIN_2; 1
          6 (Rel. 33, Created)
6 (Rel. 33, Last sequence update)
6 (Rel. 33, Last annotation updat
precursor (Endothelial leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
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66.7%;
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N-LINKED (GL
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C-TYPE LECTIN (SHORT FORM)
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                             update)
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.3e-39;
les 29;
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            adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain; Lectin;
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CRC64;
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        Gaps
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      C --- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1-3)FUCOSYLATED DERIVATIVES OF POLYCACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF C POLYCACTOS INVOLVED IN CAPILLARY MORPHOGENESIS BY BINDING TO A CONTINE CAPILLARY ENDOTHELIAL (BCE) CELL SIALYL LEWIS-X AND/OR SIALYL LEWIS A-CONTAINING LIGAND (PROBABLY).

C SUBCELLULAR LOCATION: Type I membrane protein.

C SIMILARITY: CONTAINS 1 EXECTIN FAMILY DOMAIN.

C SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS; BOVINE E-LECTIN LACKS

THE HUMAN SUSHI-4 AND 5 EQUIVALENTS.
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0343; SELECTIN.
SMART; SM00034; CCP; 4.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; PR00181; EGF=1; 1.
PROSITE; PS01186; EGF=2; 1.
PROSITE; PS00615; C_TYPE_LE
    DOMAIN
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InterPro;
InterPro;
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L12039; AAA02991.1; -. HSSP; P16581; 1ESL.
                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                          Selectin;
                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 365:267-269(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A role for sialyl Lewis-X/A glycoconjugates morphogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nguyen M., Strubel N.A.,
"A role for sialyl Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Adrenal gland;
MEDLINE=93382537; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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(CD62E).
                                                                                                                                                                                                                                                                                                                  adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00059; lectin_c; 1. PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         PS50041; C_TYPE_LECTIN_2; 1
esion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5581; 1ESL.; IPR000561; F; IPR000742; F; IPR002396; S; IPR000436; S; IPR0001304; 
                                                                                                                                                                                                                                                                                        Signa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Bovine).
Metazoa;
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                                                                                                                                                                                                                                                                                                                                                  ; EGF_1; 1.
; EGF_2; 1.
; C_TYPE_LECTIN_
                                                                                                                                                                                                                                                                                          Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7690465;
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EGF_2.
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Sushi_SCR_CCP.
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                                                                                                                                              CYTOPLASMIC (POCTIVE LECTINE)
  SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
BY SIMILA
BY SIMILA
BY SIMILA
                                                                                                                                                                                                          EXTRACELLULAR POTENTIAL.
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Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
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                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                           EGF-like domain;
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Best Local S
Matches 77
 Furie B.;
"Structure a
                                                                                                                                                                                       MEDLINE-89168432; PubMed-2466574; Johnston G.I., Cook R.G., McEver R.P.; "Cloning of GMP-140, a granule membrane protein endothelium: sequence similarity to proteins invadhesion and inflammation."; Cell 56:1033-1044(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                             LEM3_HUMAN P16109;
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CARBOHYD
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01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140)
(CD62P) (Leukocyte-endothelial cell adhesion molecul
SELP OR GMRP.
Homo sapiens (Human)
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                                                                                    Fujimoto T., Stroud E., Whatley R.E., Prescott Laposata M., McEver R.P.; Laposata M., McEver R.P.; Preselectin is acylated with palmitic acid and cysteine 766 through a thicester linkage."; J. Biol. Chem. 268:11394-11400(1993).
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89168432; PubMed-246657
Johnston G.I., Cook R.G., McEve
"Cloning of GMP-140, a granule
                                                STRUCTURE BY NMR (MEDLINE 97057176;
                                                                                                                                                     PALMITOYLATION. MEDLINE-93266599;
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                     Freedman S.J.,
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                            R OF 160-155;
6; PubMed-8901515;
Sanford D.G., Bach
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             function
                                     Sanford
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                        PubMed=7684381;
ud E., Whatley R.E.,
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                                    Bachovchin W.W., Furie B.C.,
                                                                                                                                                                                                                                                                                                           Craniata; V
Catarrhini;
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*LINKED (GLCNAC. ..
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                                                                                                                                         Prescott S.M.,
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i; Hominidae;
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.2e-38;
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             growth
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             factor
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                                                                                                                                                                                                                                                                                                              Homo.
             domain
                                      Baleja J.D.,
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 9.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCLECT; 1.
SMART; SM000181; EGF; 1.

Pfam;

EGF;

PF00008; PF00059; PF00084;

InterPro; InterPro;

173610;

01-APR-97. 03-APR-96. A30359

InterPro; InterPro;

; IPR000561; ; IPR002396; ; IPR000436; ; IPR001304;

; EGF-like. ; Selectin. ; Sushi_SCR_CCP. lectin_c.

EMBL; EMBL; PIR; PDB;

AAA35911 AAA35910

EMBL;

EMBL; EMBL; EMBL; EMBL;

PROSITE; PROSITE; PROSITE;

PS00022; PS01186; PS00615;

EGF_1; 1. EGF_2; 1. C_TYPE_LECTIN_1;

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94093388; PubMed=7505680; Bajorath J., Stenkamp R., Aruffo A. "Knowledge-based model building of
                                                                                                                                                                                                                                                                                                           EMBL;
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SIMILARITY: TO OTHER S

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SIMILARITY: CONTAINS 1

SIMILARITY: CONTAINS 9
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FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BIT TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCCITLOUAR LOCATION: Type I membrane protein.
SUBCCILCULAR LOCATION: Type I membrane PROTEIN.
TISSUE SPECIFICITY: STREED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.lsb-slban email to license@isb-sib.ch).
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1 C-TYPE LECTIN FAMILY
1 EGF-LIKE DOMAIN.
9 SUSHI (SCR) DOMAINS.
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L outstation -
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SIGNAL
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                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                 830
    Conservative
                                                                                                                                                                                                                           640
                                                                                                                                                                                                                                                                       603
                                                                                                                 ΑA;
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                    66.8%;
                                                                                                                 90844
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                                                                                                                 W.
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EXTRACELLULAR (
POTENTIAL.
CYTOPLASMIC (PC
C-TYPE LECTIN (
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 6.
SUSHI 7.
SUSHI 7.
SUSHI 8.
SUSHI 9.
Score 445; DB
Pred. No. 4e-3
L1; Mismatches
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BY SIM
                                                                                                                                   T -> P (REDUCED WITH MYOCARDIAL /FTId=VAR_004195
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N -> D.
                                                                                                                                                                                                                                                                                                                ENDOCYTOSIS
S -> N.
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FBC407BA2579F6EB
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L -> V.
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                         4e-38;
                                              DВ
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                                                                                                                                                      FREQUENCY IN PATIENTS INFARCTION).
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                                         Length 830;
                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                     (PROBABLE).
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Gaps
0;
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Pfam; Pfuvuo,, ...

R PRINTS; PR00343; SELECTIN.

R SMART; SM00032; CCP; 8.

R SMART; SM00034; CLECT; 1.

DR PROSITE; PS00181; EGF; 1.

DR PROSITE; PS001186; EGF=2; 1.

DR PROSITE; PS001186; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

KW Cell adhesion; Transmembrane; Glycoprotein; EGF-1

KW Cell adhesion; Signal; Sushi; Repeat; Lipoprotein; Pal

"Selectin; Signal; Sushi; Potential.

"Selectin; Signal; Sushi; Potential.
             C TISSUE-Lung;

X MEDLINE-94333817; PubMed=7520013;

A Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;

A Ruchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;

T "Cloning, sequence comparison and in vivo expression of the gene
at encoding rat p-selectin.";

T "Gene 145:251-255(1994).

CC -: FUNCTION: CA(2+)-DEDENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS

TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE

CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES WITH

CC LEUKOCYTES. THE LIGAND RECOGNIZED IS STALYL-LEWIS X.

CC -: SUBCELLULAR LOCATION: Type I membrane protein.

CC -: SUBCELLULAR LOCATION: Type I membrane protein.

CC -: TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,

CC -: TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,

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LEM3_RAT
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                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
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01-FEB-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L23088;
HSSP; P16109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SINDUCTION: BY ACCUTE INFLAMATION (PROBABLE). SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAINS;
HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWVGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALC
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                                                                                                                                                                                                                                                                                                                                           PF00059; lectin_c; 1.
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5; IPR000561; EGF-like.
5; IPR002396; Selectin.
6; IPR000436; Sushi_SCR_CCP.
7; IPR001304; lectin_c.
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Rodentia;
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                                                                                     EGF-like domain;
                                                             Palmitate
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Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration -
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                                      LEM2_RABIT STANDARI
p27113;
01-AUG-1992 (Rel. 23, 0
01-AUG-1992 (Rel. 23, 1
16-OCT-2001 (Rel. 40, 1
E-selectin precursor (ELAM-1) (Leukocyte-end
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CARBOHYD
CARBOHYD
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DISULFID
                (CD62E).
SELE.
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SEQUENCE
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LIPID
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CARBOHYD
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TRANSMEM
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DOMAIN
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                            l Similarity
75; Conserv
                                                                                                                                                                                                                                                                                                                                         cuniculus (Rabbit)
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                 STANDARD;
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23, Last sequence update)
40, Last annotation update)
or (Endothelial leukocyte ad)
e-endothelial cell adhesion r
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PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
ENDOCYTOSIS SIGNAL (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (PC
C-TYPE LECTIN (
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 5.
SUSHI 6.
SUSHI 6.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 8.
BY SIMILARITY.

                                                                                                                                                                                                                                                                                        Score 442;
Pred. No. 7
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                                          cell adhesion
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                 551
                                                                                                                                                                                                                                                                                        DB 1.5e-3
                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                   adhesion molecule 1)
                                                                                                                                                                                                                                                                            38;
29;
                                         molecule
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                         2)
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                              101
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                                                                                                                                                                                                                                                                            0,
     DOMAIN
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DISULFID
DISULFID
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                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M91004;
EMBL; M91005;
HSSP; P16581;
                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92189729; PubMed-1372169;
Larigan J.D., Tsang T.C., Rumberger J.M.,
"Characterization of cDNA and genomic sequ
ELAM-1: conservation of structure and func
leukocytes.";
                                                                                                                                                                                                                                                                                                                                       SMART; SM00032; CCP; 5.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + + + +
                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                               Selectin;
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 5.
PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                            adhesion;
                                                                                                                                                                                                                                                                       PS00022; EGF_1; 1.
PS001186; EGF_2; 1.
PS001615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
PS50041; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561; EGF-like.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
                                                                                                                                                                                                                                                               Signal;
                                                                                                                                       141
181
243
305
     113
145
150
167
182
212
244
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA31243.1;
AAA31244.1;
1KJA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                              Sushi;
   Chordata; Craniata; Vertebrata; Euteleostomi; Lagomorpha; Leporidae; Oryctolagus.
E-SELECTIN.
EXTRACELLULAR (
POTENTIAL.
CYTOPLASMIC (PC
CYTYPE LECTIN (
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 4.
SUSHI 5.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .M., Burns D.K.; sequences encoding rabb: functional interactions
                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                       (SHORT
                                                                                                                                                                                                                                                                           EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAL CELLS AND DERIVATIVES COMPARATION
                                                                                                                                                                                                                                                                            domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rabbit
tions with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration -
                                                                                                                                                                                                                                                                            Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in no way
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Query Match
Best Local S
Matches 74
                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Aortic endothelium;
TISSUE=4271236; PubMed=7516159;
Tsang Y.T.M., Haskard D.O., Robinson
"Cloning and expression kinetics of pubmed and pubmed 
                                                                                                                                                                                                                                                                                                                                                                                                   Matis L.A., Rother K.F.;

"Molecular and functional analysis of porcine potential role in xenograft rejection.";

potential role in xenograft 204:763-771(19)
                Biochem. Biophys. Res. Commun. 201:805-805(1994).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS ANI
MEDIATES THEIR BINDING TO LEUKROCYTES. THE LIGAND RECOGNIZED I
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
(CD62E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Aortic endothelium;

MEDLINE-95071392; PubMed-7526854;

Rollins S.A., Evans M.J., Johnson

Matis L.A., Rother R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SELE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                Commun.
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BY SIM
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Pred. No. 3.4e-37;
3; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.K.,
                                                                                                                                                                                                           n M.K.;
porcine
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AAA31244).
AAA31244).
E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi; Sus.
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(POTENTIAL).
                                                                                                                                                                                                                 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             reveals
                                                                                                                                                                                                              adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.P.,
                                                                                                                 AND
                                                                                   ВУ
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                                                   OH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                               DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00
InterPro; IPR00
Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
DOMAIN
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1;

PROSITE; PS50041; C_TYPE_LECTIN_2;

Cell adhesion; Transmembrane; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P165
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00032; CCP; 4.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUROpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOLIPIDS).

-I FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR. REJECTION AND PROBABLY ALSO IN XENOGRAFT REJECTION.
-I SUBCELLULAR LOCATION: Type I membrane protein.
-I SIMILARITY: TO OTHER SELECTINS/LECAMS.
-I SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-I SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS; PORCINE THE HUMAN SUSHI-1 AND -4 EQUIVALENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00343;
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U08350; AAA21541.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00059;
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6581; 1ESL.
; IPR000561; EGF-1; IPR002396; Selection Sushing Sushing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001304;
0008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal;
                23
430
452
452
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180
239
239
365
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144
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43; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sushi;
                EGF-like.
Selectin.
Sushi_SCR_CCP.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORE
SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 3.

SUSHI 3.

SUSHI 3.

SUSHI 3.

SUSHI 3.

SUSHI 4.

BY SIMILARITY.

BY S
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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E-selectin precursor (F
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MEDLINE-90175359; PubMed-1689848;

Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C

Hession C., Tizard R., Goelz S., McCarthy K.,
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                     3D-STRUCTURE MODELING OF LECTIN DOMAIN MEDLINE-93202275; PubMed-7681016;
                                                    "ELAM-1 mediates cell adhesion ligand, sialyl-Lex."; Science 250:1130-1132(1990).
                                                                                    Phillips M.L., Nudelman I
Hakomori S., Paulson J.C
                                                                                                         MEDLINE-91068005;
                                                                                                                                                                        Gimbrone M.A.
                                                                                                                                                                                  Collins T., Williams A.,
                                                                                                                                                                                           MEDLINE-91115870;
                                                                                                                                                                                                                           Bevilacqua M.P., Stengelin S., Gimbrone M. Endothellal leukocyte adhesion molecule neutrophils related to complement regulatication ce 243:1160-1165(1989).
                                                                                                                                                                                                                                                                    MEDLINE-89162047;
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                  "Endothelial leukocyte adhesion molecule and functional interactions."; Proc. Natl. Acad. Sci. U.S.A. 87:1673-167
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
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Stengelin S., Gimbrone M.A. Jr., Seed B.;
Stengelin S., Gimbrone M.A. Jr., Seed B.;
Stengelin S., Gimbrone M.A. Jr., Seed B.;
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InterPro; IPR000
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Pfam; PF00008; 1
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Ye S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., G
"A PStI polymorphism detects the mutation of serine-128
CD 62E gene - a risk factor for coronary artery disease.
J. Biomed. Sci. 6:18-21(1999).
-- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND REC
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DER
POLYLAGTOSAMINE THAT ARE FOUND AT THE NONREDUCING TE
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MEDLINE-95179107; PubMed-7533025;
Wenzel K., Felix S., Kleber F.X., Brachold R.,
Schulte K.L., Glaser C., Rohde K., Baumann G.,
"E-selectin polymorphism and atherosclerosis: (
Hum. Mol. Genet. 3:1935-1937(1994).
                                                                                             InterPro;
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                          Pfam; PF00059; Pfam; PF00084;
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                                                                                                                                                                                                            EMBL;
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SIMILARITY: TO OPHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD62E entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm"
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SUBGELLULAR LOCATION: Type I membrane protein.

SUBGELLULAR LOCATION: Type I membrane protein.

POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED WITH AN
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A38615; A38615.
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E -> Q (IN DBSNP:5366).

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H -> Y (IN DBSNP:5368).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like domain;
                                                                                                                                                    Length 610;
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                                                                                                              Indels
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                                                                                                       Gaps
                                                                60
                          81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000
InterPro; IPR001
Pfam; PF00008; I
                                                                                                                                                                                         Selectin;
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELE OR ELAM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEM2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOLIPIDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L25527;
                                                                                                                                                                                                                                                     Signal;
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Pfam; PF00099; lectin_C; 1.
Pfam; PF00084; sushi; 5.
SMART; SM00032; CCE; 5.
SMART; SM00034; CLECT; 1.
SMART; SM00031; EGF; 1.
PROSITE; PS00186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Fransmembrane; Glycoprotein; EG
    TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RISSUE-Lung;
Rosenbloom C.L., Auchampach J.A., Anderson D.C., Manning A.M.;
Rosenbloom C.L., Auchampach J.A., Anderson D.C., Manning A.M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED ELAM-1 IS SIALVL-LEWIS X (ALPHA(1--3)FUCOSYLATED DERIVATIVES
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P98105;
P98105;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000561; EGF-like.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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TO OTHER SELECTINS/LECAMS.
CONTAINS 1 C-TYPE LECTIN FAMILY CONTAINS 1 EGF-LIKE DOMAIN.
CONTAINS 5 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                Sushi;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lectin_c.
                                                                                                                                                                                                                                                                Repeat
POTENTIAL.

CYTOPLASMIC (PC
C-TYPE LECTIN (
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
                                                                                                                                                                                                 EXTRACELLULAR
                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549
                                                                                                                                                         (POTENTIAL)
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                                                                                                                                (SHORT
                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                  EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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; Murinae; Rattus.
                                                                                                                                                                                                                                                                                  domain;
                                                                                                                                                                                                                                                                                     Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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A Manning A.M., Lane C.L., Auchampach J.A., Kukielka G.L.,

A Rosenbloom C.L., Anderson D.C.;

A Ro
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Best Local S
Matches 71
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CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SELE.
Canis familiaris (Dog).
Canis familiaris (Dog).
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p33730;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
(CD62E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Carnivora;
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154
1154
1163
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Pred.
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BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y SIMILARITY.
Y 
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No. 1
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.6e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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SMART; SM00032; CCP; 6.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 2.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS001186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1

PROSITE; PS00614; C_TYPE_LECTIN_2; 1

Cell adhesion; Transmembrane; Glycop; Selectin; Signal; Sushi; Repeat.
   CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
SEQUENCE
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Pfam; PF
PRINTS;
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DOMAIN
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWI
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                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00059; le
PF00084; su
TS; PR00343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001304;
0008; EGF;
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IPR000436;
                   ; lectin_c; 1.
; sushi; 6.
43; SELECTIN.
    ĀΑ;
 Selectin.
Sushi_SCR_CCP.
lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like.
      ₩.
 SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 5.
SUSHI 5.
SUSHI 5.
BY SIMILARITY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
E-SELECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like domain; Lectin;
.) (POTENTIAL).
6 CRC64;
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RESULT 20

LEMZ_MOUSE

ID LEMZ_MOUSE

AC Q00690

DT 01-APR

DT 01-APR

DT 01-PEB

DE (ELAM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weller A., Isenmann S., Vestweber D.;

"Cloning of the mouse endothelial selectins. Expression of both E-
rand P-selectin is inducible by tumor necrosis factor alpha.";

L. J. Biol. Chem. 267:15176-15183(1992).

- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND

C. HEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY

ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERLYATIVES OF

C. POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF

C. GLYCOLIPIDS).

C. SUBCELLULAR LOCATION: Type I membrane protein.

C. SUBCELLULAR INCATION: Type I membrane protein.

C. SIMILARITY: CONTAINS 1 CTYPE LECTIN FAMILY DOMAIN.

C. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

C. SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
                            PRINTS;
SMART; S
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                                                                                                                                                                                                                                                                                                    EMBL; M80778; AAA37547.1;
EMBL; M87862; AAA37577.1;
HSSP; P16581; 1KJA.
MGD; MGI:98278; Sele.
     PROSITE;
                                                                                                                                                                         InterPro; IPR000561; EGF-1ike.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR
InterPro; IPR001304; lectin_c.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92340571; PubMed-1378846; Weller A., Isenmann S., Vector's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Murine endothelial leukocyte-adhesion structural and functional homologue of Eur. J. Blochem. 206:401-411(1992).
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01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte ad
(ELAM-1) (Leukocyte-endothelial cell adhesion
(CD62E).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on the EMBL outstation - European Bioinformatics Institute. There are no restrictions on way non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial
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SM00034; CLECT;
SM00181; EGF; 1.
                                                                                                F00059; lectin_c; 1.
F00084; sushi; 6.
PR00343; SELECTIN.
     PS00022;
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     EGF_1; 1
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van Huijsduijnen
                                       , 6.
¶: 1.
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Sciurognathi;
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thi; Muridae;
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molecule 2) (LECAM2)
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MANR_HUMAN
ID MANR_H
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DT 01-AUG
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OS Homo s
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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SEQUENCE
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CARBOHYD
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                                                                                    Macrophage
                                                    Homo sapiens (Human)
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DOMAIN
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PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
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                                                                                                                                                                                                                                                           82 IWVGTGKPLTEEAQNWAPGEPNNKQRNEDCVEIYIQRTKDSGMWNDERCNKKKLALC
                                                                                                                                                                                                                                                                                               61
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                                                                                      mannose
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(Rel. 19, Last sequence up
(Rel. 41, Last annotation
mannose receptor precursor
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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148
165
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179
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                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sushi;
                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...) (POT
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C-TYPE LECTIN (SHORT FORE
EGF-LIKE.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 4.

SUSHI 5.

SUSHI 5.

SUSHI 6.

SUSHI 6.

SUSHI 6.

SUSHI 7.

SUSHI 7.

SUSHI 8.

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SUSHI 8.

SUSHI 8.

SUSHI 8.

SUSHI 1.

SUSHI 2.

SUSHILARITY.

BY SIMILARITY.

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Pred. No. 3.7e
L4; Mismatches
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                                                                                  (CD206 antigen)
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                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 612;
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SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

IN SIGNILANEOUS: CRDS 1-3 HAVE AT MOST VERY WEAK AFFINITY FOR CARBOHYDRATE. CRD 4 SHOWS THE HIGHEST AFFINITY BINDING AND HAS MULTISPECIFICITY FOR A VERIETY OF MONOSACCHARIDES. AT LEAST 3 CRD (4, 5, AND 7) ARE REQUIRED FOR HIGH AFFINITY BINDING AND ENDOCYTOSIS OF MULTIVALENT GLYCOCONJUGATES.

SIMILARITY: CONTAINS 8 C-TYPE LECTIN FOMAINS.

SIMILARITY: CONTAINS 8 C-TYPE LECTIN DOMAINS.

SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.

DATABASE: NAME-PROW; NOTE-CD guide CD206 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/1644341535_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of a C-type carbohydrate recognition macrophage mannose receptor.";
J. Biol. Chem. 275:21539-21548(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor M.E., Bezouska K., Drickener K.;
"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1728(1992).
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SEQUENCE
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Kim S.J., Ruiz N., Bezouska K., Drickamer K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resembling carr
Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feinberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Organization of the gene encoding receptor (MRC1)."; genomics 14:721-727(1992).
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TRANSMEM
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PIR;
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                                                                                            CARBOHYD
                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                              SMART; SM00034; CLECT;
SMART; SM00059; FN2; 1
SMART; SM00458; RICIN;
                                                                                                                                                                                                                                                                                                                    pfam; pF00059; lectin_c; 8;
pfam; pF00652; Ricin_B_lectin;
pRINTS; PR00013; FNTYPEII.
proDom; PD000995; FN_Type_II; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                    CARBOHYD
                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                         Receptor;
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M93220;
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M93213;
M93214;
M93215;
M93216;
M93217;
M93218;
                                                                                                                                                                                                                                                                                                                                                    PF00040;
l Similarity 30.8
37; Conservative
                                                                                                                                                                                                                                                                                 PS50041;
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                                                                                                                                                                                                                                                        PS50231; RICIN_B_LECTIN; 1.
Signal; Calcium-binding; Transmembrane; Repeat;
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30-AUG-00.
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                                     C_TYPE_LECTIN_1;
C_TYPE_LECTIN_2;
FIBRONECTIN_2; 1
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Ricin_B_lectin.
lectin_c.
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POTENTIAL
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C-TYPE LECTIN 2 (LONG FORM).
C-TYPE LECTIN 3 (LONG FORM).
C-TYPE LECTIN 4 (LONG FORM).
C-TYPE LECTIN 5 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 7 (LONG FORM).
Score 157; DB
Pred. No. 3.4e
29; Mismatches
                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). RICIN B-TYPE LECTIN.
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        DB 1;
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OS Homo s
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OC Mammal
OX NCBLIT
RN [1]
RP SEQUEN
RA IKUta
RA Yamasa
RA TSUNAS
RI GOLI 4
RN [2]
RP SEQUEN
RX MEDLIN
RA IKUta
RA YAMAS
RI GOLI
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RA GOSE K
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RT Cloni
RA KILChh
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                                         Bajorath J., Aruffo A.;
"Structure-based modeling of the cell surface receptor CD23 and derived molecular models.";
Protein Sci. 5:240-247(1996).
-i- FUNCTION: THIS RECEPTOR HAM
                                                                                                                                                                                                                                                                                                                                                                                   Suemura M., Kishimoto I., "Two species of human Fc epsilon receptor II tissue-specific and IL-4-specific regulation
                                                                                                                                                                  3D-STRUCTURE MODELING MEDLINE=96276216; Pub
                                                                                                                                                                                                            "Padlan E.A., Helm B.A.;
"Modeling of the lectin-homology
affinity Fc epsilon receptor (Fc
Receptor 3:325-341(1993).
[7]
                                                                                                                                                                                                                                                                                                                                                                              tissue-specific and II Cell 55:611-618(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE SPLICING.
MEDLINE=89028672; PubMed=2972386;
7:1-1-201 H. Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luedin C., Hofstetter H., Sarfati M., Kilchherr E., Frost H., Delespesse G.; "Cloning and expression of the cDNA coreceptor.":
                                                                                                                                                                                                                                                                                                              MEDLINE=94191542; PubMed=8142907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 47:657-665(1986).
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Yamasaki K., Kaisho T.,
Yamasawa S., Sakiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Partial characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rose K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93038513;
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"Human lymphocyte Fc receptor for cloned cDNA with animal lectins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P06734
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01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Low affinity immunoglobulin epsilon FC receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular structure of
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               FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT I
B-CELL-SPECIFIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L SEQUENCE, AND DISULFIDE BONDS.
E=93038513; PubMed=1417742;
Turcatti G., Graber P., Pochon
K.U., Magnenat E., Aubonney N., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6:109-114(1987).
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Kaisho T., Uchibayashi N., Hardy R.R., Hirano T.,
Sakiyama F., Suemura M., Kishimoto T.;
ructure of human lymphocyte receptor for immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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PubMed=8745401;
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M., Kim C.W., Honjo
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EMBL; X04772; CAA28465.1; -.
EMBL; X03562; AAA52433.1; -.
PIR; A26067; LNHUER.
PIR; A26164; A26164.
PIR; A26189; A26589.
PIR; A31924; A31924.
PIR; A31924; A31924; A31924.
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use by non-profit institutions as long a
modified and this statement is not removed.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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-!- MISCELLANEOUS: THERE ARE TWO DIFFER IN BOTH STRUCTURE AND BASOPHILS AND MAST CELLS AND AND MONOCYTES.
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SIMILARITY: CONTAINS
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ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                            269
321
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162
149
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163
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259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Transmembrane; Glycoprotein; Rev
tin; Signal-anchor; Alternative splicing;
                                                                                                                                                  AA;
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Score 154.5; I
Pred. No. 1.1e
20; Mismatches
                                                                                                                                            C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR C-TYPE LECTIN CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                      SIMILARITY SIMILARITY
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D FUNCTION: HIG
D LOW AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A (SHOWN HERE)
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                                                               DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL). (LONG FORM).
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                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; B-cell; 19; 3D-structure.
                                                                                                                                                                                              ) (POTENTIAL).
ISOFORM B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in no way
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Query Match
Best Local Similarity
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SEQUENCE
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DOMAIN
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P49300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for galactose/N-acetyl-galact J. Blochem. 104:600-605(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetylgalactosamine-specific lectin on mouse tumoricidal macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-galactose/N-acetylgalactosamine-specific lectin)
                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S36676; AAB22171.1; -. HSSP; P06734; IKJE. MGD, MGI:96975; MG1. InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGL.
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oda S., Sato M., Toyoshima S., Osawa T.;
"Purification and characterization of a lectin-like
"palactose/N-acetyl-galactosamine from tumoricida"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92268032; PubMed-1587794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89197865; PubMed=3241002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato M., Kawakamyi K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                    ectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMO-OLIGOMER.
SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: IS EXPRESSED ON THE SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECOGNIZES TERMINAL UNITS. MAY PARTICIPATE IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00059; lectin_c;
                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                   PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
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172
173
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274
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288
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Rodentia;
                                                                                             34596
  23
29
                                                                                                                                                                                                                                                                                             Transmembrane; Calcium; Signal-anchor.

CYTOPLASMIC (POTENTIAL).

GIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osawa T.,
  . 5%;
                                                                                             ¥
                                                                                 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

OF COLUMN (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)
  Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toyoshima S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALACTOSE AND N-ACETYLGALACTOSAMINE INTERACTION BETWEEN TUMORICIDAL
  153
No.
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  1.3e-08;
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tumoricidal macroph
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in) (MMGL).
                                                                                                                .) (POTENTIAL).
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                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     olecule specific macrophages.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Macrophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                              DOMAIN
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DISULFID
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01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takezawa R., Wagatsuma H., Nomoto C., Watanabe Y., Akaike Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
-I- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND COULD BE INVOLVED IN ENDOCYTOSIS.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                    CARBOHYD
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                    Endocytosis
DOMAIN
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: KUPFFER CELLS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUCR_MOUSE P70194;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D88577; BAA13647.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                      , P20693; 1HLJ.
MGI:1859834; Kclr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                          PS00615; C_TYPE_LECTIN_1; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                        Transmembrane;
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(See http://www.isb-sib.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M11025; AAB59519.1; PIR; A25179; LNHU2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; \IPR001304; lectin_c.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=86016723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWO receptor genes during evolution.";

OC. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).

FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSEAME UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AN TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE CHESSASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE CHESSASSOCIATED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 108361;
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(Rel. 07, Last sequence update)
(Rel. 39, Last annotation updat
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EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
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No. 2.9e-08;
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91268022; PubMed=2050668;
MEDLINE=91268022; PubMed=2050668;
Bezouska K., Crichlow G.V., Rose J.M., Taylor M.E., Drickamer K.
"Evolutionary conservation of intron position in a subfamily of encoding carbohydrate-recognition domains.";
J. Biol. Chem. 266:11604-11609(1991).
                                   ++
                                                                                                                                                                  MEDLINE=81215504;
                                                                                                                                                                                                                      Mellow T.E., Halberg D., Drickamer K.; "Endocytosis of N-acetylglucosamine-containing glycoproteins fibroblasts expressing a single species of chicken liver glyc
                                                                                                                                                        Drickamer
                                                                                                                                                                                                                   fibroblasts expressing
receptor.";
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Gallus gallus (Chicken).
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21-JUL-1986
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                              SUBCELLULAR LOCATION: Type II membrane protein. PTM: SOME OR ALL OF THE CYSTEINES ARE INVOLVED SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOM
                                                                    coproteins. Sequence of the chicken hepatic lectin.";
Biol. Chem. 256:5827-5839(1981).
FUNCTION: HEPATIC LECTIN IS A MEMBRANE RECEPTOR PROTEIN THAT RECOGNIZES AND BINDS EXPOSED N-ACETYLGLUCOSAMINE MOIETIES OF PLASMA GLYCOPROTEINS, THUS MEDIATING THEIR CLEARANCE (FROM TICLICALION) AND ENDOCYTOSIS.
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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SEQUENCE
"Mouse asialoglycoprotein receptor cDNA sequence: conservation receptor genes during mammalian evolution."; Biochim. Biophys. Acta 1087:259-261(1990).
-!- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGI
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                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-91027942; PubMed-2223888;
Sanford J.P., Doyle D.;
                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-1992 (Rel.
30-MAY-2000 (Rel.
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CARBOHYD
CARBOHYD
SEQUENCE
                                                           01-AUG-1988 (Rel.
01-NOV-1990 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
Rattus norvegicus (| Eukaryota; Metazoa;
                        ASGR2 OR ASGR-2.
                                               Asialoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88082; Asgr2.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53042; CAA37211.1; PIR; S13165; S13165.
                                      (ASGPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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SIMILARITY: CO
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SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: EX
CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AN TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                          VDGTD--YRSNYRNWAFTQPDNWQGHEQGGGEDCAEIL----SDGHWNDNFCQQVNRWV
                                                                                                                                                                                                                                                 V-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAAL
                                                                                                                                                                                                                                                                                        YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW 62
                                                                                                                                                                                                                                                                         YWFSRDGLTWAEADQYCQLENAHLLVINSREEQDFVVKHR--SQFHIWIGLTDRDGSWKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P06734; 1KJE.
                                                                                                                                                                                               117
                                                                                                                                                                          293
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1 58
M 59 79
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                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                             STANDARD;
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                                                           39,
39,
                                                 receptor
Chordata;
                                                                                                                                                                                                                                                                                                                                      21.5%;
28.1%;
                                               Last sequence update)
Last annotation update)
ceptor R2/3 (Hepatic lec
                                                                                     Created)
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EXPRESSED
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C-TYPE LECTIN (LONG I
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
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Pred.
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 Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane protein.
EXCLUSIVELY IN HEPATIC PARENCHYMAL
                                                                                                                                                                                                                                                                                                                                      143.5; DB 1
No. 1.4e-07;
                                                                                                             301
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                                                 lectin
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 Euteleostomi;
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                                                 (RHL-2)
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EMBL; M16347; AAA42038.1; -.
EMBL; J02762; AAA41522.1; -.
EMBL; X07636; CAA30476.1; -.
PIR; AA5417; LNRT2.
PIR; AA5488; A26888.
PIR; A26888; A26880.
PIR; A38462; A28462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-84111334; rubero-13.000;
Drickamer K., Mamon J.F., Binns G., Leung J.O.;
Primary structure of the rat liver asialoglycoprotein receptor.
Structural evidence for multiple polypeptide species.";
J. Biol. Chem. 259:770-778(1984).
-i- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
CARBOHYDRATE MOIETLES HAS BEEN REMOYED. THE RECEPTOR RECOGNIZES
TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND
BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
              PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                               Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
    Lectin; Glycoprotein;
                                                                                                                                                                                                                                                         entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loeb J.A., Holland E.C., Drickamer K.;
"Major and minor forms of the rat liver asialoglycoprotein recare independent galactose-binding proteins. Primary structure glycosylation heterogeneity of minor receptor forms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=84111554; PubMed=6319386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE=87250656; PubMed=3597443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halberg D.F., Wager
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McPhaul M., Berg P.; "Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                       tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
MISCELLANEOUS: TWO TYPES OF RAT HEPATIC LECTIN HAVE BEEN
IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDANCE OF
RHL-2 AND RHL-3 ONLY DIFFERS IN THIR CARBOHYDRATE STRUCTURES.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: CALCIUM IS MISCELLANEOUS: TWO TYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type II TISSUE SPECIFICITY: EXPRESSED
                                                                            A31601; A31601.
; P06734; 1KJE.
rPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:721-728(1988).
                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3600647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodentia;
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Endocytosis; Transmembrane;
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EXCLUSIVELY IN HEPATIC
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FCE2_MOUSE
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Best Local :
                                                                                                the
                                                                                                                                                            Conrad D.H.;
"Molecular structure and expression of the murine affinity receptor for IgE (Fc epsilon RII).";
proc. Natl. Acad. Sci. U.S.A. 86:7566-7570(1989).
  Kondo H., Ichikawa Y., Nakamura K., Ts
"Cloning of cDNAs for new subtypes of
for IgE (Fc epsilon RII/CD3).",
Int. Arch. Allergy Immunol. 105:38-48
                                                       STRAIN-DBA/2
                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Low affinity immunoglobulin epsilon FC
receptor) (FC-epsilon-RII) (CD23).
FCER2 OR FCER2A.
                                                                                                                   Moore K.W.;
                                                                                                                             Gollnick S.O.,
                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DISULFID
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                                           MEDLINE=94372613; PubMed=8086828;
                                                                                                                                        MEDLINE=90171598;
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                                                                                                                                                                                                                                                                                                                                                            FCE2_MOUSE STANDARD;
P20693; Q61556; Q61557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
SEQUENCE
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                                                               SEQUENCE FROM N.A. (FORMS B AND
                                                                                                          "Isolation,
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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DOMAIN
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                                                                                   olation, characterization, and mouse Fc receptor for IgE (Fc Immunol. 144:1974-1982(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
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105:38-48(1994).
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R -> A (IN REF. 1).

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Pred. No. 2.2
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Sciurognathi; Muridae;
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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SIGNAL-ANCHOR
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                                                                                                                            Yamashita L.C.,
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                                                                                                                                                                                                            Yokoyama
                               Tsuchiya
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DR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                      murine
                                                                                                                                                                                                            W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                  S.;
low-affinity Fc receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1).
2 AND 3).
2 AND 3).
                                                                                                                            Kehry M.R.,
                                                                                                                                                                                                                                                                                                                  (Lymphocyte
                                                                                                                                                                                                           Kilchherr F.,
                                                                                                                                                                                       lymphocyte low-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                      clones
                                                                                                                                                                                                                                                                Murinae;
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                                                                                                     encoding
                                                                                                                                                                                                                                                                Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
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SEQUENCE
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DOMAIN
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Padlan E.A., Helm B.A.;
Modeling of the lectin-homology
affinity Fc epsilon receptor (Fc
Receptor 3:325-341(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M99371; AAA74898.1; -. EMBL; M34163; AAA37603.1; -. EMBL; X64223; CAA45532.1; -. EMBL; X64224; CAA45533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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3D-STRUCTURE MODELING OF LECTIN DOMAIN.
MEDLINE-94191542; Pubmed-8142907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1HLJ; 31-JAN-94.
MGD; MGI:95497; Fcer2a.
InterPro; IPR001304; lectin_c.
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                                                                                   198
256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS A B-CELL-SPECIFIC ANTIGEN).

SUBCELLULAR LOCATION: Type II membrane protein.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE PRODUCED BY ALTERNATIVE SPLICING.

PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).

MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON DASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES I OF IGE PRODUCTION AND IN THE DIFFERENTIATION
                                                                                                                         YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A43518;
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VWSDGSPVGYS--
                                      TW-----VGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHK-LKA 114
                                                                                   YYFGKGSKQWIQARFACSDLQGRLVSIHSQKEQDFLMQHI--
                                                                                                                                                                      . Similarity 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ing
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                                                                                                                                                                                                                                                                                331
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185
71
92
113
1183
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214
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282
114
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor; Alternative splicing;
23 CYTOPLASMIC (POTENTIAL),
49 SIGNAL-ANCHOR (TYPE-II N
                                                                                                                                                                                                                                                                                                                               331
298
298
112
133
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197
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30.1%;
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OF COMMENTAL:
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OF COMMENTAL:
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
NEENEYS -> MUSQNQ (IN ISOFORM B).
N-CDB2 CRC64;
NWNPGEPNNGGQGEDCVMM----
                                                                                                                                                                    Score 141.5;
Pred. No. 2.5e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
EXTRACELLULAR
C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domains epsilon
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                                                                                   NKKDSWIGLQDLNMEGEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure
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                                                                                                                                                                      23;
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Matches 34
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CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY SEQUENCE OF 3421964;
MEDLINE-88339956; PubMed=3421964;
II M., Kawasaki T., Yamashina I.;
"Structural similarity between the macrophage lectin spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMGL_RAT STANDARD; PRT; 306 AA.

P49301;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BP)
galactose/N-acetylgalactosamine-specific lectin) (MMGL).
                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactose/N-acetylgalactosamine
binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and sequence analysis macrophage lectin specific for galactose J. Biol. Chem. 265:11295-11298(1990).
                                                                                                                                                                                                                             Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILINE-90293078; PubMed=2358462;
                                                                                                                                            DOMAIN
                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                              EMBL; J05495; AAA41216.1;
HSSP; P06734; 1KJE.
                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Type II membrane protein.
-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                    InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ii M., Kurata H.,
                                                                                                                                                                                          .ectin; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
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                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT:
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                                                                                                                                                                                                     PS00615;
PS50041;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Biophys. Res. Commun. 155
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174
175
203
276
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                                                       306
300
186
298
290
76
168
34242
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C_TYPE_LECTIN_2; 1.
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58
             20
27
                                                                                                                                                                                           Transmembrane;
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             . 68;
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                                                          (POTENTIAL).

EXTRACELLULAR (POTENT EXTYPE LECTIN (LONG E BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...
Score 133.5; |
Pred. No. 1.5e
20; Mismatches
                                                                                                                                                                   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                 155:720-725(1988).
             133.5;
No. 1.
                                                                                                                                                                               Calcium; Signal-anchor.
 ; DB 1;
.5e-06;
les 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawasaki T.; of cDNA encoding the and N-acetylgalactosamine.";
                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                              http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                        Usage
                                                            CRC64;
                                                                                                                                 FORM).
                      Length
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; Murinae; Rat
                                                                       (POTENTIAL)
                                                                                   (POTENTIAL)
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Similarity

Conservative

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Indels

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Gaps

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RESULT
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                                                                     EMBL; AF119097; AAD17252.1; -.
HSSP, P05451; ILIT.
GlycoSuiteDB; Q9YGP1; -.
InterPro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 MOD_RES
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Q9YGP1;
30-MAY-2000
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                                                   SIGNAL
                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu Q., Wu X.-F., Xia Q.-C., Wang "Cloning of a galactose-binding stejnegeri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Galactose-binding lectin precursor (TSL).
Trimeresurus stejnegeri (Chinese green tree viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                           DOMAIN
                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                     venom using liquid chromatography-electrospray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRIST
                                                                                                                                                                                                                                                                                                                                                                                                                             Zeng R., Xu Q., Shao X.-X., Wang K.-Y., Xia Q.-C.; "Characterization and analysis of a novel glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10561575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99348038; PubMed=10417338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, CARBOHYDRATE-LINKAGE SITE,
                                                              ectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
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                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER; DISULFIDE-LINKED MASS SPECTROMETRY: MW=17924.2; MW_ERI
                                                                                                                                                                                                                                                                                                                                       . J. Biochem. 266:352-358(1999).
FUNCTION: GALACTOSE-BINDING PROTEIN WHICH RECOGNIZES SPECIFIC CARBOHYDRATE STRUCTURES AND AGGLUTINATE A VARIETY OF ANIMAL CELLS BY BINDING TO CELL-SURFACE GLYCOPROTEINS AND GLYCOLIPIDS. MAY BE CALCIUM-DEPENDENT LECTIN.
                                                                                                                                                                                                                                                                                                       RANGE=24-158.
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                                                            Signal;
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                   EMBL; J03734; AAA4147;
EMBL; M55532; AAA4089;
PIR; A28166; A28166.
PIR; A38674; A38674.
HSSP; P20693; 1HLJ.
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01-APR-1990
01-APR-1990
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Hoyle G.W., Hill R.L.;
Molecular cloning and sequencing of a
binding receptor unique to rat Kupffer
r Riol. Chem. 263:7487-7492(1988).
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-- FUNCTION: RECEPTOR WITH AN AFFINITY FOR-
COULD BE INVOLVED IN ENDOCYTOSIS.
-- SUBCELLULAR LOCATION: Type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of the gene for a carbohydrate-binding rat Kupffer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91107689; PubMed=1846367; Hoyle G.W., Hill R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=88227939; PubMed=2836387;
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                                                                                                                                                                  entities requires a license agreement
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                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-FEB-1994 (Rel. 28,
15-JUL-1998 (Rel. 36,
30-MAY-2000 (Rel. 39,
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                                                                                                                                   Monroe R.S., Huber B.E.;
"The major form of the murine asialoglycoprotein receptor:
sequence and expression in liver, testis and epididymis.";
Gene 148:237-244(1994).
                                                                                                                                                                                                            STRAIN-BALB/C; TISSUE-Liver; MEDLINE-95047431; PubMed-7958950;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                         sequence.
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FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AN TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWVDGTPFDYVQSRRFWRKGQPDNWRHGNGEREDCV--HLQR-----MWNDMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYFSRDKKSWHEAENFCVSQGAHLASVTSQEEQAFLVQIT--NAVDHWIGLTDQGTEGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00615; C_TYPE_LECTIN_1; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                       FROM
                                                                                                                                                                                                                                                                                         Biophys.
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438
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132
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69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
Last annotation
ceptor 1 (Hepation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                         1172:220-222(1993)
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BY SIMILARITY.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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EXTRACELLULAR
C-TYPE LECTIN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 132; DB 1;
Pred. No. 4.3e-06;
1; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                 Υ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                 Akaike
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lectin; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
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                                                                                                                                                                                                                                                                                                                             receptor
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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Best Local S
Matches 33
                                            PSPD_MOUSE STAI
P50404;
01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
15-JUL-1999 (Rel.
                   U1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D prescript OR SFTPO OR SFTP4.
                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                       MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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MGD; MGI:8808; Asgrl.
InterPro; IPRO01304; lectin_c.
Pfam; PF00059; lectin_c; l.
SMART; SM00034; CLECT; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
 Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00615; CLEVE; L.

PROSITE; PS50041; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D13517; BAA02734.1;
EMBL; U09362; AAB60441.1;
EMBL; U08372; AAB60440.1;
EMBL; S29855; S29855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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SUBCELLULAR LOCATION: Type II
TISSUE SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS:
SIMILARITY: COM
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                                                                                                                                                                                                   WVDGTD.
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                                                                                                                                                                                                                                                YWFSSSVRPWTEADKYCQLENAHLVVVTSRDEQNFLQRHMGPLNT---WIGLTDQNGPWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                             l Similarity
33; Conser
                                                                                                                                                      275
                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long
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283 /
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180
180
253
74
77
                                                                                                                                                                                                   --YETGFQNWRPEQPDNWYGHGLGGGEDCAHF
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1HLJ.
                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US: CALCIUM IS REQUIRED FOR LIGAND BIND: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN
                                                                                                                                                                                                                                                                                                                                                163
275
267
74
77
145
150
32472
                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
277
7
Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
59
                                                                                                                                                                                                                                                                                                        19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                              ENDOCYTOSIS SIGNAL (POTENTIAL).

BY SIMILARITY.

OLIVED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

I -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                            Score 129.5;
Pred. No. 3.6e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                      982A5D305AAE0D8F
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                                                                                             374
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                                                                                                                                                                                                                                                                                             .6e-06;
les 52;
                                                                                            ₹
                                   precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content
                                                                                                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                                   -TTDGRWNDDVCRRPYRW
                                                                                                                                                                                                                                                                                                                                                      CRC64;
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                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                              Indels
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  Euteleostomi;
                                   (SP-D)
                                                                                                                                                                                                                                                                                                                     283;
                                                                                                                                                                                                                                                                                             17;
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RESULT 3
PSPD_RAT
ID PSPD
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Best Local S
Matches 32
PSPD_RAT STANDARD;
P35248;
01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                    DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                       Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
or send a
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange;
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01391; Collagen; 3. Pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L40156; AAA92021.1;
HSSP; P35247; 1B08.
MGD; MGI:109515; Sftpd.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000087; Collagen.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u> . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96094460; PubMed=7499852;
MCtWani M., White R.A., Guo N., Dowler L.L., Tauber A.I., Sa.
"Mouse surfactant protein-D. cDNA cloning, characterization, localization to chromosome 14.";
J. Immunol, 155:5671-5677(1995).
                                                                          326
                                                                                                                  269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                               64
                                            <u>ω</u>
                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lities requires a license agreement (See http://www.isb-sib.ch/announcesend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROORGANISMS. BINDS STRONGLY MALFOSE RESIDUES AND TO A LESSER EXTENT OTHER ALPHA-GLUCOSYL MOIETIES. IT COULD PARTICIPATE IN THE EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT. SUBCLILIAR LOCATION: EXTRACELIULAR SOF 4 SET OF HOMOTRIMERS. SUBCELLULAR LOCATION: EXTRACELIULAR. SURGELLULAR LOCATION: EXTRACENTIAT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                          GTNKSLTEEAENWGDGEPNNKKNKEDCVETYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                SEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIWTWV
                                                                        PTGEPLV--YSNWAPGEPNNNGGAENCVEIFTN-----GQWNDKACGEQRLVIC
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A
                                                                                                                FEDAQEMCKQAGGQLASPRSATENAAIQQLITAHNKAAFLSMTDVGTEGKFTY-
                                                                                                                                                                                                                                45
222
278
280
350
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                         ; Collagen; :
1 19
0 374
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                                                                                                                                                                                                                                                                                                                                                                                                        Sftpd
                                                                                                                                                                                                                     221
253
374
372
364
89
                                                                                                                                                                                                           37688
                                                                                                                                                                   18.9%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                            MW:
                                                                                                                                                                                                                                                                                                    Repeat; Coiled coil.
BY SIMILARITY.
                                                                                                                                                         24;
                                                                                                                                                   Score 126; ин
Pred. No. 1.1e
24; Mismatches
                                                                                                                                                                                                                             COILED COIL (PC
C-TYPE LECTIN (
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                       D.
COLLAGEN-LIKE
                                                                                                                                                                                                                                                                                         PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                          LINKED (GLCNAC. . .) (P FE034261263F43E4 CRC64;
                       374
                                                                                                                                                                DB 1;
                      A
                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                 (SHORT
                                                                                                                                                        46;
                                                                                                                                                                          Length 374;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                   FORM)
                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                        Hydroxylation;
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on, and
                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outstation
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                                                                                                                                                       Gaps
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                                                                                                                                  63
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InterPro; IPR000087; Collagen.
InterPro; IPR001304; lectin_c.
Pfam; PF01391; Collagen; 3.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00611; C_TYPE_LECTIN_2; 1.
MOD_RES
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                                                                                               DOMAIN
DOMAIN
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DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                            Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagenous surfactant-associated protein.";
Biochemistry 28:6361-6367(1989).
-!- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFE
                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deduced amino acid sequence.";
J. Biol. Chem. 267:1853-1857(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pulmonary surfa
(CP4).
SFTPD OR SFTP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persson A., Chang D., Rust K., Moxley M., Longmore "Purification and biochemical characterization of (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90001186; PubMed=2675969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 73-95 AND 153-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of rat pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimizu H., I
Voelker D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92112913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROPROANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER MICROPROANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER EXTENDENT OTHER ALPHA-GLUCOSYL MOISTIES. IT COULD PARTICIPATE IN THE EXTRACELLULAR REDROANIZATION OR TURNOVER OF PULMONARY SURFACTANT. SUBJUIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
SUBJUIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
SUBJUIT: OLIGOMERIC COMPLEX OF 5 SET OF HOMOTRIMERS.
MISCELLANGEDUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL UNVOCCHOORST DEOTERNS OF 50.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D)
HYDROPHOBIC PROTEINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGEMOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A42046; A42046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M81231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P35247;
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99 (Rel. 38, Last annotation update)
surfactant-associated protein D precursor (SP-D) (PSP-D)
    45
222
278
280
280
350
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89
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                                                                                                                                                                                                                                                                                               Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA42170.1;
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                                                                                                                                                                                                                                                                          Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1370483;
221
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HYDROXYLATION.
HYDROXYLATION.
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BY SIMILARITY
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                                                                           N-LINKED (GLCNAC.
HYDROXYLATION.
                                                                                                                                                                                               COLLAGEN-LIKE
                                                                                                                                                                                                                                    PULMONARY SURFACTANT-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ρ,
                                                                                                                                                                                                                                                                                               film;
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                                                                                                                                                                                                                                                                                         Gaseous exchange; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions in as its content is in
                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                        (SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
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                                                                                                                                                        FORM).
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Best Local S
Matches 32
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P41317;
P41317;
P41317;
P41317;
Ol-FEB-1995 (Rel. 31, Createu,
Ol-FEB-1996 (Rel. 33, Last annotation update)
Ol-FEB-1996 (Rel. 33, Last annotation update)
Mannose-binding protein C precursor (MBP-C) (Mannan-binding
Mannose-binding protein C precursor (MBP-C) (Mannan-binding Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein C precursor (MBP-C) (MANNAN-B) (MBP-C) (MBP
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CONFLICT
SEQUENCE
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Mus musculus (Mouse).
Mus musculus (Mouse).
Mouse).
Mouse).
Mouse).
Mouse).
Mousella;
Mous
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STRAIN-CBA/J; TISSUE-Liver;
STRAIN-CBA/J; TISSUE-Liver;
MEDLINE-91302823; PubMed-1712818;
Sastry K., Zahedi K., Lelias J.M., Whitehead A.S., Ezekow
"Molecular characterization of the mouse mannose-binding
The mannose-binding protein A but not C is an acute phase
J. Immunol. 147:692-697(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95284466; PubMed-7766991; Sastry R., Wang J.S., Brown D.C., Sastry K.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mamaiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                              SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MC
SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MC
PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULUM AND IN THE GOL
APPRARTUS, AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES
LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11ya G., Kawakami M.;
hitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
FUNCTION: BINDS MANNOSE AND N-ACETYLGLUCOSAMINE IN A CALCIUM-
DEPENDENT MANNER. IS CAPABLE OF HOST DEFENSE AGAINST PATHOGENS,
BY ACTIVATING THE CLASSICAL COMPLEMENT PATHWAY INDEPENDENTLY OF
                                                                                                                                                          SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                   European
                                                                                                                                                                                                                                                                                                                                                                                                                                               THE ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s.,
   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reveals
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32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ihara S., Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 AA;
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89
164
                                                                                                                                                                                                                                                    THE ORGANELLES, PROBABLY
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28.1%;
                                                                                                                                                       A COLLAGENOUS DOMAIN.

1 C-TYPE LECTIN FAMILY DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mannose-binding protein to other collectin gene
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N -> E (IN REF

K -> C (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 125; DB 1;
Pred. No. 1.4e-05;
5; Mismatches 45
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Sciurognathi; Muridae;
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Eukaryota; Metazoa; Arthropoda; Cru
Thoracica; Sessilia; Balanomorpha;
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01-OCT-1996 (Rel. 34, Li
16-OCT-2001 (Rel. 40, Li
Lectin BRA-3 precursor
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Hydroxylation; Liver; Glycoprotein;
Calcium; Collagen; Repeat; Signal.
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eda T., Kojima M.,
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Matches 37
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Biochim. Biophys. Acta 874:285-295(1986).

-i- FUNCTION: SUGAR-BINDING PROTEIN WHICH RECOGNIZES SPECIFIC CARBOHYDRATE STRUCTURES AND AGGLUTINATE A VARLETY OF ANIMAL CELLS BY BINDING TO CELL-SURFACE GLYCOPROTEINS AND GLYCOLIPIDS.

THIS IS A CALCIUM-DEPENDENT LECTIN. INVERTEBRATE LECTINS MAY BE INVOLVED IN DEFENSE FUNCTIONS.
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SMART; SM00034; CLECT; 1.
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MISCELLANEOUS: THIS LECTIN BINDS GALACTOSE.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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sen the Swiss Institute of Bioinformatics and the EN
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EMBL; M18962; AAA42028.1; -.
EMBL; D26164; BAA05149.1; -.
PIR; A28351; A28351.
PIR; PL0147; PL0147.
PIR; PL0147; PL0147.
PIR; A39081; A39081.
PIR; S34618; S34618.
PIR; S34618; S34618.
PIR; S34618; S34618.
                 InterPro; IPR03990; pancreatitis_assoc. Pfam: PF00059; lectin_c; 1. PRINTS; PR01504; PNCREATITSAP. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                               entities requires a license agreement (som send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90031455; PubMed-2680252; Adrich Z., de Caro A.M., Guidoni A.A., Wounderstand in rat pancreatic juice the human pancreatic stone protein."; Comp. Biochem. Physiol. 93B:793-797(1989).
                                                                                                                                                                                                                                                                                                                    entities requires
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Miyashita H.,
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Yonekura H., Okamoto H.;
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Mammalia; Eutheria;
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FUNCTION: MIGHT ACT AS AN INHIBITOR
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                                                                                                                  SEQUENCE OF 1856-2124 FROM N.A.

**MEDLINE=86250698; PubMed=2424893;

**A Doege K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;

**A Doege K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;

**A Doege K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;

**A Doege K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;

**Partial CDNA sequence encoding a globular domain at the C terminu T of the rat cartilage proteoglycan.";

**J Station Comparison of the Component of Extracellu T of the rat cartilage. IT BINDS AVIDLY TO IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

**C SUBCELULIAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY)

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Doege K., Sasaki M., Horigan E., Hass
"Complete primary structure of the ra
protein deduced from cDNA clones.";
Di Biol. Chem. 262:17757-17767(1987).
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      EMBL; M13518; AAA418:
EMBL; J03485; AAA2100
PIR; A23835; A23835.
PIR; A28452; A28452.
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between
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InterPro;
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SMART; SM00034; CLECT; 1
SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 4 LINK DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PF00084; 
; PF00193;
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PF02339;
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; IPR003596; Ig_v.
; IPR000358; Link.
; IPR0003324; SGXXSG.
; IPR000436; Sushi_SCR_CCP.
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PS00615;
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0059; lectin_c; 1.
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Xlink; 4.
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SGXXSG; 58.
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IG-LIKE V
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  Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lectin; Signal; Sushi;
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Best Local
                                                                                                                                        The aggrecan gene.";

Nat. Genet. 7:154-157(1994).

Nat. Genet. 7:154-157(1994).

Nat. Genet. 7:154-157(1994).

IS FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF THIS PROTEIN MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A PEGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGCA_MOUSE STANDARL
Q61282; Q64021;
Q1-NOV-1997 (Rel. 35, C
Q1-NOV-1997 (Rel. 35, L
Q1-NOV-1997 (Rel. 35, L
                                                                                                                                                                                                                                                                                                                     MEDLINE=95004579; PubMed=7920633; Watanabe H., Kimata K., Line S.,
                                                                                                                                                                                                                                                                                                                                                                                             localization, and structural analysis of murine aggrecan. Genomics 22:364-371(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Walcz E., Deak F., Erhardt P., Coul
Doege K.J., Glant T.T.;
"Complete coding sequence, deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUE=Cartilage; MEDLINE=95104847; PubMed=7806222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                   "Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion
                                                                                                                                                                                                                                                                                                            Yamada
                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SV;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 211-326 FROM N.A.
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                   DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS, G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WT-----YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGI-
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                              G3
          CONTAINS MOSTLY CHONDROITIN SULFATE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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annotation updat
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N-LINKED (GLCNAC. .)
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Pred. No. 0.00
L7; Mismatches
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InterPro; IPR001304; Lectin_c.
InterPro; IPR001304; Lectin_c.
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-I- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF CARTILAGE MATRIX DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF CARTILAGE MATRIX DEFICIENCY (CMD), AN AUTOSOMAL RECESSIVE SYNDROME CHARACTERIZED BY CLEFT PALATE, SHORT LIMBS, TAIL AND SNOUT. MUTATION IN STRAIN CMD CAUSES ABSENCE OF AGGRECAN BY TRUNCATION OF THE PROTEIN (MUTATION IN THE G1 DOMAIN).

-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

-I- SIMILARITY: CONTAINS 4 LINK DOMAINS.

-I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

-I- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

-I- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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Kupffer cell recep	A28166	N	550	19.8	132	3
lectin M-ASGP-BP p	A42230	N	306	20.0	133.5	30

ALIGNMENTS

RESULT S09702

N;Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-ral lymph node homing receptor Leu-8 C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 26-May-2000 C;Accession: S09702

leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc

A; Description: binds with low affinity to oligosaccarides like heparan sulfate and siment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homolog C; Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammat F;1-51/Domain: signal sequence #status predicted <SIG>F;42-168/Domain: C-type lectin homology <CCH>F;2-323/Product: L-selectin #status predicted <MAT>F;52-323/Product: L-selectin #status predicted <EXT>F;52-300/Domain: extracellular #status predicted <EXT>F;17-204/Domain: complement factor H repeat homology <FH1>F;210-267/Domain: complement factor H repeat homology *Fi27-323/Domain: intracellular #status predicted <INNP
F;319-333/Domain: complement factor H repeat homology *Fi39-333/Domain: intracellular #status predicted <INNP
F;319-333/Domain: complement factor H repeat homology *Fi39-333/Domain: intracellular #status predicted <INNP
F;319-333/Domain: complement factor H repeat homology *Fi39-333/Domain: compl A;Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1 A;Cross-references: GDB:120157; GDB:118834; OMIM:153240 A;Map position: 1q22-1q23 A;Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 303/2 C;Function: NATURE 342, 78-82, 1989
A;Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor. A;Reference number: S06798; MUID:90044046
A;Accession: S09702 Дb A; Note: this translation is not annotated in GenBank entry HSLEU8, C; Comment: For an alternative splice form, see PIR: A34015. C; Genetics: Š Ş A; Cross-references: EMBL:X17519; NID:g34344 A; Molecule type: mRNA A; Residues: 1-323 <CAM> A; Status: not compared with conceptual translation Query Match Best Local Similarity Matches 117; Conser 61 52 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 111 site: phosphate (Ser) Conservative 100.0%; 0; Score 666; DB 1; Pred. No. 2.8e-58; Mismatches 0; (covalent) #status Length predicted Indels 0 release 111.0 Gaps 60 0

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C;Genetics:
A;Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1
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A;Gene: GDB:LAM1, LAM1, LAM
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A; Cross-references: GB:M25280; NID:g187182; PIDN:AAC63053.1; C; Comment: For an alternative splice form, see PIR:S09702.
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A;Molecule type: mRNA
A;Residues: 14-49,'Y',51-190,'H',192-205,'L',207-226,'F',228-385
A:Cross-references: GB:X16070; NID:g38092; PIDN:CAA34203.1; PID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; ACCESSION.

A; ACCESSION.

A; Molecule type: mRNA
A; Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TED>
A; Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TED>
A; Rolecule type: mRNA
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F<sub>*</sub>173-204/Domain:
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: I55333; S06798; JL0104; A34015; A33912
R;Ord, D.C.; Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertini, O.; Griffin, O.
J. Biol. Chem. 265, 7760-7767, 1990
A;Title: Structure of the gene encoding the human leukocyte adhesion molecul A;Reference number: I55333; MUID:90243637
A;Accession: I55333
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A; Residues: 1-225,'S',227-385 <CAM>
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A;Residues: 14-385 <ORD)
A;Cross-references: GB:M32414; NID:g187259; P:
A;Cross-references; S.P.; Stamenkovic, I.;
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R;Qian, Biochem.
                                                    L-selectin precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998
                                          C; Accession:
                                                                                                                      JC4892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;39-157/Domain: calcium-binding #status predicted <CAB>
F;160-191/Domain: EGF homology <EGF>
F;197-254/Domain: complement factor H repeat homology <FH1>
F;259-316/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;39-372/Product: L-selectin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This receptor is involved in sites of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 37-43;142-148 <TSU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: A; Accession: PC4315
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A; Residues: 1-372 <TSU1>
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R;Tsurushita, N.; Fu, H.; B
Gene 181, 219-220, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JC5377
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F;272-329/Domain:
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Best Local
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                  J.; Huang,
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complement factor H repeat homology <FH2>
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                      Marks,
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Pred. No. 3.4e-58;
406-412,
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225,

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submitted to the EMBL Data Library, October 1991

A; Reference number: $22123

A; Reference number: $22124

A; Reference number: $22124

A; Reference number: $22124

A; Recession: $22124

A; Status: preliminary

A; Molecule type: mRNA

A; Cross-references: EMBL:X62882; NID:g515; PIDN:CAA44676.1; PID:g516

A; Malcheck, B:, White, MI:x Kurk, S.; Kishimoto, T.K.; Jutila, M.A.

Eur. J: Immunol. 22, 469-476, 1992

A; Title: Characterization of the bovine peripheral lymph node homing received as a constant of the covine peripheral lymph node homing received as a covine 
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A;Accession: JC4892
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-376 <QIA>
A;Cross-references: GB:U26535; NID:9847787; PIDN:AAA67896.1; PID:9847788
A;Cross-references: GB:U26535; NID:9847787; PIDN:AAA67896.1; PID:9847788
C;Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhesion C;Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology; F;1-37/Domain: Signal sequence #status predicted <SIG>F;29-155/Domain: C-type lectin homology <LCH>F;38-376/Product: L-selectin homology <LCH>F;10-11/Domain: EGF homology <LGEP>F;107-254/Domain: complement factor H repeat homology <FH1>F;197-254/Domain: complement factor H repeat homology <FHP>F;299-316/Domain: complement factor H repeat homology <FHP>
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N;Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S22124; A46531
R;Bosworth, B.T.
R;Bosworth, B.T.
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Best Local S
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                                  TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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TWVGTNKSLTEEAKNWGAGEPNNRKSKEDCVEIYIKRNKDSGKWNDDACHKAKTALC
                                                                                                                                   WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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Pred. No. 8.3e-50;
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No. 1.8e-51;
7;
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A; Title: Mouse lymph node homing receptor cDNA clone encodes a glycoprotein revealing A; Reference number: A40167; MUID:89162048
A; Reference number: A40167; MUID:89162048
A; Recession: A40167
A; Molecule type: mRNA
A; Residues: 1-372 <SIE2>
A; Molecule type: mRNA
A; Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
A; Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
A; Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
A; Note: part of this sequence, including the amino end of the mature protein, was con R:Stegelman, M: Bond, M.W.; Gallatin, W.M.; St.John, T.; Smith, H.T.; Fried, V.A.; W Science 231, 823-829, 1986
A; Title: Cell surface molecule associated with lymphocyte homing is a ubiquitinated b. A; Reference number: A60906; MUID:88122900
A; Accession: A60906
A; Muid: Accession: Accession:
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A32375; A35102; A40107; A60906
R;Lasky, L.A.; Singer, M.S.; Yednock, T.A.; Dowbenko, D.; Fennie, C.; Rodrig Cell 56, 1045-1055, 1989
A;Title: Cloning of a lymphocyte homing receptor reveals a lectin domain. A;Reference number: A32375; MUID:89168433
A;Accession: A32375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;197-254/Domain: complement factor H repeat homology <FH1>F;259-316/Domain: complement factor H repeat homology <FH2>F;259-316/Domain: complement factor H repeat homology <FH2>F;332-355/Domain: transmembrane #status predicted <TMM>F;332-3572/Domain: intracellular #status predicted <INT>F;366-372/Domain: intracellular #status predicted <INT>F;60,104,216,246,278,308,320/Binding site: carbohydrate (Asn) F;364/Binding site: phosphate (Ser) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-372 <SIE1>
A;Cross-references: GB:M36005; NID:g199735; PIDN:AAA39722.1;
R;Stegelman, M.H.; van de Rijn, M.; Weissman, I.L.
Science 243, 1165-1172, 1989
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A; Residues: 1-372 <LAS>
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Local :
TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                             WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                   WTYHYSEKPMNWENARKFCKQNYTDLVAIQNKREIEYLENTLPKSPYYYWIGIRKIGKMW
                                                                                                                                                                                                                                                                                                                                                97; Conserv
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82.9%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                          565; DB 1;
No. 3.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 372;
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predicted
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TWVGTNKTLTKEAENWGAGEPNNKKSKEDCVEIYIKRERDSGKWNDDACHKRKAALC

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R;Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.

Blood 80, 795-800, 1992

A;Title: Molecular cloning and analysis of in vivo expression of murine P-se
A;Reference number: A44899; MUID:92345617

A;Accession: A44899

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-723, 'E',725-768 <SAN>
A;Cross-references: GB:M72332; NID:g193565; PIDN:AAA37712.1; PID:g193566
A;Note: sequence extracted from NCBI backbone (NCBIP:109900)
C;Superfamily: unassigned EGF-related proteins; complement factor H repeat hom
C;Reywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; rf-41/Domain: signal sequence #status predicted <NGT>
F;1-41/Domain: GGF homology <EGF>
F;200-257/Domain: complement factor
F;262-319/Domain: complement factor
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$23936
L-selectin precursor - rat
L-selectin precursor - rat
N;Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-C;Accession: $23936
R;Watanabe, T.; Song, Y.; Hirayama, Y.; Tamatani, T.; Kuida, K.; Miy
Blochim. Blophys. Acta 1131, 321-324, 1992
A;Title: Sequence and expression of a rat cDNA for LECAM-1.
A;Reference number: $23936; MUID:92329548
A;Accession: $23936
A;Accession: $23936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-372 <WAIP
A;Common control of the control of 
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A; Molecule type: mRNA
A; Residues: 1-768 <WEL>
A; Residues: 1-768 <WEL>
A; Cross-references: GB:M87861; NID:g200552; PIDN:AAA40008.1; PID:g200553
A; Experimental source: endothelial cells
A; Note: sequence extracted from NCBI backbone (NCBIP:109467)
A; Note: sequence extracted from NCBI backbone (NCBIP:109467)
D: Canadara W F: Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: CD62; granule membrane protein 140; PADGEM C;Species: Mus musculus (house mouse) c;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 19-May-2000 C;Accession: A42755; A44899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins.
A;Reference number: A42755; MUID:92340571
A;Accession: A42755
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A42755
P-selectin precursor
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Pred. No. 2e-47;
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RESULT 10 S36772 E-selectin C; Species:

bovine
 Bos primigenius

taurus

(cattle)

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           Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Strubel, N.A.; Nguyen, M.; Kansas, G.S.; Tedder, T.F.; Bischoff, J. Biochem. Biophys. Res. Commun. 192, 338-344, 1993
A;Title: Isolation and characterization of a bovine cDNA encoding a functional homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;324-381/Domain: complement factor H repeat homology <FH03>
F;386-443/Domain: complement factor H repeat homology <FH04>
F;488-505/Domain: complement factor H repeat homology <FH05>
F;510-567/Domain: complement factor H repeat homology <FH06>
F;580-637/Domain: complement factor H repeat homology <FH07>
F;642-699/Domain: complement factor H repeat homology <FH08>
F;710-733/Domain: complement factor H repeat homology <FH08>
F;710-733/Domain: transmembrane #status predicted <TMN>
F;734-768/Domain: intracellular #status predicted <TMN>
F;745,54,107,212,347,398,456,467,663,654,661,679/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                            Query Match
Best Local
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Best Local
102 TWYGTKKTLTEEAENWADNEPNNKRNNQDCVEIYIKSLSAPGKWNDEPCWKRKRALC
                                               61 TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                      42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                        WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGGIW 60
                                                                                                             WTYHYSNKTYSWNYSRAFCOKYYTDLVAIQNKNEIAYLNETIPYYNSYYWIGIRKINNKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWVGTNKTLTEEAENWADNEPNNKKNNQDCVEIYIKSNSAPGKWNDEPCFKRKRALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTYNYSTKAYSWNNSRVFCRRHFTDLVAIQNKNEIAHLNDVIPFFNSYYWIGIRKINNKW 101
                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-646 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JN0473; MUID:93249394
                                                                                                                                                                                                                                                            67.7%;
66.7%;
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                                                                                                                                                                                                                           Score 451; DB 2;
Pred. No. 1.1e-36;
D; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 455; DB 2; Pred. No. 5.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                           Gaps
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A; Map position: 1922-1925
C; Superfamily: unassigned EGF-related proteins; complement C; Keywords: cell adhesion; glycoprotein; phosphohistidine; F; 1-41/Domain: signal sequence #status predicted <SIG>F; 42-830/Product: P-selectin #status experimental <MAT>F; 163-194/Domain: EGF homology <EGF>F; 200-257/Domain: complement factor H repeat homology <FH01F; 200-257/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L12039; NID:g402913; PIDN:AAA029 (;Superfamily: unassigned EGF-related proteins; C-type F;13-139/Domain: C-type lectin homology <LCH> F:181-237/Domain: complement factor H repeat homology <F;242-299/Domain: complement factor H repeat homology <F;342-299/Domain: complement factor H repeat homology <F;367-421/Domain: c
                                                                                                                                                                                                                                                                                  F;572-629/Domain:
F;642-699/Domain:
                                                                                                                                                                                                                                                                                                                                                   F;448-505/Domain:
F;510-567/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 56, 1033-1044, 1989
A;Title: Cloning of GMP-140, a granule membrane
A;Reference number: A30359; MUID:89168432
A;Accession: A30359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 18-Oct-1989 #sequence_revision
C;Accession: A30359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-selectin precursor - human
N;Alternate names: CD62 antigen; granule membrane protein
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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A;Molecule type: mRNA
A;Residues: 1-485 <NGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 365, 267-269, 1993
A;Title: A role for sialyl Lewis-X/A glycoconjugates
A;Reference number: S36772; MUID:93382537
A;Accession: S36772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 10-Dec-1993
C;Accession: S36772
R;Nguyen, M.; Strub
                                                                                                                                                                                                             F;772-795/Domain:
                                                                                                                                                                                                                                                 F;704-761/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                       F;324-381/Domain:
F;386-443/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: SELP; GRMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M25322
A;Note: parts of this sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Johnston, G.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Query Match
Best Local Similarity
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                                                                                                                              n: complement factor H repeat homology <FH04>
n: complement factor H repeat homology <FH05>
n: complement factor H repeat homology <FH05>
n: complement factor H repeat homology <FH06>
n: complement factor H repeat homology <FH07>
n: complement factor H repeat homology <FH08>
n: complement factor H repeat homology <FH09>
n: complement factor H repeat homology <FH09>
n: transmembrane #status predicted <TMN>
n: intracellular #status predicted <CYT>
,219,411,460,518,665,716,723,741/Binding site: <
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   Score
Pred.
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Pred. No. 3.
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   445;
No. 5
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   DB 2;
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                                                                                                                                            A; Nolecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-307,'T',309-327,'T',329-490,'A',492-551 <LAR2>
A;Residues: GB:M91004; NID:g165004; PIDN:AAA31243.1;
                                                                                                                                     A;Cross-references: GB:M91004;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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A; Map position: 1
A; Introns: 13/1;
C; Superfamily: ur
                                                                                                            A; Gene:
                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                           A; Accession: I46708
                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: M91005; NID: g165006; PIDN: AAA31244.1;
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-551 <LAR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: I46709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Characterization of cDNA and genomic A; Reference number: I46708; MUID:92189729
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1: 1q22-q25 /1; 143/1; 17 : unassigned

179/1; 241/1; ed EGF-related

303/1; 366/1; 429/1; 488/1; 525/1; proteins; C-type lectin homology; c

complement

fa

from

GB/EMBL/DDBJ

PID: 9165007

PID: g165005

GB/EMBL/DDBJ

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endothelial leukocyte adhesion molecule 1 - rabbit c;Species: oryctolagus cuniculus (domestic rabbit) C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 C;Accession: 146709; 146708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 145, 251-255, 1994
A;Title: Cloning, sequence comparison and in vivo expression A;Reference number: I53821; MUID:94333817
A;Accession: I53821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-selectin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
               R; Larigan, J.D.; Tsang, T.C
DNA Cell Biol. 11, 149-162,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         F; 642-699/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;510-567/Domain:
F;580-637/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F; 262-319/Domain:
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F;163-194/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L23088; NID:g349552; PIDN:AAA60325.1; C;Superfamily: unassigned EGF-related proteins; C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-768 < RES>
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Best Local S
Matches 75
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                                                                                                                                                                                                          TWVGTNKTLTAEAENWADNEPNNKRNNQDCVEIYIKSNSAPGKWNDEPCFKRKRALC
                                                                                                                                                                                                                              TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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                                 J.D.;
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                                                                                                                                                                                                                                                                                                                                                            75; Conservative
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complement factor H repeat
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                                   T.C.; Rumberger,
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                   1992
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Pred. No. 1e-3
13; Mismatches
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                                     J.M.; Burns,
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                                                                      #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                              Length 768;
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rabbit ELAM-1: Conse
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rat

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N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELC;Species: Homo sapiens (man) C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change C;Accession: A38615; A35046; A32606 R;Collins, T.; Williams, A.; Johnston, G.I.; Kim, J.; Eddy, R.; J. Biol. Chem. 266, 2466-2473, 1991 A;Title: Structure and chromosomal location of the gene for endo A;Reference number: A38615; MUID:91115870
                                                                                                                                                                                                RESULT 15
A35046
E-selectin precursor -
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JC5092
LT-selectin - pig
E-selectin - pig
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 19-May-2000
C.Accession: JC5092
R.Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Barrange 19-May-2000
R.Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Barrange 19-May-2000
R.Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Barrange 19-May-2000
R.Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Barrange 19-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-482 <WIN>
A; Cross-references: GB:U37521; NID:g1052974; PIDN:AAC48680.1; PID:g1052
A; Cross-references: GB:U37521; NID:g1052974; PIDN:AAC48680.1; PID:g1052
A; Cross-references: GB:U37521; NID:g1052974; PIDN:AAC48680.1; PID:g1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 176, 67-72, 1996
A;Title: The intron-exon structure of the porcine E-selectin-encoding A;Reference number: JC5092; MUID:97075911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: duplication; glycoprotein: tandem repeat F;14-140/Domain: C-type lectin homology <LCH> F;18-239/Domain: complement factor H repeat homology <FH1> F;244-301/Domain: complement factor H repeat homology <FH2> F;306-364/Domain: complement factor H repeat homology <FH3> F;369-427/Domain: complement factor H repeat homology <FH4> F;432-486/Domain: complement factor H repeat homology <FH4> F;432-486/Domain: complement factor H repeat homology <FH4> F;432-486/Domain: complement factor H repeat homology <FH5> F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 13/1; 1421; 178/1; 237/1; 300/1; 363/1; 422/1; 459/1; 466/1
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Best Local :
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Best Local
                                                                                                                                                                                                                                                                                                                                         83
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                                                                                                                                                                                                                                                                                                                                                                                                                              23 WSYSASTETMTFDDASAYCQQRYTHLVAIQNHAEIEYLNSTFNYSASYYWIGIRKINGTW 82
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                                                                                                                                                                                                                                                                                                                            TWIGTKKALTPEATNWAPGEPNNKQSNEDCVEIYIKRDKDSGKWNDERCSKKKLALC 139
                                                                                                                                                                                                                                                                                                                                                         TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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                                                                                                                                                                   names: endothelial leukocyte adhesion molecule 1 (ELAM-1); LECAM-2
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63.2%;
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No. 2.9e-34;
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Pred. No. 4.3e-35;
3; Mismatches 30
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                                                                       Eddy, R.; Shows, T.; Gimbrone Jr
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                     endothelial-leukocyte
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                                                                                                                                           A; Reference number: A; Accession: S23174
                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                A; Title:
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F:12-138/Domain: C-type lectin homology <LCH>
F:22-610/Product: endothelial leukocyte adhesion molecule 1 #status |
F:143-174/Domain: EGF homology <EGF>
F:180-237/Domain: complement factor H repeat homology <FH01>
F:242-299/Domain: complement factor H repeat homology <FH02>
F:304-362/Domain: complement factor H repeat homology <FH03>
F:304-362/Domain: complement factor H repeat homology <FH04>
F:304-362/Domain: complement factor H repeat homology <FH05>
F:403-488/Domain: complement factor H repeat homology <FH05>
F:430-488/Domain: complement factor H repeat homology <FH06>
F:430-488/Domain: complement factor H repeat homology <FH06>
F:457-578/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-21/Domain: signal sequence #status predicted
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A;Map position: 1q22-1q25
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A;Title: Endothelial leukocyte adhesion molecule 1: A;Reference number: A32606; MUID:89162047
A;Accession: A32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: duplication; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-467,'Y',469-610 <BEV>
A;Cross-references: GB:M24736; NID:g537523; PIDN:AAA52376.1; PID:g537524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Cross-references: GB:M61893; GB:M58017; NID:g182043; PIDN:AAA52375.1; PID:g182046 R;Hession, C.; Osborn, L.; Goff, D.; Chi-Rosso, G.; Vassallo, C.; Pasek, M.; Pittacl Proc. Natl. Acad. Sci. U.S.A. 87, 1673-1677, 1990 A;Title: Endothelial leukocyte adhesion molecule 1: direct expression cloning and fu A;Reference number: A35046; MUID:90175359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: SELE; ELAM; ESEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-610 <HES>
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                                                                                                                                557-578/Domain: transmembrane #status predicted <\brace{TV}.25,145,160,179,199,203,265,312,332,503,527/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement; Keywords: duplication; glycoprotein; tandem repeat; transmembrane protein
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   62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMIM:131210
Score 415; DB 2;
Pred. No. 3.6e-33;
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                                                                                                                                   site: carbohydrate
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B.
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A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015 R;Weller, A.; Isenmann, S.; Vestweber, D. J. Biol. Chem. 267, 15176-15183, 1992
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000
C;Accession: S23174; B42755
                                                                                                   A; Molecule type: DNA
A; Residues: 1-612 <BEC>
                                                                                                                                                                                                                                                                                                                                 R; Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter,
                                                                                                                                                                                                                  . Biochem. 206, 401-411, 1992
s: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and
rence number: S23174; MUID:92283265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor - mouse
e names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
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Mismatches

33;

Indels

0;

Gaps

0

117

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A;Title: Cloning of the mouse endothelial selectins. Expression of b A;Reference number: A42755; MUID:92340571
A;Recession: B42755
A;Reterence number: A42755; MUID:92340571
A;Recession: B42755
A;Ccession: B42755
A;Ccession: B42755
A;Coss-references: GB:M87862; NID:g193107
A;Rote: Lipe sequence endothelial cells
A;Note: sequence extracted from NCBI Dackbone (NCBIP:109470)
A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PID A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PID A;Note: it is uncertain whether the initiator is Met-1 or the AUG co Csuperfamily: unassigned EGF-related proteins; C-type lectin homolog (Superfamily: unassigned EGF-related protein crype lectin homology (F12-121/Domain: signal sequence #status predicted <SIG>F;12-138/Domain: C-type lectin homology <CCH>F;21-138/Domain: complement factor H repeat homology <FH1>F;21-5139/Domain: complement factor H repeat homology <FH3>F;305-363/Domain: complement factor H repeat homology <FH4>F;305-363/Domain: complement factor H repeat homology <FH5>F;491-548/Domain: complement factor H repeat homology <FH5>F;255.391,528/Binding site: carbohydrate (Asn) (covalent) #status pre
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A;Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)
C;Superimmily: C-type lectin homology
F;256-377/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A46274
R;Curtis, B.M.; Scharnowske, S.; Watson, A.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992
A;Title: Sequence and expression of a membrane-associated A;Reference number: A46274; MUID:92390446
A;Accession: A46274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV gp120-binding C-type lectin - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
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A; Residues: 1-404 <CUR>
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Best Local
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     113
                                                                                                                                                              260 WTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLS
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                                                                                                                                                                                                                   WT----YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIR 54
KAALC 117
                                                          DLNQEGTWQWVDGSPLLPSFKQYWNRGEPNN-VGEEDCAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WYYNASSELMTYDEASAYCQRDYTHLVALQNKEEINYLNSNLKHSPSYYWIGIRKVNNVW
                                                                                                         KIG--GIWTWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKL 112
                                                                                                                                                                                                                                                                        1 Similarity
37; Conserv
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Pred. No. 3.
                                                                                                                                                                                                                                                                     Score 161.5; DB 2;
Pred. No. 2.7e-08;
6; Mismatches 57;
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.6e-32;
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                                                    -SGNGWNDDKCNLA 372
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INHUER

IGE FC receptor II, low-affinity [validated] - human

IGE FC receptor II, low-affinity [validated] - human

N; Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IgE receptor

N; Contains: IgE Fc receptor II, splice form a; IgE Fc receptor II, splice fc

C; Species: Homo sapiens (man)

C; Species: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 15-Sep-2000

C; Accession: A26067; S03279; S39442; S39443; A26184; A26589; A31924; JI00132;

C; Kikutani, H.; Inui, S.; Sato, R.; Barsumian, E.L.; Owaki, H.; Yamasaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: No.lecular characterization of the human macrophage mannose receptor: demonst A;Reference number: A60926; MUID:91079783
A;Accession: A60926
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1333, 'T', 1335-1456 <EZE>
A;Cross-references: GB:X55635
A;Cross-references: GB:X55635
A;Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 4
A;Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 4
R;Kim, S.J; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A;Reference number: A44255; MUID:93052405
A;Accession: A44255; MUID:93052405
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A36563; A60926; A44255; B44255; C44255; D44255; E44255; R7aylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A;Title: Primary structure of the mannose receptor contains multiple motifs 1A;Reference number: A36563; MUID:90324192
A;Accession: A36563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type C;Keywords: duplication; lectin; tandem repeat; transmembrane protein F;1-18/Domain: signal sequence #status predicted <SIG>F;168-209/Domain: fibronectin type II repeat homology <2F1>
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A;Residues: 155-233,'KSAL',238-283;346-428;492-569;631-714,716-719;783-820,'N',822-86
A:Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:1184
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A;Residues: 1-1456 <TAN>
A;Residues: 1-1456 <TAN>
A;Cross-references: GB:J05550; NID:g188675; PIDN:AAA59868.1; PID:g188676
A;Cross-references: GB:J05550; NID:g188675; PIDN:AAA59868.1; PID:g188676
A;Note: parts of this sequence, including the amino end of the mature protein,
R;Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;223-340/Domain: C-type lectin homology <LCH1>F;362-486/Domain: C-type lectin homology <LCH2>F;945-1079/Domain: C-type lectin homology <LCH3>
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A;Cross-references: GDB:133759; OMIM:153618
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37; Conser
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Pred. No. 3e-07;
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Kaisho,

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A;Reference number: JL0132; MUID:90220558

A;Accession: JL0132

A;Molecule type: protein
A;Residues: 1-321 <LETY
A;Residues: 1-321 <LETY
A;Experimental source: lymphoblastoid B cell line
R;Rose, K; Turcatti, G; Graber, P; Pochon, S; Regan
Biochem. J. 286, 819-824, 1992
A;Title: Partial characterization of natural and recomb
A;Reference number: S29107; MUID:93038513
A;Accession: S29107
A;Molecule type: protein
A;Residues: 152-166;173-179;189-212;230-263;268-306 <RC
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A;Title: Molecular structure
A;Reference number: A26067; M
A;Accession: A26067
A;Molecule type: mRNA
A;Residues: 1-321 <KIK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 55, 611-618, 1988
A;Title: Two species of human Fc-epsilon receptor A;Reference number: A31924; MUID:89028672
A;Accession: A31924
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EMBO J. 6, 109-114, 1987
A:Title: Cloning and expression of the cDNA coding
A:Reference number: A26164; MUID:87218454
A:Accession: A26164
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A; Cross-references: GB:M23562; NID:g182444
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A;Note: the codon given for 269-Asn (ACC) is inconsistent with the authors' translation A;Note: part of this sequence, including the amino end of soluble forms of the protein, R;Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Yode, C. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987
A;Title: Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with A;Reference number: A26589; MUID:87118255
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A: Residues: 1-7,'D',47-50 <MAS1>
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A;Accession: S39442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 157-284 <SUT>
A; Cross-references: GB: X06049; NID: g31316
A; Note: all exon sequences were determined
A; Note: all exon sequences were determined
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A; Cross-references: GB:M14766; NID:g182449; PIDN:AAA52435.1; F
A; Experimental source: EBV-transformed B lymphoblastoid cells
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A;Residues: 1-268,'T'
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lectin, galactose/N-acetylgalactosamine-specific c;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 C;Accession: JX0209; pX0009
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JX0209
lectin,
A;Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T. J. Biochem. 104, 600-605, 1988
                                                                                                  A; Molecule type: mRNA
A; Residues: 1-304 <SAT>
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F:163-282/Domain: C-type lectin homology <LCH>
F:63-81/Binding site: carbohydrate (Asn) (covalent) #status predicted F:147-148/Cleavage site: Lys-Leu (unidentified proteinase) #status exp F:149-150/Cleavage site: Arg-Met (unidentified proteinase) #status exp F:191-282,259-273/Disulfide bonds: #status experimental
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C; Superfamily: IgE receptor II; C-type lectin homology
C; Superfamily: IgE receptor II; G-type lectin homology
C; Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macr
F; MNPPSQD', 47-321/Product: IgE Fc receptor II, splice form b' #status predicted <SFB
F; MNPPSQD', 8-321/Product: IgE Fc receptor II, splice form b #status predicted <SFB>
F;1-321/Product: IgE Fc receptor II, splice form a #status predicted <SFB>
F;1-23/Domain: intracellular #status predicted <INT>
F;1-7, 'D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted <SFAI>
F;14-20/Region: stop-transfer sequence
F;22-45/Domain: transmembrane #status predicted <TMM>
F;46-321/Domain: extracellular #status predicted <TMM>
F;46-321/Domain: extracellular #status predicted <TMM>
F;46-321/Product: soluble IgE-binding factor (37K) #status predicted <IGE>
F;85-105/Region: 21-residue repeat
F:10-321/Product: soluble IgE-binding factor (37K) #status predicted <IGE>
                                                                                                                                                                  A; Accession: JX0209
                                                                                                                                                                                          A; Title: Molecular cloning and expression A; Reference number: JX0209; MUID:92268032
                                                                                                                                                                                                                                                       R;Sato, M.; Kawakami, K.; Osawa
J. Biochem. 111, 331-336, 1992
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C;Comment: T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Brookhaven Protein Data Bank, June 1993 A; Reference number: A51791; PDB:lHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Bajorath,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYFGKGTKQWVHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGS--WIGLRNLDLKGEF 232
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Pred. No. 1e-07;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                         Toyoshima,
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by proteolytic cleavage of IgE
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characterization

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lectin-like

molecule specific

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A; Reference number: PX0009; MUID: 0717/0002

A; Accession: PX0009

A; Molecule type: protein
A; Residues: 102-120;137,'x',139-151 <ODA>
C; Superfamily: hepatic lectin; C-type lectin homology
C; Keywords: 9lycoprotein; lectin; macrophage; transmembrane protein
F; 36-61/Domain: transmembrane #status predicted <TRA>
F; 173-296/Domain: C-type lectin homology <LCH>
- 74 166/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: hepatic lectin H2a
N;Contains: ASGPR; asialoglycoprotein receptor H2a; asialoglycoprotein recept
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 10-Dec-1999
C;Accession: A25179; A39100; B39100; I37995; A49466; B49466; S14525
R;Spiess, M.; Lodish, H.F.
R;Spiess, M.; Lodish, H.F.
R:Yuk, M.H.; Lodish, H.F.
J. Cell Biol. 123, 1735-1749, 1993
A:Title: Two pathways for the degradation
A:Reference number: A49466; MUID:94103329
A:Accession: A49466
A:Molecule type: protein
A;Residues: 78-98 <YUK>
                                                                                                                                                                            R; Paietta, E; Stockert, R.J.; Racevskis, J.
Hepatology 15, 395-402, 1992
A; Title: Differences in the abundance of variably spliced
A; Reference number: I37995; MUID: 92184202
A; Accession: I37995
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-23,43-81,87-311 <PAID
A; Residues: 1-23,43-81,87-311 <PAID
                                                                                                                                                                                                                                                                                                                                                             A;Accession: B39100
A;Molecule type: DNA; mRNA
A;Residues: 69-81.87-99 <LE2>
A;Cross-references: GB:M38420; NID:g184395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A39100;
A; Accession: A39100
A; Molecule type: DNA; mRNA
A; Residues: 69-99 <LED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M11025; NID:g179080; R;Lederkremer, G.Z.; Lodish, H.F. J. Biol. Chem. 266, 1237-1244, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 82, 6465-6469, 1985
A;Title: Sequence of a second human asialoglycoprotein receptor: conservation A;Reference number: A25179; MUID:86016723
A;Accession: A25179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-311 <SPI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WTEHEGSCYWFSESEKSWPEADKYCRLENSHLVVVNSLEEQNFLQNRL--ANVVSWIGLT 234
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A; Note: Some or all of the cysteines are involved in disulfide bonds A; Note: residues 24-48 form an uncharged, hydrophobic region that may int R; Mellow, T.E.; Halberg, D.; Drickamer, K.

J. Biol. Chem. 263, 5468-5473, 1998

A; Title: Endocytosis of N-acetylglucosamine-containing glycoproteins by 1 A; Reference number: A28194; MUID:88186849

A; Molecule type: mRNA
A; Residues: 1-207 <MEL>
A; Residues: 1-207 <MEL>
A; Cross-references: GB.J03188; NID:g212246; PIDN:AAAA8937.1; PID:g212247
A; Cross-references: GB.J03188; NID:g212246; PIDN:AAA8937.1; PID:g212247
A; Cr
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A;Gene: GDB:ASGR2; L-H2
A;Cross-references: GDB:11875; OMIM:108361
A;Map position: 17p13-17p11
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: alternative splicing; endocytosis; glycoprotein; lectin; liver; phosphopr
F;1-311/Product: asialoglycoprotein receptor H2a #status predicted <MAT2>
F;1-81,87-311/Product: asialoglycoprotein receptor H2b #status predicted <MAT2>
F;1-58/Domain: intracellular #status predicted <INT>
F;1-23,43-81,87-311/Product: asialoglycoprotein receptor H2c #status predicted <MAT3>
F;59-78/Domain: transmembrane #status predicted <TMM>
F;59-311/Domain: extracellular #status predicted <EXT>
F;177-300/Domain: c-type lectin homology <LCH>
F;177-305/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                      and endocytosis. C; Genetics:
                                                                                                                                                                        A;Cross-references: GB:M63225; GB:M63226; GB:M63227; GB:M63228; GB:M63229; GB:M63230; C;Comment: Hepatic lectin is a membrane receptor protein that recognizes and binds ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-207 < DRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 256, 5827-5839, 1981
A;Title: Complete amino acid sequen
A;Reference number: A03167; MUID:81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatic lectin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 22-Jun-1999
C;Accession: A03167; A28194; A40427
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A;Molecule type: protein
A;Residues: 87-98 <YU2>
C;Comment: The functioning ligand-binding unit of this receptor is thought to be C;Genetics:
                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-207 <BEZ>
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A;Reference number: A48925; MUID:93043353
A;Accession: A48925
A;Accession: A48925
A;Status: not compared with conceptual translation
A;Residues: 1-1455 <HAR>
A;Residues: 1-1455 <HAR>
A;Residues: 1-1455 <HAR>
A;Rote: sequence extracted from NCBI backbone (NCBIP:118733)
R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.B
                                                                                                                                                                                   mannose receptor precursor, macrophage - mouse (:Species: Mus musculus (house mouse) (:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (:Accession: A48925; S21320; Pc2245 R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.A. Blood 80, 2363-2373, 1992 A;Title: Characterization of the murine macrophage mannose receptor: demonstration that
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1479 <MUK>
A;Residues: 1-1479 <MUK>
A;Cross-references: EMBL:U56734; NID:g1336073; PID:g1336074; PIDN:AAC52729.1
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin
C;Keywords: membrane protein; receptor
C;Keywords: membrane protein; receptor
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J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the rate characterization of a novel member of the rate characterization of a novel member 22235; MUID:96355501
A;Reference number: 22235; MUID:96355501
A;Recession: T42710
A;Status: preliminary; translated from GB/EMBL/DDBJ
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N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculius (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
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Pred. No. 2.3e-06;
4; Mismatches 47
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                                                                                                                                                                                        21.5%;
28.1%;
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A;Cross-references: EMBL:x53042; NID:g53104; PIDN:CAAC;Superfamily: hepatic lectin; C-type lectin homology C;Keywords: glycoprotein; liver; transmembrane proteir;170-293/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                              R;Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990
A;Title: Mouse asialoglycoprotein receptor
A;Reference number: S13165; MUID:91027942
A;Accession: S13165
                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: hepatic lectin
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S13165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A: Map position: 2

C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin C:Keywords: membrane protein; receptor

F:168-209/Domain: fibronectin type II repeat homology <2F9>
F:361-455/Domain: C-type lectin homology <LCHI>
F:361-455/Domain: C-type lectin homology <LCHI>
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A;Title: The exon-intron structure and chromosomal localization
A;Reference number: PC2245; MUID:94128116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-302, 'W', 303-1117, 'E', 1119-1455 <HA2>
A; Cross-references: EMBL: Z11974; NII: 952997; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, April 1992 A;Description: Characterization of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              962 NEEKKSWQDARQACKGLKGNLVSIENAQEQAFVTYHMRDSTFNAWTGLNDINAEHMFLWT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 WYGTNKSLTEEAENWGDGEPNNKKNK-----EDCVEIYIKRNKDAGKWNDDACHKLKAAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGG----IWT 61
YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NWGKGYPGGRRSSLSYEDADCVVVIGGNSREAGTWMDDTCDSKQGYI 1076
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                                                      22;
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                                                 Score 143.5; DB 2;
Pred. No. 1.2e-06;
2; Mismatches 50;
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Pred. No. 5.
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5.7e-06;
51;
                                                                                                                                                                                                                                                     PIDN:CAA37211.1; PID:g53105
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ts, M.; Raspberry, D.; Eichbaum,
                                                                                                                                                                                                 protein
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                                                    Indels
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-KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAAL: | | | | | | | : : : :

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IgE Fc receptor II, low-affinity - rat
N;Alternate names: CD23; lymphocyte IgE receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
C;Accession: S34198
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S34198
IGE FC
                                                                                                   A;Cross-references: GB:M34163; NID:g193242; PIDN:AAA37603.1; PID:g309227 R;Bettler, B.; Hofstetter, H.; Rao, M.; Yokoyama, W.M.; Kilchherr, F.; Cl Proc. Natl. Acad. Sci. U.S.A. 86, 7566-7570, 1989 A;Title: Molecular structure and expression of the murine lymphocyte low A;Reference number: A33840; MUID:90017519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IgE Fc receptor, low-affinity - mouse
N;Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IgE
C;Species: Mus muscullus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 28-Oct-1994 #text_change
C;Accession: A43518; A33840
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F;24-46/Domain: transmembrane #status predicted <TMM>
F;47-309/Domain: extracellular #status predicted <EXT>
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                                                                       A; Accession: A33840
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A; Residues: 1-331 <GOL>
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                                                                                                                                                                                                                                                                                                                                                                             A; Title: Isolation, characterization, and A; Reference number: A43518; MUID: 90171598
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J. Immunol. 144, 1974-1982, 19
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A; Accession: S34198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 e, M.L.; Yamashita, L.C.;
1990
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Pred. No. 1.5
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                                                                                                                                                                                                          Conrad,
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                                                                                                                                                                                                              D.H.
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A; Accession: A26888
A; MOID:87257885
A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: I-152, 'A', 154-201, 'I', 203-259, 'C', 261-301 < MGP> A; Residues: I-152, 'A', 154-201, 'I', 203-259, 'C', 261-301 < MGP> A; Cross-references: GB:M16347; NID:g206648; PIDN:AAA42038.1; A; Note: the authors translated the codon GCA for residue 153 R; PICA A; MARCHAR A; MA
                                                                                                                                                                                                                                                                                                                                                                          R;McPhaul, M.; Berg, Mol. Cell Biol. 7, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Asialoglycoprotein A;Reference number: A31601; A;Accession: A31601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-301 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNRT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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F;47-331/Domain: extracellular #status pr
F;66-86/Region: 21-residue repeat
F;87-107/Region: 21-residue repeat
F;108-128/Region: 21-residue repeat
F;129-149/Region: 21-residue repeat
F;186-305/Domain: C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: IgE receptor II; C-type lectin homolo C;Keywords: B-cell; glycoprotein; immunoglobulin rec F;1-25/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                           F;65,114/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                        F;14-22/Region: stop-transfer sequence F;26-46/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Comment: This f B-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M99371; NID:g193245; C;Comment: This receptor for the Fc portion
                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 37; Conserv
303
                                  115
                                                                      256 VWSDGSPVGYS---
                                                                                                                                            198
                                                                                                        61
                                                                                                                                                                              ω
WVC
                                  ALC
                                                                                           TW-----VGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHK-LKA 114
                                                                                                                                            YYFGKGSKQWIQARFACSDLQGRLVSIHSQKEQDFLMQHI--NKKDSWIGLQDLNMEGEF
                                                                                                                                                                 117
305
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                           carbohydrate
                                                                                                                                                                                                                                   21.2%;
                                                                    -NWNPGEPNNGGQGEDCVMM-----RGSGQWNDAFCRSYLDA
                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                     Score 141.5; DB Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -type lectin homology
immunoglobulin receptor;
                                                                                                                                                                                                                                                                                                         (Asn) (covalent) #status
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                                                                                                              <LCH>
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                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                       <EXT>
                                                                                                                                                                                                                  40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage;
                                                                                                                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                  Gaps
                                                                      302
                                                                                                                                            255
                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tandem
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                                                                                                                                                                                                                    6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat;
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1988 #sequence_revision 09-Apr-1998 #text_change
C:Accession: B28462; A28462; A31801; A26888; A25417 A;Molecule type: protein A;Residues: 88-96,'X',98-118,'X',120;129-158;177-182,'X',184,'X',186-189;192-290,'C' R;Sanford, J.P.; Elliott, R.W.; Doyle, D. DNA 7, 721-728, 1988 R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb J. Biol. Chem. 262, 9828-9838, 1987
A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are indep A;Reference number: A28462; MUID:87250656 A; Accession: A28462 A; Cross-references: A; Molecule type: mRNA A; Residues: 1-301 <HA A; Reference number: A28462; N;Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3) A; Accession: B28462 hepatic lectin 1-301 <HAL> GB:J02762; NID: g205162; PIDN:AAA41522.1; PID:g205163 22-Jun-1999

1841-1847, 1987

of. CDNA

clones

encoding two

homologous

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NID: g57066;

PIDN:CAA30476.1;

PID:957067

asialoglycoprotein

receptor:

PID:g206649 as Arg and

ATT

for

resid

receptor genes MUID:89170119

are linked

9

chromosome

11

'n

the

mouse

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C;Genetics:
A;Gene: src1-I
C;Keywords: colled coll; glycoprotein; transmembrane protein
F;10-19/Region: internalization signal YKRF
F;40-56/Domain: transmembrane #status predicted <TMM>
F;57-112/Domain: extracellular #status predicted <COC>
F;113-335/Domain: colled coll #status predicted <COC>
F;369-384/Region: serine/threonine-rich #status predicted
F;443-589/Domain: collagen-like #status predicted <COL>
F;607-732/Domain: collagen-like #status predicted <COL>
                                                                           QΥ
                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-742 < NAK>
A; Cross-references: DDBJ:AB038518
C; Comment: This receptor, a membe:
important role in host defense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Nakamura, K.; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T. Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001
A; Title: Molecular cloning and functional characterization of a human scavenger receptor A; Reference number: JC7595; MUID:21092718; PMID:11162630
A; Contents: Placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scavenger receptor with C-type lectin type I - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A25417
A;Molecule type: protein
C;Comment: Calcium is required for ligand binding.
C;Comment: Calcium is required for ligand binding.
C;Comment: Calcium is required for ligand binding.
C;Comment: Calcium is required for lectin; liver; receptor; transmembrane protein
F;2-60,Domain: intracellular #status predicted <INT>
F;61-77,Domain: catracellular #status predicted <EXT>
F;170-293,Domain: C-type lectin homology <LCH>
F;170-293,Domain: C-type lectin homology <LCH>
F;77,119,165,Mainding site: carbohydrate (Asn) (covalent) #status predicted
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JC7595
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Best Local S
Matches 34
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Best Local
                      678 KWLDGT----SPDYKNWKAGQPDNWGHGHGPGEDCAGLIY---
                                                                                                                                    619
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                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 YWFSRDGLTWAEADQYCQMENAHLLVINSREEQEFVVKHR--GAFHIWIGLTDKDGSWKW
                                                                                                                                                                                                                                            Local Similarity
nes 34; Conser
                                                                                                                                                                        3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGI--RKIGGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 V-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW
                                                                      TWV-GTNKSLTEEAENWGDGEPNNKKN----KEDCVEIYIKRNKDAGKWNDDACHKLKAA 115
                                                                                                                           YYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQM-VGRESHWIGLTDSERENEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor, a member of the scavenger receptor family, belonging to the ty in host defense. It forms a timer and plays a role in recognizing infect
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                               20.5%;
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                                                                                                                                                                                                                                      Score 136.5;
Pred. No. 1.5e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 140.5; DB 1;
Pred. No. 2.3e-06;
"""matches 53;
                                                                                                                                                                                                                                                                  1.5e-05;
                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ane protein predicted .
                      AGQWNDFQCEDVNNF
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                       domain #status
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                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                      6;
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                                                                                                                                                                                                                                                                                                                                                                       <CRD>
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A;Cross-references: GB:J03734; NID:g205050; PIDN:AAA41472.1; C;Superfamily: C-type lectin homology C;Keywords: transmembrane protein C;Keywords: transmembrane protein F;412-536/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-550 < HGD>
A;Residues: 1-550 < HGD>
A;Residues: 1-550 < HGD>
A;Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363
A;Cross-references: GB:M55532; NID:g203362; PIDN:AAA40892.1; PID:g203363
B;Hoyle, G.W.; Hill, R.L.
J. Biol. Chem. 263, 7487-7492, 1988
A;Hoyle, G.W.; Hill, R.L.

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A; Residues: 1-550 <HOY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Ii, M.; Kurata, H.; Itoh, N.; Yamashina, I.; Kawasaki, T.
J. Biol. Chem. 265, 11295-11296, 11990
A;Title: Molecular cloning and sequence analysis of cDNA encoding the macrophage lect
A;Reference number: A42230; MUID:90293078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lectin M-ASGP-BP precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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A; Residues: 1-306 <IIA>
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           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WESQSGKPWPEADKYCQLENSNLVVVNSLAEQNFLQTHM--GSVVTWIGLTDQNGPWRW 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDGTDYEKGFT----HWAPKQPDNWYGHGLGGGEDCAHF----TSDGRWNDDVCQRPYR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IC.
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19.8%; Score 132; DB 2; 28.9%; Pred. No. 3.1e-05;
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Pred. No. 1.2e-05;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-Sep-1989 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           for a carbohydrate binding recept
                                       Length 550
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Conservative

21;

Mismatches

Indels

16;

6

60

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RESULT 32
S78774
perlucin - Haliotis 1
C;Species: Haliotis 1
C;Date: 04-Feb-2000 #
C;Accession: S78774
R;Mann, K.
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                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D13517; NID:g220480; PIDN:BA:C;Superfamily: hepatic lectin; C-type lectin homology C;Keywords: glycoprotein; transmembrane protein F;153-276/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-284 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asialoglycoprotein receptor 1 - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision C;Accession: S29855
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                                                                                 밁
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Matches 33
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wa, R.; Shinzawa, K.; Watanabe, Y.; Akaike, T. Biophys. Acta 1172, 220-222, 1993
Determination of mouse major asialoglycoprotein nce number: S29855; MUID:93176818
                                                                                                                                        YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTL-PFSRSYYWIGIRKIGGIWT 61
                                                                                 YWFSSSVRPWTEADKYCQLENAHLVVVTSRDEQNFLQRHMGPLNT---WIGLTDQNGPWK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKPSHFIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YWFSTIKSSFAEAAGYCRYLESHLAIISNKDEDSFI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWVDGTPFDYVQSRRFWRKGQPDNWRHGNGEREDCV--HLQR-----MWNDMAC
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laevigata
#sequence_revision 04-Feb-2000 #text_change
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                                                                                                                                                                                                      Score 129.5;
Pred. No. 2.66
Pred. Mismatches
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Pred.
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                                                                                                                                                                                            2.6e-05;
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:BAA02734.1;
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                                                                                                                                                                                                                                                                    284;
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A; ACCESSACH.
A; MOLECULE type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2, 'L', 4-14, 'A', 16-244 <SAS2>
A; Residues: 1-2, 'L', 4-14, 'A', 16-244 <SAS2>
A; Residues: 1-2, 'L', 4-14, 'A', 16-244 <SAS2>
A; Cross-references: GB:S42294; NID:9233017; pIDN:AAB19343.1; pID:9233018
A; Cross-references: GB:S42294; NID:92 A; PIDN:AAB19343.1; pID:9233018
A; Experimental source: inbred CBA/J, acute phase liver library, pTZ 19 ve
A; Note: sequence extracted from NCBI backbone (NCBIN:42294, NCBIP:42295)
A; Note: sequence extracted from NCBI backbone (NCBIN:42294, NCBIP:42295)
A; Note: sequence extracted from NCBI backbone (NCBIN:42294, NCBIP:42295)
A; Note: sequence extracted from NCBI backbone (NCBIN:42294, NCBIP:42295)
A; Title: CDNAs and deduced amino acid sequences of subunits in the bindiparticles of subunits in the
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R;Sastry, K.; Zahedi, K.; Lelias, J.M.; Whitehead, J. Immunol. 147, 692-697, 1991
A;Title: Molecular characterization of the mouse ma A;Reference number: A46466; MUID:91302823

mannose-binding

proteins.

The

mannos

binding

component

vector

T.; Mamiya, G

A;Cross-references: EMBL:U09016; NID:g773286; PIDN:AAA82010.1; PID:g773288 R;Sastry, K.; Zahedi, K.; Lelias, J.M.; Whitehead, A.S.; Ezekowitz, R.A.

A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-244 <SAS1>

A;Title: Characterization of murine mannose-binding A;Reference number: I48650; MUID:95284466 A;Accession: I48651

from

GB/EMBL/DDB:

protein genes

Mbl1 and Mbl2 revea

A; Accession: B46466

```
mannose-binding lectin C precursor - mouse
M;Alternate names: Ra-reactive factor P28a
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 20-Feb-1998 #text_change 16-Jun-2000
C;Accession: I48651; B46466; A42574; C42574
R;Sastry, R.; Wang, J.S.; Brown, D.C.; Ezekowitz, R.A.; Tauber, A.I.; Sastry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-374 <SHI>
A; Cross-references: GB:M81231; NID:g207035; PID
A; Experimental source: lung
A; Note: sequence extracted from NCBI backbone (C; Superfamily: pulmonary surfactant protein D; F; 253-372/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Shimizu, H.; Fisher, J.H.; Papst, P.; Bens J. Biol. Chem. 267, 1853-1857, 1992
A;Title: Primary structure of rat pulmonary A;Reference number: A42046; MUID:92112913
A;Accession: A42046
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surfactant protein D - rat
C;Species: Rattus norvegicus (Norway ra
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: A42046
R;Shimizu, H.; Fisher, J.H.; Papst, P.;
R; Sastry, R.; Wang, J.S.; Brow
Mamm. Genome 6, 103-110, 1995
                                                                                                                                                                                                                                    밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                  269
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                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                PTGEALV--YSNWAPGEPNNNGGAENCVEIFTN----GQWNDKACGEQRLVIC
                                                                                                                                                                                                                                                                         GTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                  SEEP--FEDAKEMCRQAGGQLASPRSATENAAVQQLVTAHSKAAFLSMTDVGTEGKFTY-
                                                                                                                                                                                                                                                                                                                                                    SEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIWTWV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVDGTD--YETGFQNWRPEQPDNWYGHGLGGGEDCAHF----TTDGRWNDDVCRRPYRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WV-GTNKSLTEEAENWGDGEPNN-----KKNKEDCVEIYIKRNKDAGKWNDDACHKLKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein D - rat
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%;
                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 125; DB 1; Pred. No. 9.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benson, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN: AAA42170.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surfactant protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NCBIN: 76027,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lau, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                     Tauber, A.I.; Sastry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g207036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mason, R.J.; Voelker,
                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA and deduced
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A; Molecule type: protein
A; Residues: 25-162 < MUR>
A; Residues: 25-162 < MUR>
A; Note: 116-Arg was also found
C; Comment: This three galactose-binding lectin is isolated from the coelomic fluid.
C; Comment: This protein plays important roles in defense mechanisms and in development
C; Comment: The molecule is a tetramer of identical chains.
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: hemolymph; homotetramer; lectin
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-162/Product: lectin BRA3-2 #status experimental <MAT>
F; 26-19/Domain: C-type lectin homology <LCH>
F; 26-39, 56-150, 125-142/Disulfide bonds: #status experimental
F; 16-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-31, 56-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Residues: 1-162 <TAK>
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-;
A;Title: The amino-acid sequence
A;Reference number: A26094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure ar
A;Reference number: JC1503; MUID:93292994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 31-Dec-1988 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999 C;Accession: JC1504; A26094 R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lectin BRA3-2 precursor - barnacle (Megabalanus rosa) C;Species: Megabalanus rosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;38-94/Region: collagen-like
F;124-240/Domain: C-type lectin homology <LCH>
F;29,34/Disulfide bonds: interchain #status predicted
F;69/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 59/1; 98/1; 121/1
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: calcium; endoplasmic reticulum; Golgi apparatus; homohexar
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-244/Product: mannose-binding lectin C #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note:
C; Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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A; Molecule type: mRNA; protein
A; Molecule type: mRNA; Protein
A; Residues: 1-244 < KUG>
A; Cross-references: GB:D11440; NID:g220585; PIDN:BAA02005.1; PID:g220586
A; Experimental source: BALB/c, liver
A; Note: sequence extracted from NCBI backbone (NCBIP:110137)
A; Note: parts of the sequence, including the amino end of the mature pro
A; Accession: C42574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: Mb12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 19,'X',21-28
           √Best
                                             Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SVKKMSLDRVKALCSEFQGSVATPRNAEENSAIQKV--
               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VGTNKSLTEEAENWGDGEPNNKKNKEDCVETYIKRNKDAGKWNDDACHKLKAALC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A26094
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                                                                                                                                                         bonds: interchain (to 160) bonds: interchain (to 157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
       18.3%;
30.6%;
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sence of a
       Score
Pred.
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Pred. No. 8.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lectin
   122; DB 1;
No. 7.9e-05;
                                                                                                                                                 #status experimental
#status experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the acorn barnacle Megabalanus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AKDIAYLGITDVRVEGSFEDL
                                                                                                                                                         experimental
                                                                                                                                                                                       experimental
                                      Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.; Kamiya, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydroxyproline
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γQ
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Matches

Similarity

18.2%; 27.6%;

Score 121; DE Pred. No. 0.00 24; Mismatches

DB 2;

Indels

12;

Gaps

6,

54

Conservative

WTYHYSEKPMNWQRARRFCRD-NYTDLVAIQNKAEIEYLEKTLPFS---RSYYWIGIR--

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A;Cross references: EMBL:LO7512; NID:g393208; PIDN:AAA41533.1; PID: C;Comment: This protein is found in pancreatic calculi of mammals. rotein into an insoluble protein at a neutral pH of 5.5 to 7.5. C;Genetics:
A;Introns: 21/1; 60/3; 106/3; 144/1
C;Superfamily: tetranectin; C-type lectin homology
                                                                                                         C;Superfamily: tetranectin; C-type lectin homology C;Keywords: pyroglutamic acid F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L. Biochim. Biophys. Acta 1174, 99-102, 1993
A;Title: Rapid PCR cloning and sequence determination of the A;Reference number: S34618; MUID:93326645
A;Accession: S34618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463 R;Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M. Comp. Biochem. Physiol. B 93, 793-797, 1989
A;Title: Characterization in rat pancreatic juice of a protein homologous to the huma; Reference number: PL0147; MUID:90031455
               F;22/Modified site:
                                       F;35-161/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-165 < DUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M18962; NID:g206604; R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Biol. Chem. 266, 786-791, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #sequence_r
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A28351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: 'Rat pancreatic stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-165 <TER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: A novel gene activated in regenerating islets A; Reference number: A92704; MUID:88115343
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on 31-Mar-1990 #text_change
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acid (Gln) (in
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A; Molecule type: mRNA
A; Residues: 1-2124 <DOE>
R; Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Noege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Noege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; J. Biol. Chem. 261, 8108-8111, 1986
A; Title: Partial cDNA sequence encoding a globular don A; Reference number: A23835; MUID:86250698
A; Accession: A23835
                                                                                                                                                                                                                                                                                                                                                              F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;2041-2097/Domain: complement factor H repeat homology <FHD>
F;2041-2097/Domain: complement factor H repeat homology <FHD>
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A;Residues: 1856-2124 <CDO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
A;Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
J. Biol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term A;Reference number: A28453; MUID:88087071
A;Accession: A28453
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A; Residues: 20-37, 'W', 39-60, 'E', 62-64, 'X', 66-69; 70-83; 84, 89-148, 'L', 150-238, 'S', 240, 'A'
C; Superfamily: aggreen; C-type lectin homology; complement factor H repeat homology; E
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A;Title: Complete primary structure of the rat cartilage proteoglycan core protein
A:Reference number: A92623; MUID:88087070
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N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
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Best Local
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                                                     54 -RKIGGIWTWVGTNKSLTEEAENWGDGEPNN-KKNKEDC-VEIYIKRNKDAGKWNDDACH 110
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                                                                                                                                                                    1 WT-----YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGI- 53
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  DRTIEGDFRW-SDGHSL--QFEKWRPNQPDNFFATGEDCVVMIWHER---
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                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                     18.2%;
                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                             Score 121; DB 2;
Pred. No. 0.0016;
7; Mismatches 45
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                                                                                                                                                                                                                                45; Indels
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C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; C;Keywords: cartilage; extracellular matrix
E;1-19/Domain: signal sequence #status predicted <SIG>E;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: immunoglobulin homology <IMK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;268-349/Domain: link protein repeat homology <LNK3>
F;504-581/Domain: link protein repeat homology <LNK4>
F;504-581/Domain: link protein repeat homology <LNK4>
F;1922-2042/Domain: C-type lectin homology <LOHS
F;2049-2105/Domain: complement factor H repeat homology <FHD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-567, 'G', 569-1728, 'I', 1730-2132 <WAT1>A; Cross-references: GB:U22901; NID:9886014 R; Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, l Biochim. Biophys. Acta 1219, 613-622, 1994 A; Title: Analysis of aggrecan and tenascin gene exp. A; Reference number: S50206; MUID:95035091 A; Accession: S50207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-2132 <WAL>
A;Residues: 1-2132 <WAL>
A;Cross-references: GB:L07049; NID:g678541; PIDN:AAC37670.1; PID:g191772
R;Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
Biochem. J. 308, 433-440, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA A;Rolecule type: DNA A;Rolecule type: DNA A;Residues: 211-240,'MCTASLRRWRVRSFMRHPQRNSPSRRQPTS','AGGWGHAWPPQASSTWPGRAVWTCAALAGW'A;Cross-references: GB:S73720; NID:g765211; PIDN:AAB32159.1; PID:g765212
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A; Residues: 350-383, 'CPWMSQRERPWAA'
A; Cross-references: EMBL:x80279
R; Watanabe, H.; Kinata, K.; Line, S.
Nature Genet. 7, 154-157, 1994
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A;Station: S55329
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A55182; S5529; S50207; S51355; I78532; I58123
R;Walcz, E; Deak, F; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, Genomics 22, 364-371, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:S73722; NID:g765215; PIDN:AAB32160.1; PID:g765216
A;Accession: I58123
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A; Residues: 350-481, 'R', 483-506 <GLUl>
A; Cross_references: EMBL: X80279; NID: g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 253/1
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A; Residues: 211-326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <GLU2>
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YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGI53

Query Match Best Local : Matches 3

Similarity

18.2%;

Score 121; Pred. No. 0.

DB 1;

Length 2132; ; Indels 2

20;

Gaps

8

17;

Mismatches

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A, Excludes: 1-0, K, 702-240 NOW.

A, Experimental source: clone 22; clone 1

A, Accession: B94020

A; Molecule type: mRNA

A, Residues: 92-804 (RO2>
A; Molecule type: mRNA

A, Residues: 92-804 (RO2>
A; Note: clone 22 codes for a terminator at residue 210

R; Matts, C.

Biosci. Rep. 6, 527-534, 1986

A, Title: Isolation and expression of cDNA clones for a rat liver asialoglycoprotein rece
A; Matts, C.

Biosci. Rep. 6, 527-534, 1986

A; Matts isolation and expression of cDNA clones for a rat liver asialoglycoprotein rece
A; Matts, C.

Biosci. Rep. 6, 527-534, 1986

A; Matts isolation and expression of cDNA clones for a rat liver asialoglycoprotein rece
A; Matts, C.

Biosci. Rep. 6, 527-534, 1986

A; Molecule type: mRNA

A; Reference number: A54727; MUID:87026895

A; Molecule type: mRNA

A; Residues: 12-284 (WAT>
A; Cross references: GB:M21770; NID:9202985; PIDN:AAA40764.1; PID:9202988

A; Molecule type: mRNA

A; Residues: 12-284 (WAT>

A; Cross references: GB:M21770; NID:9202985; PIDN:AAA40764.1; PID:9202988

A; Molecule type: mRNA

A; Residues: 12-284 (WAT>

A; Cross references: GB:M21770; NID:9202985; PIDN:AAA40764.1; PID:9202988

A; Molecule type: mRNA

A; Residues: 12-284 (WAT>

A; Molecule type: mRNA

A; Residues: 12-284 (WAT>

A; Molecule type: mRNA

A; Residues: 12-284

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N;Alternate names: ASGP; asialoglycoprotein receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1986 #sequence_revision 04-Dec-1986 #text_change 22-Jun-1999
C;Accession: A92497; A94020; B94020; A54727; A03166
R;Leung, J.O.; Holland, E.C.; Drickamer, K.
J. Biol. Chem. 260, 12523-12527, 1985
A;Title: Characterization of the gene encoding the major rat liver asialog1:
A;Reference number: A92497; MUID:86008335
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Proc. Natl. Acad. Sci. U.S.A. 81, 7338-7342, 19
A;Title: Rat liver asialoglycoprotein receptor
A;Reference number: A94020; MUID:85063786
A;Accession: A94020
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A; Residues: 1-60,'R',62-210 <HOL>
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A; Residues: 1-284 <LEU>
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                                       116 LC
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                                                                                                     WVDGTD--YETGFKNWRPGQPDDWYGHGLGGGEDCAHF----TTDGHWNDDVCRRPYRW
                                                                                                                                                                                                                                              YWFSSSVKPWTEADKYCQLENAHLVVVTSWEEQRFVQQHMGPLNT--
                                                                                                                                                                                                                                                                                                               YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTL-PFSRSYYWIGIRKIGGIWT 61
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                                                                                                                                                                                                                                                                                                                                                                                       32;
                                           117
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Pred. No. 0.0002;
0; Mismatches 53;
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Db 275 VC 276

Search completed: September 7, 2002, 10:15:25 Job time: 203 sec

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                                               11328, Ap
11158, Ap
11158, Ap
22816, A
25139, A
US-10-211-364-1171

Sequence 1171, Application US/10211364

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ16C10, VUMBER: US/10/211,364

CURRENT APPLICATION NUMBER: US/10/211,364

CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 09/760,486
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-32

PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
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Best Local Similarity
Matches 117; Conserv
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	121834,	22813, A	357, App	916, App	23269, A	93873, A	50405, A	111285,	41672, A	14651, A	121836,	44925, A	86038, A	35618, A	22819, A	32024, A	32023, A	32025, A	004047

ALIGNMENTS

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Sequence 53485, Application US/09791537

Sequence 53485, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 53485
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-53485
100.0%; Score 666; DB 5; ilarity 100.0%; Pred. No. 1.8e-64; Conservative 0; Mismatches 0;
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; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any
US-10-212-054-1328
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US-10-212-054-1328
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; NAME/KEY: misc_feature
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-211-364-1171
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                                                                                                            Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PJZ12C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1778
SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                                 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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Pred. No. 2e-64;
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 58446
LENGTH: 363
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Best Local
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Best Local Similarity
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LENGTH: 341
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PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
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NUMBER OF SEQ ID NOS: 1478
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CURRENT FILING DATE: 2002-08-07
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                               Local Similarity
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                    1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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Homo sapiens
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                                                                              Conservative
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                                                                      Score 666; DB 5;
Pred. No. 2.1e-64;
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US-09-791-537-22816
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIA PROTEIN VERSION 3.0
SEQ ID NO 22816
LENGTH: 372
TYPE: PRT
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SEQ ID 4657
LENGTH: 372
TYPE: PRT
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAMILICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                    61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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Local Similarity 100.0%; Pred. No. 2.2e-64;
nes 117; Conservative 0; Mismatches 0;
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TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                            WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 98
                                                                                                                                                        al Similarity
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                                                                                                                                                    Score 666; DB 5;
Pred. No. 2.2e-64;
Pred. No. 2.2e-64;
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RESULT 10
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US-09-791-537-84593
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APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
LENGTH: 372
TYPE: PRT
Sequence 152667, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 117; Conservative (
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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Pred. No. 2.2e-64;
0; Mismatches 0;
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RESULT 12
US-09-791-537-53844
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (11). (11)
; OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-152667
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-791-537-51391
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US-09-791-537-51391
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Sequence 53844, Application US/09791537 GENERAL INFORMATION:
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 51391
LENGTH: 385
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 15305
SOFTWARE: Patentin version 3.0
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APPLICANT:
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Pred. No. 2.3e-64;
0; Mismatches 0;
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                                                                                                          ; Sequence 42659, Appl
; GENERAL INFORMATION;
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 113060
LENGTH: 385
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 53844
LENGTH: 385
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Matches
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TYPE: PRT
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Pred. No. 2.3e-64;
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US-09-791-537-42659
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APPLICANT: Debe, Derek
APPLICANT: METHODS OF USE THEREOF
FILE REFERENCE: 261.210
CURRENT FILING DATE: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEO ID NO 42655
LENGTH: 372
TYPE: PRT
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Best Local Similarity 94.0
Matches 110; Conservative
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 42659
APPLICANT: Bionomix, Inc.
APPLICANT: Dobe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 15305
SOFTWARE: Patentin version 3.0
SEQ ID NO 42658
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Best Local Similarity
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Pred. No. 6e-64;
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Pred. No. 1.4e-60;
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US-09-791-537-50403
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US-09-791-537-42658
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNMEER: US/99/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50403
LENGTH: 370
TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOETWARE: PatentIn version 3.0
SEQ ID NO 132144
LENGTH: 376
                                                                                                                                                                                                                                                                               Sequence 50403, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103;
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Best Local Similarity 94.0%;
Matches 110; Conservative
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 132144, Application US/09791537
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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Pred. No. 5.9e-57;
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Pred. No. 1.4e-60;
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; ORGANISM: Mus musculus US-09-791-537-37750
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GENERAL INFORMATION:
APPLICANT: Bionomix,
APPLICANT: Debe, De
APPLICANT: Danzer,
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37750
LENGTH: 372
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                        Matches
                                      Query Match
Best Local
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Best Local Similarity 82.9%;
Matches 97; Conservative
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILLOATION NUMBER: US/09/791,537
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                                    Local Similarity
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                        97;
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Debe, Derek
                       Conservative
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                                  84.8%;
82.9%;
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82.9%;
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                     9;
                                 Score 565; DB 5; Pred. No. 2.3e-53;
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Pred. No. 2.3e-53;
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Pred. No. 4.2e-55;
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                                               Length 372;
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; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 81233

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-791-537-81233
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US-09-791-537-6693
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US-09-791-537-6693
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Best Local
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6693
LENGTH: 372
                                                                                                                                                                                                                                                                               APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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Best Local
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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                                                                                      Local Similarity
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1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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                                                                Conservative
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                                                                                    83.6%;
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81.2%;
                                                                11; Mismatches
                                                                               Score 557; DB 5;
Pred. No. 1.8e-52;
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 29989
US-09-791-537-20989
US-09-791-537-20989
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US-09-791-537-20989
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Best Local S
Matches 79
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50409
LENGTH: 769
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Best Local Similarity
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                           102 TWVGTNKTLTEEAENWADNEPNNKKNNQDCVEIYIKSNSAPGKWNDEPCFKRKRALC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 TWVGTKKTLTEEAENWADNEPNNKKNNQDCVEIYIKSPSAPGKWNDEPCGKRKRALC 158
                                                                              61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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                                                                                                                                                                                                                                        68.3%; Score 455; DB 5; 67.5%; Pred. No. 5.7e-41;
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Pred. No. 6e-42;
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US-09-791-537-50404
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US-09-791-537-84829
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 37753
LENGTH: 768
TYPE: DEM
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APPLICANT: Danzer, JOSeph
APPLICANT: Danzer, JOSeph
TITLE OF INVENTION: THESE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 153055
SOFTWARE: PAtentin version 3.0
SEQ ID NO 84829
LENGTH: 646
TYPE: PRT
                                      Sequence 50404, Application GENERAL INFORMATION:
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Best Local :
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Best Local :
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
APPLICANT: Bionomix, APPLICANT: Debe, De
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CURRENT FILING DATE: 2001-02-22
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Local Similarity 67.5%; Pred. No. 5.7e-41;
hes 79; Conservative 10; Mismatches 28
                                                                                                                                                                                                                                             42 WTYHYSNKTYSWNYSRAFCQKYYTDLVAIQNKNEIAYLNETIPYYNSYYWIGIRKINNKW 101
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Pred. No. 1.3e-40;
0; Mismatches 29;
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US-09-791-537-32023 : Sequence 32023, Application US/09791537 ; GENERAL INFORMATION:
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US-09-791-537-32025;
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        APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 66.8%; Score 445; DB 5; JB 8st Local Similarity 65.8%; Pred. No. 5.5e-40; Matches 77; Conservative 11; Mismatches 29;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 50404
CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                     APPLICANT: Bionomix, Inc.
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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Best Local
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TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
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                                                      OF PROTEIN FAMILIES AND FAMILY MEMBI
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RESULT 31
US-09-791-537-22819
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 22819 LENGTH: 830
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32024
LENGTH: 740
                                                   APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
ETILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
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SEQ ID NO 32023
LENGTH: 740
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.8%; Score 445; DB 5; 65.8%; Pred. No. 6.8e-40;
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 35618
LENGTH: 830
TYPE: PRT
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; ORGANISM: Rattus norvegicus 
US-09-791-537-86038
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                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 86038
LENGTH: 768
TYPE: PRT
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Best Local Similarity
Matches 77; Conser
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Best Local
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APPLICANT: Danzer, JOSeph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
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Pred. No. 7.8e-40;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 44925
LENGTH: 551
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LENGTH: 551
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                     Query Match
Best Local
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                CURRENT FILING DATE: 2001-0
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3
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CURRENT FILING DATE: 2001-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                   Similarity
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                 65.2%;
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64.1%; Pred. No. 1
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Score 434; DB 5;
Pred. No. 7.6e-39;
3; Mismatches 30;
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Pred. No. 7.6e-39;
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.5e-39;
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US-09-791-537-41672

Sequence 41672, Application US/09791537

GENERAL INFORMATION:
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; ORGANISM: Canis familiaris
US-09-791-537-14651
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US-09-791-537-14651
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 41672
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Best Local Similarity
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LENGTH: 754
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 15305
SOFTWARE: Patentin version 3.0
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josepl
                                                                                                                                                                                                                                                                                    LENGTH: 482
TYPE: PRT
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                                                            23 WSYSASTETMTFDDASAYCQQRYTHLVAIQNHAEIEYLNSTFNYSASYYWIGIRKINGTW
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les 76; Conserv
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    TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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                                                                                                                                       63.8%; Score 425; DB 5; Length 482; 63.2%; Pred. No. 6.2e-38; tive 13; Mismatches 30; Indels
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65.0%;
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Pred. No. 1.1e-38;
"'ematches 31; Indels
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RESULT 40
US-09-791-537-93873
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US-09-791-537-50405
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US-09-791-537-111285
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 111285
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILLE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 484
TYPE: PRT
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                                                                    83 TWIGTKKALTPEATNWAPGEPNNKQSNEDCVEIYIKRDKDSGKWNDERCSKKKLALC
                                                                                          61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                             23 WSYSASTETMTFDDASAYCQQRYTHLVAIQNHAEIEYLNSTFNYSASYYWIGIRKINGTW 82
                                                                                                                                                                                                                                 Local Similarity nes 74; Conserv
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63.2%;
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Pred. No. 6.3e-38;
13; Mismatches 30
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Sequence 93873, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Bobbe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 251/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 93873
LENGTH: 649
TYPE: PRT
ORGANISH: Oryctolagus cuniculus
US-09-791-537-93873

Query Match
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Result
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Maximum DB seq
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Listing first 45 summaries
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// Cgn2_6/ptodata/2/paa/US084_COMB.pep: *
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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         Gapext 0.5
    1 US-09-758-449-1158
1 US-09-760-443-1328
PCT-US01-26675-3
5 US-09-119-209-2
1 US-09-760-475-2123
PCT-US92-03970-2
PCT-US94-00909-2
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Sequence 1158, Ap
Sequence 1328, Ap
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		903	350	122	19, App	36,	122	2, Appl	e 2, Appl	ω	N	19, A	916,	3226	4238	1908,	1909,	4237, A	4236, A	Sequence	4	equence 4, Appli	467, Ap	9998, A	9326, A	6200, A	10011,	4, Appl	6716, A	5003, A	5823,	w	10	Sequence 523, App	10	equence 2	N	equence 2	

ALIGNMENTS

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; ORGANISM: Homo sapiens PCT-US01-26675-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-760-443-1328
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APPLICANT: Genaissance Pharmaceuticals,
APPLICANT: Anastasio, Alison E
APPLICANT: Bieglecki, Karyn M
      Matches
                    Query Match
Best Local Similarity
                                                                                                                                                    SEQ ID NO 3
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SEQ ID NO 1328
LENGTH: 341
TYPE: PRT
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Best Local
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                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US01/26675
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/228,262
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                             TITLE OF INVENTION: HAPLOTYPES OF THE SELL FILE REFERENCE: SELL MWH1116-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ12
CURRENT APPLICATION NUMBER: US/09/760,443
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2164
                                                                                                                       TYPE: PRT
                                                                                                                                    ENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Kumar, Anant Madan
                                                                                                                                                                                                                                                                                                                            Anastasio, Alison
Bieglecki, Karyn I
Kliem, Stefanie E
      Conservative
                  100.0%;
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Score 666; Db 1;
Pred. No. 1.1e-67;
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Pred. No. 9.4e-68;
); Mismatches 0;
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                              Length 372;
   Indels
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Gaps
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0;
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US-09-119-209-2
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                                                               Query Match
Best Local Similarity
Matches 117; Conserv
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                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-FEB-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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        39
                                                                                                                                                                TOPOLOGY:
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/786149 FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/
FILING DATE: 6-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 10-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 20-Jul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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Amino Acid
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                                                               100.0%; Score 666; DB 15; ilarity 100.0%; Pred. No. 1.1e-67; Conservative 0; Mismatches 0;
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ROSEN, STEVEN D.
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                                                                                                                                                                 Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-760-475-2123
Sequence 2123, Application US/09760475
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
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GENERAL INFORMATION:
APPLICANT: Dana-F
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Best Local Similarity
Matches 117; Conserv
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CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
                                                TELEFAX: (617) 451-031
TELEX: 940675
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03970
FILING DATE: 19920513
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: LEUKOCYT
            SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acid
                                                                                                   REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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AMINO ACID
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Ten Post Office Square
                                                                                 (617) 451-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dana-Farber Cancer Institute, VENTION: LEUKOCYTE-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                                                                                                                                                                                                                             Floppy disk
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Pred. No. 1.1e-67;
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RESULT 7
PCT-US94-00909-2
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                                                                                           Query Match
Best Local
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Best Local Similarity
                                                                         Matches
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                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                    TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-JUL-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1993
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/962,483 FILING DATE: 02-APR-1992
                                                                       / Match 100.0%;
Local Similarity 100.0%;
nes 117; Conservative (
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/700,773 FILING DATE: 15-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-000
 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                   WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                        amino acid
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08-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: US 07/770,608
03-OCT-1991
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29-JUL-1991
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                                                                                                                                                                                                                                                                                                  21-FEB-1989
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                                                                     Score 666; DB 1;
Pred. No. 1.1e-67;
; Mismatches 0;
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                                                                                                      Length
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                                      Best Local Similarity Matches 117; Conserv
                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,483
FILING DATE: 02-APR-1992
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 21-FEB-1989
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Heine, Holliday C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-JUL-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/737,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes STREET: Ten Post Office Square
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                                                                                                                                                                      u: 385 amino acids amino acid
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                                                                                                                                                                                                                                                             (617) 451-0313
                                        Conservative
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                                                      100.0%;
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                                 ; Score 666; DB 4; I; Pred. No. 1.1e-67; O;
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                                                                    Length 385;
                                   Indels
                                   0;
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; MOLECULE TYPE: US-08-340-539-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
APPLICATION DATE: 15-MAY-1991
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                       REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEPHAX: (617) 451-0313
                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 FILING DATE: 21-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US OF FILING DATE: 29-JUL-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 03-OCT-1991 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                            TYPE:
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                               TOPOLOGY:
                                                        LENGTH:
                                                                                                                                                                                        REGISTRATION NUMBER:
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STREET: Ten Post Office Square
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SYSTEM: PC-DOS/MS-DOS
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             protein
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25-JAN-1993
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CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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                                                                                                                                                                Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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APPLICANT: Spertini, Olivier G.
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   112
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                 61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 52
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                                                                                                                                                                                                                                                               TYPE: amino acid
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ZIP: 02109
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les 117; Conserv
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                                                               WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 111
                                                                                                                               al Similarity
117; Conserv
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                                                                                                                                               100.0%;
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100.0%; Pred. No. 1.1e-67;
tive 0; Mismatches 0;
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                                                                                                                             Score 666; DB 8;
Pred. No. 1.1e-67;
Mismatches 0;
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                                   RESULT 13
US-60-230-435-1751
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SEQ ID NO 428
LENGTH: 1078
Sequence 1751, Application US/60230435 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 117; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL000674
CURRENT APPLICATION NUMBER: US/60/212,659
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 879
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TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1078
TYPE: PRT
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                                                                                                                          61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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                                                                                                        TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beasley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/60212659
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                                                                                                                                                                                                                                                 Score 666; DB 26;
Pred. No. 4.1e-67;
); Mismatches 0;
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Pred. No. 4.1e-67;
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                                                                                                                                                                                                                                                                                 Length 1078;
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APPLICANT: Beasley, TITLE OF INVENTION:

ISOLATED HUMAN PROTEASE PROTEINS.

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US-60-169-867-5823
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US-60-160-189-8687
; Sequence 8687, Application US/60160189
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN

APPLICANT: HONAZZI, VIVIEN

TOLLATED HUMAN DR
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; NAME/KEY: VARIANT
; LOCATION: (1)...(119)
; OTHER INFORMATION: Xaa = Any
US-60-160-189-8687
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Sequence 5823, Application US/60169867
GENERAL INFORMATION:
APPLICANT: BONGZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: HUMAN US-60-230-435-1751
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SOFTWARE: FastSEQ for
SEQ ID NO 1751
LENGTH: 1078
TYPE: PRT
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Best Local Similarity
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LENGTH: 119
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Best Local Similarity
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CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 10162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-09-06
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TITLE OF INVENTION:
FILE REFERENCE: CLO
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                                                                                                                                                                                                                             61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                    1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                          TWVGTNKSLTEEAENWGDGEPNNKKTKEDCVEIYIXRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                              WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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98.3%;
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Pred. No. 6e-67;
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Pred. No. 4.1e-67;
; Mismatches 0;
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                                     TARGET PROTEINS
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(119)
; OTHER INFORMATION: Xaa
US-60-169-867-5823
US-60-169-840-6716
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; NAME/KEY: VARIANT
; LOCATION: (1)...(119)
; OTHER INFORMATION: Xaa
US-60-160-203-5003
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CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 6374
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5003
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5003, Application US/60160203
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING F
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000116
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Best Local Similarity
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Best Local Similarity
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SEQ ID NO 5823
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CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 8230
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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ORGANISM: Human
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                                                                            TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                          WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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94.9%;
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98.3%;
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                                                                                                                                                                                          Score 633; DB 26;
Pred. No. 1.6e-64;
1; Mismatches 5;
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                                                                                                                                                                                                                         Length 119;
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Sequence 6716, Application US/60169840 GENERAL INFORMATION:

APPLICANT: Bonazzi, Vivien TITLE OF INVENTION: ISOLATI TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: USES TO

ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND USES THEREOF

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Best Local S
Matches 111
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CURRENT FILING DATE: 1999-12-09
NUMBER OF SEO ID NOS: 9628
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6716
LENGTH: 119
TYPE: PRT
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NAME/KEY: VARIANT

LOCATION: (1)...(119)

OTHER INFORMATION: Xaa - Any Amino Acid

-60-169-840-6716
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           FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                     PRIOR APPLICATION DATA:
07/315015
                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/786149
                                                                                                                                                                                       APPLICATION NUMBER: 08/5: FILING DATE: 10-AUG-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARB: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MAK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                            APPLICATION NUMBER: 08/0 FILING DATE: 6-MAY-1993
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/119,209 FILING DATE: 20-Jul-1998
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REGISTRATION NUMBER: 34,659 REFERENCE/DOCKET NUMBER: PO
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San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LASKY, LAURENCE A. STACHELL, SCOTT E.
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94.9%;
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P0565D1C3
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Pred. No. 1
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1.6e-64;
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Best Local S
Matches 97
                                                                                                                                                                 Sequence 6200, Appli GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10011
LENGTH: 116
TYPE: PRT
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FILE REFERENCE: CL000116
CURRENT APPLICATION NUMBER: US/60/160,203
CURRENT FILLING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 6374
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM TITLE OF INVENTION: AND USES THEREOF
                                                                                         APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING I
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL000112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BONAZZI, VIVIEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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82.9%;
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Pred. No. 1.1e-53;
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Pred. No. 4.8e-56;
9; Mismatches 11;
                                                                                                                 ENCODING HUMAN SECRETED PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(116)
; OTHER INFORMATION: Xaa = Au
US-60-169-840-9326
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; DOTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-203-6200
                                           Sequence 7998, Application US/60169867
GENERAL INFORMATION:
APPLICANT: BONAZZI, Vivien
TITLE OF INVENTION: USCLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000160
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCS THEREOF
TITLE OF INVENTION: USCS THEREOF
FILE REFERENCE: CL000164
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Best Local :
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Best Local S
Matches 95
       CURRENT APPLICATION NUMBER: US/60/169,867
CURRENT FILING DATE: 1999-12-09
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NUMBER OF
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CURRENT FILLING DATE: 1999-12-09
NUMBER OF SEO ID NOS: 9628
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 116
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96.0%;
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Pred. No. 1.1e-53;
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                                                                        TARGET PROTEINS
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; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; HAME/KEY: VARIANT
; LOCATION: (1)...(116)
; OTHER INFORMATION: Xaa
US-60-169-867-7998
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; NAME/KEY: VARIANT
; LOCATION: (1)...(700)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-207-315-467
                                                                                                                                                     RESULT
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Best Local S
Matches 77
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SEQ ID NO 467
LENGTH: 700
                                                                                                Sequence 4, Application PC/TUS9409395 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL006601
FILE REFERENCE: CL006601
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Best Local
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CURRENT FILING DATE: 2000-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: HUMAN
                                TITLE OF INVENTION: EX NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                             APPLICANT: Board of Regents of the University of Oklahoma TITLE OF INVENTION: Expression Control Sequences of the P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 116
 STREET:
             ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                               94 TWYGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALC
                                                                                                                                                                                                                  61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                           71 TWVGTNKSLTEEAENWGDGEPNNKKTKEDCVEIYIKEKQ 109
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nes 95; Conserv
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                                                                                                                                                                                                                                                                                                                                   Similarity 77; Conserv
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1100 Peachtree Street, Suite 2800
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Pred. No. 1.1e-53;
Pred. No. 1.1e-53;
                                                                                                                                                                                                                                                                                                                                               Score 445; DB 26; Pred. No. 7.5e-42;
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                                                               P-Selectin
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                                                                                                                                                                                                                                                                                                                            Gaps
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US-08-449-687B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08449687B GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,687B
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
DEFICE ADDITION: 435
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pan, Junliang
TITLE OF INVENTION: Expression Control Sequences of the
TITLE OF INVENTION: P-Selectin Gene
TITLE OF INVENTION: 17
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CURRENT APPLICATION DATA:
APPLICATION NIMBERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              APPLICATION NUMBER: US 08 FILING DATE: 20-AUG-1993 PRIOR APPLICATION DATA:
                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McEver, Rodger P. APPLICANT: Pan, Junliang
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
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                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 19-AUC CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC-SOFTWARD.
APPLICATION NUMBER: US 0 FILING DATE: 08-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 WTYHYSTKAYSWNISRKYCONRYTDLVAIONKNEIDYLNKVLPYYSSYYWIGIRKNNKTW 101
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USA
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(404)-815-6555
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linear
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                                                                   US 08/110,158
               US 07/320,408
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Pred. No. 9.3e-42;
ll; Mismatches 29;
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RESULT 27
US-60-196-718-4236
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                                                Sequence 4236, Application US/60196718
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fa
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APPLICANT: McCarthy, Jeanette
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/327,485
PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/020,141
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ableson, Allen
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 21
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INFORMATION FOR SEQ ID NO: 4:
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TYPE: PRT
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                                                                                                                                                                  102 TWVGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALC
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nes 77; Conserv
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                                                                                                                                                                                                                                                    1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING FUSES THEREOF
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65.8%;
                                                                                                                                                                                                                                                                                                   66.8%; Score 445; DB 24; 65.8%; Pred. No. 9.3e-42; tive 11; Mismatches 29;
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                   HUMAN SECRETED PROTEINS,
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; ORGANISM: HUMAN
US-60-196-718-4237
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                                                                                                                                                                                                  Sequence 1909, Application US/60195053 GENERAL INFORMATION:
                     SEQ ID NO 1909
                                               TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING H
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000427
CURRENT APPLICATION NUMBER: US/60/195,053
CURRENT FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 2836
COURTENED FOR THE PROTEIN OF SEQ ID NOS: 2836
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 133
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Best Local
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CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4236
LENGTH: 129
                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000456
CURRENT FILENCATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER: FastSEQ ID NOS: 7494
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local (
LENGTH: 128
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mes 77; Conserv
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                                    FastSEQ for
                                                                                                                                                                             Bonazzi, Vivien
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                                Windows Version 4.0
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65.8%;
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Pred. No. 2.9e-42;
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                                                                                                                                     ENCODING HUMAN SECRETED PROTEINS, AND
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; ORGANISM: HUMAN US-60-196-718-4238
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Sequence 4238, Application US/60196718
GENERAL INFORMATION:
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; ORGANISM: HUMA
US-60-195-053-1909
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 Query Match
Best Local Similarity
                                                                                                                                        SOFTWARE: Fai
SEQ ID NO 4238
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CURRENT FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 2836
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1908
LENGTH: 129
TYPE: PRT
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TITLE OF INVENTION: ISOLATI
TITLE OF INVENTION: NUCLEIO
TITLE OF INVENTION: USES TI
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Best Local :
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                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                      LENGTH: 138
TYPE: PRT
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLO
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NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
USES THEREOF
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65.8%;
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Score 439.5; DB 2
Pred. No. 4.1e-42;
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US-60-192-739-3226
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CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 4532
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3226
LENGTH: 134
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: BODASZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USCS THEREOF
FILE REFERENCE: CL000406
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 916
LENGTH: 196
TYPE: PRT
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                                                      Matches
                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                       FEATURE:
NAME/REY: SITE
LOCATION: (190)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
-09-760-498-916
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/760,498 CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC017
                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 930
                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGGIW 60
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                                                                  62.3%; Score 415; DB 21; 60.7%; Pred. No. 4.3e-39;
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Best Local
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                                                                                                                                                                                                                                                                               CITY:
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; ORGANISM: Homo sapiens PCT-US99-28965-19
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GENERAL INFORMATION:
APPLICANT: Klimuk
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CURRENT FILING DATE: 1999-12-08
EARLIER APPLICATION NUMBER: US 09/209,668
EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
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TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0424
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ATTORNEY/AGENT INFORMATION:
NAME: KEZET, WILLIAM B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 16:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FITLE OF INVENTION:
                                                                                                                           APPLICATION NUMBER: US/08/657,753 FILING DATE: Not yet assigned
                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scherrer, Peter
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Sean C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Crew LLP Center, Eighth Floor
     16303-003600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Efficacy of Liposomal Antisense
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US-08-770-435-3
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; MOLECULE TYPE: protein
US-08-657-753-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08770435 GENERAL INFORMATION:
                                                                     TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                           APPLICATION NUMBER: US 07/850,802 FILING DATE: 13-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/102,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100
CITY: Washington
STATE: DC
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gimbrone, Jr., Michael A. APPLICANT: Bevilacqua, Michael P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acid
           TOPOLOGY:
                                                                                                                                 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                        APPLICATION NUMBER: US 01 FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                        LENGTH:
                                                                                                                                                 NAME: Markowicz, Karen R. REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: herew: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVW 81
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                         amino acid
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                                        610 amino acids
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(415) 57
           linear
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29-DEC-1994
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60.7%;
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Pred. No. 1.8e-38;
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US-09-266-091-2
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GENERAL INFORMATION:
APPLICANT: Klimuk, Sandra K.
Semple, Sean C.
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Best Local Similarity
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SEQ ID NO 2
LENGTH: 610
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CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 08/657,753
PRIOR FILING DATE: 1996-05-30
NUMBER OF SEQ ID NOS: 10
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Best Local Similarity
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TITLE OF INVENTION: ENHANCED EFFICACY OF LIPOSOMAL ANTISENSE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT: Semple, Sean C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                            Hope, Michael J.
TITLE OF INVENTION: Enhanced Efficacy of Liposomal Antisense NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                       ZIP: 94111-3834
                                                                                                                            COUNTRY:
                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and STREET: Two Embarcadero Center, Eight
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                                                                                                                          USA
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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CURRENT APPLICATION DATA:

FILING DATE: 10-Mar-1999 CLASSIFICATION: <Unknown>

APPLICATION NUMBER: US/09/266,091A

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; ORGANISM: Homo sapiens
US-09-784-356-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watson, Susan R.
APPLICANT: Working Since Specific Structures of Anglogenesis, applicant: EOS Biotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Anglogenesis, TITLE OF INVENTION: Compositions and Methods of Screening for Anglogenesis TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-0071003
CURRENT APPLICATION NUMBER: US/09/784,356
CURRENT APPLICATION NUMBER: US/09/784,356
CURRENT APPLICATION NUMBER: US 60/148,425
PRIOR APPLICATION NUMBER: US 60/148,425
PRIOR APPLICATION NUMBER: US 09/637,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 122
LENGTH: 610
                                                                                                                                                                                                           Best Local Similarity 60.7 Matches 71; Conservative
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61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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                                                                                                              1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 16303-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                   WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVW 81
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Watson, Susan R.
EOS Biotechnology,
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                                                                                                                                                                                                       62.3%; Score 415; DB 21; 60.7%; Pred. No. 1.8e-38; ative 13; Mismatches 33;
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APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleyn Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 610
TYPE: PRT
ORGANISM: Homo Sapien
US-09-802-640-36
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Search completed: September Job time: 485 sec
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                                                                                                                                                                                                                                                                                                                    Best
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                                                                                                                                     61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                           82 VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC 138
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                                                                                                                                                                                                                           1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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                     2002,
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-110-158-4

US-08-340-539A-19

US-08-274-661B-37

US-08-252-493C-9

US-08-274-61B-36

US-08-340-539A-15

US-08-274-61B-36

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US-08-274-651B-36

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US-08-340-539A-14
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5514582-4
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US-08-340-539A-18
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(without alignments)
99.818 Million cell updates/sec
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Sequence 14, Appli
Sequence 14, Appli
Sequence 4, Appli
Patent No. 5514582
Sequence 12, Appli
Sequence 13, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 18, Appli
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Sequence
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Sequence 2, Appli
Patent No. 5514582
39, Appl
16, Appl
17, Appl
4, Appl
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37, Appl
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15, Appl
19, Appl
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OPERATING SYSTEM: PC-DOS/MS OF TWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/274,661B
FILING DATE: 13-Jul-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956701
FILING DATE: 10/01/1992
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 761P1C1
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415/225-3216
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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US-08-274-661B-38
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Patent No. 5593882
      Query Match
Best Local Similarity
Matches 117; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Erbe, David V.
APPLICANT: Lasky, Laurence A.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Selectin Variants
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5514582-1
US-08-365-103B-8
Score 666; DB 1; I
pred. No. 1.8e-66;
pred. No. 1.8e-66;
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                                                          Length 117;
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Sequence 8, Appli
Sequence 5, Appli
Patent No. 5514582
Sequence 14, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
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                                                                                                                                                                                           Best
                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Applic Patent No. 5840844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 56:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
                                       99
                                                                     61
                                                                                              39 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                        Local Similarity es 117; Conserv
                                                                                                             1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/786149 FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 10-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                          TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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ROSEN, STEVEN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SINGER, MARK S.
                                                                                                                                                                                                                                                                                                                                                                                           415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/513,278
10-AUG-1995
                                                                                                                                                               100.0%; Sc.
100.0%; Pr
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                                                                                                                                                                 Score 666; DB 2;
Pred. No. 7.5e-66;
Mismatches 0;
                                                                                                                                                                                                   Length 372;
                                                                                                                                                                  Indels
                                                                                                                                                                 0;
                                                                                                                                                               Gaps
                                                                                                                                                                 0,
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5514582-2
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APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE;
TITLE OF INVENTION: RECOMBINANT DNA ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08340539A Patent No. 5808025 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULINS
                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08,
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                                        COMPUTER: IBM PC COMPAT:
OPERATING SYSTEM: PC-DO:
SOFTWARE: PATENTIN Relace
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OF-1194-1111.
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tedder, TAPPLICANT: Kansas, CAPPLICANT: Kansas, CAPPLICANTION: TITLE OF INVENTION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FISH & NEAVE
ADDRESSEE: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 986,931 FILING DATE: 08-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 21-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 155
                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 666; DB 6; ilarity 100.0%; Pred. No. 7.5e-66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                          16-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geoffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                          Release #1.0, Version #1.30
                                                                                                                         us 08/008,459
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Length 372;

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INFORMATION FOR SEQ ID NO:

2

SEQUENCE CHARACTERISTICS

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; MOLECULE TYPE: protein US-08-461-592B-2
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                      TELEFAX: (212) 596-909
TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: 13mes # H11ev Tr
                                                                                                                                                                                                NAME: James F. Haley, Jr.
REGISTION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                    (212) 596-9090
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                                                                                            linear
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 100.0%;
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Pred. No. 7.8e-66;
Mismatches 0;
 Score 666; DB 2; Pred. No. 7.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1.25
              Length 385;
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RESULT 7 5514582-7

Patent No. 5514582

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APPLICANT: Tedder,
APPLICANT: Kansas,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                 Query Match
Best Local
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5808025
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
APPLICATION NUMBER: 25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14,
                                                                                                                                                                                                                                                                                                  TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            NAME: Gunnison, Jane
REGISTON NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                Local
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CITY: 1
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   61
                              61
                                                                                                                                                                                                                                    TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                          1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                                                                     LENGTH:
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WTYHYSKRPMPWEKARAFCRENYTDLVAIQNKGEIEYLNKTQPFSRTYYWIGIRKVEGVW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 168
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                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                     119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1251 Avenue
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                                                                                                                   Conservative
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SYSTEM: PC-DOS/MS-DOS
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51 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geoffrey S.
CHIMERIC S
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                                                                                                                                 86.3%;
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version
                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                             CG-104
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                                                                                                                                 Score 575; DB 1; Pred. No. 2.1e-56;
                                                                                                                   Mismatches
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                                              APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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Best Local Similarity
                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/059027
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360
COMPUTER: IBM PC compatible
                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LASKY, LAURENCE |
APPLICANT: STACHELL, SCOTT |
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
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 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TWVGTNKTLTKEÄENWGAGEPNNKKSKEDCVEIYIKRERDSGKWNDDACHKRKAALC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 315,015 FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-JAN-1994
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33,055
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RESULT 10
US-08-340-539A-12
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5514582-4
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TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TYPE: amino acid
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                                                                                                  Sequence 12, Application US/08340539A Patent No. 5808025
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Best Local 9
                                              GENERAL INFORMATION:
APPLICANT: Tedder,
APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
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APPLICATION NUMBER: 986,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 43
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                                                                                                                                                                                          APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
                                                                                                                                                                                                                                                             39 WTYHYSEKPMNWENARKFCKQNYTDLVAIQNKREIEYLENTLPKSPYYYWIGIRKIGKMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                              1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPESRSYYWIGIRKIGGIW 60
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                                                Thomas F. Geoffrey S.
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 CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION 28
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                                                                                                                                                                                                                                                                                                                                              Score 565; DB 6;
Pred. No. 1.1e-54;
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                                                                                                                                                                                                                                                                                                                                                           Length 372;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

FISH & NEAVE

New York

1251 Avenue of the Americas

FILING DATE:

16-NOV-1994

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                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08340539A Patent No. 5808025
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Best Local 9
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                TITLE OF INVENTION: CH
TITLE OF INVENTION: BL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  APPLICANT: Tedder, Thomas F. APPLICANT: Kansas, Geoffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gunnison, Jane REGISTRATION NUMBER: 38,479 REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/340,539A FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                     COUNTRY:
                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTYHYSEKPMNWENARKFCKQNYTNLVAIQNKREIEYLENTLPKSPYYYWIGIRKIGKMW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
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1251 Avenue of the Americas
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BLOCKING
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82.1%;
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US/08/340,539A
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Pred. No. 9.7e-55;
                                                                                                                                                                                                                                                   SELECTINS AS SIMULTANEOUS AGENTS FOR COMPONENT SELECTIN FUNCTION
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US-08-340-539A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08340539A Patent No. 5808025
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Best Local Similarity
                                                                                                                                                                         SOFTWARE: PALEH.C. DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION NUMBER: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tedder,
APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                              NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 25-JAN-1993
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 25-JAN-1993
                TELEPHONE:
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212-596-9090
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212-596-9090
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                  212-596-9000
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CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELE
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81.2%;
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Pred. No. 2.1e-54;
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Best Local Similarity
Watches 79; Conserve
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 07/320408

FILING DATE: 08-MAR-1989

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/554199

FILING DATE: 17-JUL-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                              TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                               AYPOTHETICAL: YI
                                                                                     MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTANDED: PATCHAFTE PC-DOS/MS-DOS
COMPUTANDED: PATCHAFTE PATCHAFTE
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05059
FILING DATE: 19910717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEB: Kilpatrick & Cody
STREET: 100 Peachtree Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Regents of the Board of the, University of APPLICANT: Oklahoma
TITLE OF INVENTION: Functionally Active Selectin-Deri-
TITLE OF INVENTION: Peptides
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                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
               TISSUE TYPE:
                            ORGANISM:
                                                                                                                              TYPE: AMINO ACID
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                           LENGTH:
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STATE: Georgi
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Y: US
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               Homo sapien
E: Blood
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Endothelial
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YES
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67.5%; Pred. No. 3.9e-43;
470: Mismatches 28;
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  Disulfide-bond 540..567
                                          Disulfide-bond 523..536
                                                                               Disulfide-bond 510..554
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354..381
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292..319
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275..288
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262..306
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213..226
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200..244
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185..194
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168..183
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131..150
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LOCATION: 460
OTHER INFORMATION:
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LOCATION: 54
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734..761
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717..730
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585..616
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glycosylation site"
                        /note= "Potential asparagine-linked
glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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RESULT 14
5378464-2
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US-08-274-661B-39
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APPLICANT: MCEVER, RODGER P.

TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES
BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140

NUMBER OF SEQUENCES: 32

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/320,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/08274661B Patent No. 5593882
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Best Local :
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Best Local :
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Erbe,
           SOFTWARE: WinPatin (Gene
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 13-Jul-1994
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb:
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                           APPLICANT: Lasky, Laurence A.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Selectin Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                            ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/320,408 FILING DATE: 08-MAR-1989
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                STATE:
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nes 77; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
CLASSIFICATION:
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                                                                                                                                                 94080
                                                                                                                                                                              California
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Presta, Leonard G.
                                                                                                                                                               USA
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65.8%;
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glycosylation site"
                                                             (Genentech)
                              US/08/274,661B
                                                                                                           1.44 Mb floppy
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Pred. No. 3.2e-41;
1; Mismatches 29
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Pred. No. 3.2e-41;
1; Mismatches 29
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FILING DATE: 10/01/1992 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER:

07/956701

761P1C1

MOLECULE TYPE:

protein

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US-08-340-539A-16
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Patent No. 5808025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 65.8 Matches 77; Conservative
                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/340,539A FILLING DATE: 16-NOV-1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/008,459 FILING DATE: 25-JAN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                     TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                      NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC S
TITLE OF INVENTION: BLOCKING A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dreger, Ginger R. 33,055 REGISTRATION NUMBER: 365 REFERENCE/DOCKET NUMBER: 76: TELECOMMUNICATION INFORMATION: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
               STRANDEDNESS:
                                                                                                                            TELEPHONE:
                                                      LENGTH:
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                                 amino acid
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                                                  119 amino acids
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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US-08-340-539A-17
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                                                                                                                              Query Match
Best Local
                                                                                                                Matches
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TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
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Best Local 9
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                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/ACENT INFORMATION:
NAME: CREATON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tedder, APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
61 TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVELYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                            Local
                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                 STRANDEDNESS:
                                             NAME: Gunnison, Jane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
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                                                                                                                           Similarity
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1251 Avenue of t
                                                                                                            Conservative
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                                                                                                                       66.8%; Score 445; DB 1 65.8%; Pred. No. 5e-42;
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                   38,479
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                                                                                                                                                                                                                                                                                             17:
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                                                                                                           Mismatches
                                                                                                                                      DB 1;
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                                                                                                                                      Length 119;
                                                                                                           Indels
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                                                                                                                                                                                                                Sequence 19, Appli
Patent No. 5808025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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Patent No. 560582
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                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (404)-815-659
INFORMATION FOR SEQ ID NO:
                                                                             APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC S
TITLE OF INVENTION: BLOCKING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 08-MAR-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      102 TWVGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 830 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
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1100 Peachtree Street,
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FISH & NEAVE
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65.8%; Pred. No. 5.4e-41;
67. Mismatches 29;
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                                                                             CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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; Sequence 37, Applicat
; Patent No. 5593882
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UPPLICATION DATE: 16-NOV-11
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UPPLICATION NU
                                                                          SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Erbe, David V.
APPLICANT: Lasky, Laurence A.
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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OPERATING SYSTEM: PC-DOS/MS-DOS
                      APPLICATION NUMBER: US/0 FILING DATE: 13-Jul-1994
                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gunnison, Jane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 66.7%; Score 444; DB 1; Length 119; Similarity 65.8%; Pred. No. 6.4e-42;
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RESULT 21
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US-08-274-661B-37
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                                      TELEFAX: (203) 772-36
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                   FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING TOTAL
                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION STREET
                                                                                  NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rother, Russell P. APPLICANT: Evans, Mark J. APPLICANT: Matis, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 76.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10/01/1992
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IWVGTHKPLTEGAKNWAPGEPNNKQNNEDCVEIYIKRPKDTGMWNDERCSKKKLALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/2-9881
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Seth A. Fidel
25 Science Park, Box 15
                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rollins,
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                                                                            (203)
                                                            772-3655
                                                                            776-1790
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                                          9:
                                                                                                                                                                                                                                                                                                                                  750 Kb storage
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Pred. No. 8.3e-41;
3; Mismatches 30
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RESULT 22
US-09-276-197-9
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Query Match
Best Local Similarity 63.2
74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (203) 776-
TELEFAX: (203) 772-36:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fidel Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Fidel, Seth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 25 CONTROL OF THE CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: PC compatible OPERATING SYSTEM: DOS 6.2 SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 63.2 nes 74; Conservative
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TOPOLOGY: Lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                  Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rother,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rollins, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seth A. Fidel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear
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predicted amino acid sequence
Porcine E-selectin
                                                                                                                                                                                                                                                                                                                                             Single
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63.8%; Score 425; DB 3; 63.2%; Pred. No. 4.5e-39; Live 13; Mismatches 30

30;

Indels

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Gaps

0

Length 484;

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RESULT 24
US-08-274-661B-36
; Sequence 36, Application US/08274661B
; Patent No. 5593882
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Watches 71; Conserve
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; MOLECULE TYPE:
US-08-340-539A-15
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US-08-340-539A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tedder, THOMAS S. APPLICANT: Kansas, Geoffrey S. APPLICANT: Kansas, Geoffrey S. TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/340,539A FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1251 Aven
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                        61 TWVGTNKSLTEBAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                   1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                   WSYNTSTEAMTYDEASAYCOORYTHLVAIONKEEIEYLNSILSYSPSYYWIGIRKVNNVW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 amino acids
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                                                                                                                                                                                                                                                                                       62.3%; Score 415; DB 1; 60.7%; Pred. No. 1e-38;
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US-08-365-470-3
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                                                                                                                                                                                                                                                                 Sequence 3, Application US/08365470 Patent No. 5632991
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gimbrone
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lasky, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 76.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                                                                      61 VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC
                                                                                                                                                                                                                                                                                                                                                                                                       61 TWYGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/
FILING DATE: 10/01/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0:
FILING DATE: 13-Jul-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                        ZIP:
                                                                      COUNTRY:
                                                                                       STATE:
                                                                                                                         STREET:
                                                                                                                                           ADDRESSEE:
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r: 460 Point San Bruno
South San Francisco
                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino Acid
                                                                                        R
                                                                                                                       E: STERNE, KESSLER, 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 amino acids
                                                                                                                                                                                          Gimbrone, Jr., Michael A.
VENTION: Antibodies Specific For E-selectin
VENTION: Thereof
                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; Score 415; DB 1; Length 120; 60.7%; Pred. No. 1e-38;
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                                                                                                                           GOLDSTEIN & FOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09209668A Patent No. 6114517 GENERAL INFORMATION:
                                                                                                                                                    Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/209,668A CURRENT FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 610 amino acids
                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/102/510
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
           82
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                                                                                                                                                                 Local Similarity 60.7%;
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                                                                                          1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKABIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Markowicz, Karen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 13-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC 138
                                 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                       WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVW 81
                                                                                                                                                                                                                                                                                                610
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                                                                                                                                                                Score 415; DB 3; Length 610; Pred. No. 7.7e-38;
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; TYPE: Amino Acid
; STRANDEDMESS: Sing
; TOPOLOGY: Linear
; ANTI-SENSE: no
US-09-009-490A-89
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US-09-009-490A-89
; Sequence 89, Application US/09009490A
parent No. 6300491
                                                                                                                                                                                                                                                                                  Matches 71;
                                                                                                                                                                                                                                                                                                                                                      Query Match
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EILING DATE: May 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 969,151
FILLING DATE: February 10, 1993
PRIOR APPLICATION NUMBER: 007,997
APPLICATION NUMBER: 007,997
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APPLICANT: Bennet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
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FILING DATE: September 937,757
PRIOR P
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: Windows
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,740
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                  61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                 1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 08053
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                                                                                                                        WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                   Score 415; DB 4; Length 610;
Pred. No. 7.7e-38;
13; Mismatches 33; Indels
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VWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALC 138

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5217870-2
; Patent No. 5217870
                                                                                  US-08-840-062-8
                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08840062 Patent No. 6117977
Query Match 35.0
Best Local Similarity 61.7
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/345,151
FILING DATE: 28-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDLIM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                  Linear
                 35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%; Score 415; DB 6; 60.7%; Pred. No. 7.7e-38; tive 13; Mismatches 33
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                 Score 237; DB 3; Pred. No. 2.4e-19;
                             Length 67;
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Gaps
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US-08-513-278-5
                                                             Matches
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                                                                                         Query Match
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                                                                               Best
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                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/319
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                           TYPE: ami
TOPOLOGY:
                                                             Local Similarity 78.4
les 29; Conservative
                                                                                                                                                                                                                                         TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 460 Point San Brui
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/0 FILING DATE: 06-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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               2 TYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYL 38
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TYHYSEKPMNWENARKFXKQNYTDLVAIQNKXXIEYL 38
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o. 5840844
                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                           910/371-7168
                                                                                                                                                                                            38 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINGER, MARK S.
YEDNOCK, TED A.
VENTION: LYMPHOCYTE HOMING RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASKY, LAURENCE A. STACHELL, SCOTT E. ROSEN, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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N: 5530
                                                                            24.68;
78.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 Kb floppy
                                                                                                                                                                                                                                                                                                            565D1C1
                                                                          Score 164; DB 2;
Pred. No. 1.4e-11;
                                                             Mismatches
                                                                                           Length 38;
                                                             Indels
                                                             0;
                                                             Gaps
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RESULT 31 5514582-5

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Patent No. 5514582

Length 31;

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US-08-140-137A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5817617
GENERAL INFORMATION:
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                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                               MOLECULE TYPE:
                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TUOMANEN, ELAINE
APPLICANT: MASURE, H. R.
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
TITLE OF INVENTION: ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                                         TELEPHONE: ZU1 30. 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 43
                DESCRIPTION:
                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/140,137A FILING DATE: 27-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 315, FILING DATE: 23-FEB-1989
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FILING DATE: 21-JAN-1994
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|||||||||||||| |||| 31
|2 TYHYSEKPMNWENARKFXKQNYTDLVAIQNKXXIEYL 38
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                                                  linear
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 peptide
hLHRc peptide segence
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                                                                                                                               Query Match
Best Local Similarity
Matches 34; Conserv
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No. 6277959
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Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                   TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-JUL-
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
208 VDGTD--YATGFQNWKPGQPDDWQGHGLGGGEDCAHFH-----PDGRWNDDVCQR 255
                                                             150 YWFSHSGMSWAEAEKYCOLKNAHLVVINSREEONFVOKYL--GSAYTWMGLSDPEGAWKW
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ADDRESSEE: DNAX Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                           63 V-GTNKSLTEEAENWGDGEPNNKKNK-----EDCVETYIKRNKDAGKWNDDACHK 111
                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                         3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW 62
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 08-JUI
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                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                   273 amino acids
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                                                                                                                           Conservative
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Lebecque, Ser
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09-JUL-1997
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                                                                                                                                          24.18; 29.68;
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Mammalian Membrane Protein Genes;
Related Reagents
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                                                                                                                           22; Mismatches
                                                                                                                                          Score 160.5; DB 4
Pred. No. 3.9e-10;
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US-08-688-342-4

Sequence 4, Application US/08688342

GENERAL INFORMATION:

Au-Young, Janice

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Best Local Similarity
                                                                                                                                                          GENERAL INFORMATION:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                 APPLICANT: Au-Young, Janice APPLICANT: Cocks, Benjamin (APPLICANT: Goli, Surya K.
                                                 APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                               CORRESPONDENCE ADDRESS
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LIBRARY: GenBank
CLONE: 1235724
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TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
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                                                                                                                                                                                                                                                                                 227 VDGTD--YATGFQNWKPGQPDDWQGHGLGGGEDCAHFH-----PDGRWNDDVCQR 274
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STREET:
                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
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Goli, Surya K.
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                                                                                                                   Benjamin G.
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29.6%; Pred. No. 4.2e-10;
Live 22; Mismatches 44
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Patent No. (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                              ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                   APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrane Protein Genes;
TITLE OF INVENTION: Related Reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 VDGTD--YATGFQNWKPGQPDDWQGHGLGGGEDCAHFH-----PDGRWNDDVCQR 274
                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 V-GTNKSLTEEAENWGDGEPNNKKNK-----EDCVEIYIKRNKDAGKWNDDACHK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW
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                                                                                                                 Palo Alto
: California
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                                                                                                                                                   901 California Avenue
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                                                                                                     USA
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Bates, Elizabeth E.M.
Ford, John
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PatentIn Release #1.0, Version #1.30
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29.6%; Pred. No. 4.2e-10;
tive 22; Mismatches 44
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PRIOR APPLICATION DATA:

CLASSIFICATION:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0: FILING DATE: 08-JUL-1998

US/09/111,470

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5514582-12
;Patent no. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
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                                                                                                                                                                                                                                                                                       SEQ ID NO:12:
                                                                                                                                  Query Match
Best Local Similarity 32.2
38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650)450 INO: 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FRIGHT: 316 amino acids
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 986,931
FILING DATE: 08 DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/053,080 FILING DATE: 09-JUL-1997 ATTORNEY/AGENT INFORMATION:
         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 YWFSHSGMSWAEAEKYCQLKNAHLVVINSREEONFVQKYL--GSAYTWMGLSDPEGAWKW 250
                                 61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDAC-HKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 VDGTD--YATGFQNWKPGQPDDWQGHGLGGGEDCAHFH----PDGRWNDDVCQR 298
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 23-FEB
                                                                      3 YYFGKGTKQWVHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGS--WIGLRNLDLKGEF 60
                                                                                                       3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW 60
                                                                                                                                                                                                                                                                     LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 V-GTNKSLTEEAENWGDGEFNNKKNK-----EDCVEIYIKRNKDAGKWNDDACHK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 29.6 nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIWTW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
IWVDGSH----VDYSNWAPGEPTSRSQGEDCVMM-----RGSGRWNDAFCDRKLGAWVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 160.5; DB 4; Length 316; 29.6%; Pred. No. 4.6e-10; ative 22; Mismatches 44; Indels 15;
                                                                                                                                                                  23.2%; Score 154.5; DB 6 32.2%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/185,670
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                                                                                                                                                    Mismatches
                                                                                                                                                                                     DB 6;
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                                                                                                                                                  Indels
                                                                                                                                                                                     Length 110;
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RESULT 39
US-07-781-248A-1
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; CELL LINE: CHO cells transformed with pCAL8-BF-ND
US-07-641-971B-1
                                                           Sequence 1, Application US/07781248A
Patent No. 5246699
GENERAL INFORMATION:
APPLICANT: Debre, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 38
US-07-641-971B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 908-277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Debre, Patrice
APPLICANT: MOSSalayi, Mohammed D
TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 908-277-4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9
FILING DATE: 24-JAN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/641,971B
FILING DATE: 19910116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Debre, Patrice
APPLICANT: MOSSALAYI, MOHAMMED D
TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
                                                                                                                                                                                                              86 IWVDGSH---VDYSNWAPGEPTSRSQGEDCVMM-----RGSGRWNDAFCDRKLGAWVC 135
                                                                                                                                                                                                                                                    61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDAC-HKLKAALC 117
                                                                                                                                                                                                                                                                                             28 YYFGKGTKQWVHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGS--WIGLRNLDLKGEF 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fishman, Irving M
REGISTRATION NUMBER: 302
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 0790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: 11v+...,
ADDRESSEE: 556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I: 174 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             23.2%; Score 154.5; DB 32.2%; Pred. No. 1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 174;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 556 CITY: Summit

556 Morris Avenue

Irving M.

Fishman, CIBA-GEIGY Corporation

COUNTRY: USA ZIP: 07901

New Jersey

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US-08-365-103B-10
; Sequence 10, Application US/08365103B
; Patent No. 5766943
; Patent No. 5766943
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                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     APPLICANT: Lynch,
APPLICANT: Nunez,
APPLICANT: Yodoi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 90103565 FILING DATE: 09-MAY-1990 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE: Human B. Cells CELL LINE: CHO cells transformed with pCAL8-BF-ND
                  COUNTRY: United States ZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                                    86 IWVDGSH----VDYSNWAPGEPTSRSQGEDCVMM-----RGSGRWNDAFCDRKLGAWVC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 174 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 908-277-4306
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REGISTRATION NUMBER: 36,170
REFERENCE/DOCKET NUMBER: 4-
                                                                        CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDAC-HKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 YYFGKGTKQWVHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGS--WIGLRNLDLKGEF 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW 60
                                                                                                                    IDDRESSEE:
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                                                          Iowa
                                                                                             E: Zarley, McKee, Tho
801 Grand Ave. Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                      Richard G
Raphael D.
                                                                                                                                                                                                                   Jungi
                                                                                                 McKee, Thomte, Voorhees & Sease
ve. Suite 3200
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Search completed:
Job time: 275 sec
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Best Local Similarity 32.2
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heldi S.

REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: U1rf

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       174 YYFGKGTKQWYHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGS--WIGLRNLDLKGEF 231
                                                                                              232 IWVDGSH---VDYSNWAPGEPTSRSQGEDCVMM-----RGSGRWNDAFCDRKLGAWVC 281
                                                                                                                           61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDAC-HKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 28-DEG CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                                                                                                                                                               3 YHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIG--GIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                  September
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                                                                                                                                                                                                                                                                  23.2%; Score 154.5; DB 1; 32.2%; Pred. No. 2.2e-09;
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                                                                                                                                                                                                                                                    47;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                    AAR22551
AAR91443
AAY961443
AAR98127
AAR98128
AAR98130
AAR98115
AAR98115
AAR98116
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T-cell speci
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Modified-site
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                                            Modified-site
                                                                                                            Modified-site
                                                                                                                                                                             Modified-site
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Human lymphocyte c	AAR98109	17	371	•	ū	
	AAR98112	17	371	•	O.	
	AAR98111	17	371		g	
	AAR22802	13	372		σ,	
Human lymphocyte c	AAR98113	17	371	•	g	
Human lymphocyte c	AAR98110	17	371		σ	
Human T-lymphocyte	AAU02447	22	405	100.0	σ	
-	AAY96138	21	385		S.	
	AAW86199	20	385	•	ď	
Leu8	AAW80452	19	385		σ	
3	AAW21657	18	385	•	σ	
ar	AAR91442	17	385	-	σ	
5	AAR56663	15	385	-	g	
Sequence en	AAR34197	14	385	•	g	
Ę,	AAR32707	14	385	•	σ	
T lymphocyt	AAR20815	13	385		g	
Hu	AAR98135	17	374		σ	
Human	AAR98134	17	374	•	σ	
Amino acid sequen	AAB68334	22	372	•	O)	
Human lymphoc	AAW73264	20	372	•	o,	
Homo sapiens	AAW37781	19	372	•	σ,	
Human	AAR98133	17	372	•	σ	
Human lymphoc	AAR98106	17	372	•	σ	
Human LHR. Homo	AAR83050	16	372	•	g	
Human LHR. Homo	AAR76506	16	372	•	σ	
Hulhr. Homo sapi	AAR38908	14	372	•	σ	
Human Lymphocyte	AAR37960	14	372	•	ð	
Human lymphocyte	AAR98129	17	371	•	g	
Human lymphocyte	AAR98124	17	371	٠	O)	
Human lymphocyte	AAR98123	17	371		g	
lymphocyte	812	17	371	•	σ	
Lymphocyte	812	17	371	00	σ	
Lymphocyt	812	17	371		666	
Human lymphocyte c	AAR98119	17	371	100.0	σ	

ALIGNMENTS

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Rapid immunoselection cloning technique; cell surface antigen; homing receptor; antigen-presenting cells.
                                  /label= N-linked_glycosylation
/note= "putative"
299.301
                                                                                            /label= N-linked_glycosylation
/note= "putative"
285..287
                                                                                                                                                    /label= N-linked_glycosylation /note= "putative" 269..271
                                                                                                                                                                                                            /label= N-linked_glycosylation /note= "putative" 230..232
                                                                                                                                                                                                                                                                    /label= N-linked_glycosylation /note= "putative" 157..159
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
/label= N-linked_glycosylation
/note= "putative"
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RESULT
AAR91443
ID AAR9
XX AAR9
XX AAR9
XX Huma
AX Cell
KW Cell
KW anti
XX Homc
OS Homc
XX Hom
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                       therapy; diagnosis; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                           Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; Leu8 antigen; T-lymphocyte;
                                               Modified-site
                                                                                                                          Modified-site
                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                    Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Leu8 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two cDNA clones encoding Leu8 determinants were isolated from a human T cell library using the rapid immunoselection cloning method (see e.g. AAQ21164 for description of method). This protein sequence was deduced from the shorter insert. The weakly hydrophobic C-terminal domain is characteristic of surface proteins that are attached to the cell membrane by covalent linkage to a phosphatidylinositol-substituted glycan.

See AAQ21184 for the larger insert and AAR20815 for the major form of the Leu8 antigen that it encodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR91443 standard; Protein; 363
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                                           /label= Glycosylation_site 229..231
                                                                                                                          /label=
156..15
                                                                                                                                                                                                 Location/Qualifiers 113..115
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/label= N-linked_glycosylation
/note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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Glycosylation_site
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Pred. No. 2.2e-63;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULT
AAY96184
ID AAY9
XX
AC AAY9
DT 19-I
XX
DE Huma
XX
KW Leuf
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                                                                                                                                                                                  δÃ
                                                                                                                                                                                                          Д
                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                         Matches
                       Human T-cell specific Leu8 antigen
                                                                                                                                                                                                                                                                                                                                             2 cDNA clones encoding Leu8 determinants (AAR91442 and AAR91443) were isolated from a human T-cell library using a novel immunoselection cloning method. The longer insert (AAR14723) contained 2,350 residues, while the shorter lacked 436 internal residues. A major transcript of 2.4 kb was present in peripheral blood monouclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukaemic T-cell lines. Leu8 antigens can be obtd. for diagnostic and therapeutic use. The presence or absence of Leu8 on CD4 T-cell subsets. Soluble forms of Leu8 can act as antiinflammatory agents by reducing tumbhoryte micratics.
     Leu8; cell
                                                   19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
18-OCT-1993;
                                                                            AAY96184;
                                                                                                  AAY96184
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins
                                                                                                                                                     lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Column 71-74; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT14723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-200279/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aruffo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5506126-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                          52
                                                                                                                                                                                                                  1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                        ω
                                                                                                                                                                                                     wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 111
                                                                                                                                                                                                                                                        al Similarity
117; Conserv
                                                                                                  standard;
     surface
                                                                                                                                                                                                                                                                                                                   363
                                                                                                                                                                                                                                                                                                                                         migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seed B;
                                                                                                                                                                                                                                                         Conservative
                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0983647.
88US-0160416.
89US-0379076.
89US-0553759.
93US-0139273.
                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88US-0160416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Glycosylation_site
324..326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Glycosylation_site 299..301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269..271
/label=_Glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285..287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= Glycosylation_site
  antigen;
                                                                                                  Protein;
                                                 entry)
                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                              .0%;
                                                                                                363
   human;
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                     Score 666; DB 17;
Pred. No. 2.2e-63;
Mismatches 0;
                                                                                                AA
immunoselection; panning;
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                     0,
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding the CD19 cell surface a useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA50632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stamenkovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6111093-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amyloidosis; multiple sclerosis; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodlagnosis; diagnosis; immunotherapy; gene therapy;
immune disorder; infection; asthma; immune-complex disease;
 112
                                 61
                                                                    52
                                                                                 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc 168
                   TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                 wtyhysekpmnwgrarrfcrdnytdlvaignkaeieylektlpfsrsyywigirkiggiw 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-586382/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEN
                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Column 69-72; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOSPITAL CORP.
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0379076.
90US-0498809.
90US-0553759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0983647
88US-0160416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0181612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed
                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                    0;
                                                                                                                                                    Score 666;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                    Mismatches
                                                                                                                                                  DB 21;
.2e-63;
                                                                                                                                    0
                                                                                                                                                                  Length
                                                                                                                                    Indels
                                                                                                                                                                     363;
                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen,
                                                                                                                                    Gaps
                                                                                                                                    0,
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RESULT
AAR98127
   22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                  encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                      A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                           Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                            immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                  Disclosure; Page 19; 41pp;
                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                   Capon
                                                                                                                                                                                                                                                                                                                                                                                              (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation,
metactact.
                                        Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5514582-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR98127 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                      1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                              ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                  Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
195..256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
257..315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159..191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF domain
                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region.
                                                                                                                                                                                                                                                                                            the ligand
- useful fr
                                                                                                                                                                                                                                                                                          useful
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Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                               22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
Nucleic acid encoding hybrid immunoglobulin comprising the ligand
                        WPI; 1996-238773/24.
                                                                  (GETH
                                                                                                                                                    23-FEB-1989;
                                                                                                                                                                        07-MAY-1996
                                                                                                                                                                                             US5514582-A.
                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; therapy; drug delive:
immunomodulator; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98128;
                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98128 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  facilitates recovery, improves aqueous solubility and remove potentially immunogenic epitopes. Variants of the human lyme cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Ser166 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                             DJ,
                                                                  ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wtyhysekpmnwqrarrfordnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                                            Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                    89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                   89US-0315015
                                                                                                                                                                                                                           /label=
354..370
                                                                                                                                                                                                                                                257..315
/label=
331..353
                                                                                                                                                                                                                                                                                         /label= EGF domain
196..256
                                                                                                                                                                                                                                                                                                                                  /label= Signal region 38..154
                                             LA;
                                                                                                                                                                                                                                                                                                              /label= Lectin domain.
159..192
                                                                                                                                                                                                                                                                           /label= Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                             .370
                                                                                                                                                                                                                                                                     315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                Cytoplasmic domain
                                                                                                                                                                                                                                     Transmembrane domain
                                                                                                                                                                                                                                                       Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 666; DB 17;
. No. 2.3e-63;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and removes human lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 2.3e-63;
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89US-0315015
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                                                                                                  Protein;
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                                                                                                    371 AA
                                                                                                                                                                                                                                                                                             Score 666; DB 17;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                           Gaps
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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
'21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the advector (representation of a light block of a control of the combines the advector (representation of a light block of a light block of a light block of the combines the advector (representation of a light block of a light block of the combines the advector (representation of a light block of a light block of the combines the advector (representation of a light block of a l
                                                                                                                                                                                                                                                                               the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidingnosis and treatment e.g. of inflammation
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Sequence
                                                                                        facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Hisl68Gln substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A hybrid immunoglobulin chain comprising the ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 19; 41pp; English.
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371
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89US-0315015.

91US-0808122.

92US-0986931.

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38..154
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Query Match Best Local Similarity

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Length 371;

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RESULT
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                   A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                               Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                  Disclosure; Page 19;
         immunoglobulin
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196..257
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258..316
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- useful for
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 22-NOV-1989;
23-FEB-1989;
                                                       23-FEB-1989;
                                                                                           07-MAY-1996
                                                                                                                           US5514582-A
                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                          Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lymphocyte cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typical applications are as antivital, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Ile174Leu substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
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wes 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
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89US-0315015
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332..354
                                                                                                                                                                                   /label=
355..371
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258..316
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glycoprotein (HuLHR) variant.

inflammation;

domain

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154

Score Pred.

Mismatches 8 666; DB 17; No. 2.3e-63; smatches 0;

Indels Length

Gaps

0,

97

371; 0;

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Matches 117
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08-DEC-1992;
21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                              Region
                                                                                                                      Homo
                                                                                                                                                                               metastasis.
                                                                                                                                                                                                    Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an information of the immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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92US-0986931.
94US-0185670.
Location/Qualifiers
1..37
/label= Signal regi
                                                                                                                                                                                                                                                                                                                     cell surface glycoprotein (HuLHR) variant.
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pred. No. 2.3e-63;
rulematches 0;
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useful for
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                 Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
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Sequence
                                                facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyt cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Thr211Ser substitution.
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371 AA;
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91US-0808122.
92US-0986931.
94US-0185670.
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196..257
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159..192
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                                  TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                                                                        Conservative
                                                                                100.0%;
                                                                       0;
                                                                      Score 666; DB 17;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                        Indels
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RESULT 1
AAR90118
ID AAR9
XX AAR9
XX AAR9
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                                                                                            encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. treating graft rejection; inflammation; metastasis of lymphoma et the immunoglobulin component increases plasma half life and
                                                                                                                                                                                                                 immunoglobulin constant region. The receptor is not immunoglobulin super family, nor a multiple subunit polypeptide immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain commonded by discrete genes.
                                                                                                                                                                                                                                                                                                                A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an active transmembrane region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DΊ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-0315015.
91US-0808122.
92US-0986931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0185670
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38..154
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332..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= EGF domain
196..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Lectin domain.
159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label = Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein (HuLHR)
                                                                                                                                                                                                                                                                                            The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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Matches
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                                                              22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                          Capon DJ,
                                            (GETH ) GENENTECH INC
                                                                                                                        23-FEB-1989;
                                                                                                                                                            US5514582-A.
                                                                                                                                                                                                                                            Binding-site
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                                                                                                                                                                                                                                                                                                                                                    metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Phe214Leu substitution.
                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                 Human lymphocyte cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98119
                                                                                                                                                                                                                                                                                                                                                             immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                          Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                             89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                      89US-0315015
                                                                                                                                                                                                                            /label=
258..316
                                                                                                                                                                                                                                                                                                                                                         transmembrane receptor; adhesion; targetting;
apy; drug delivery; antiviral; neuromodulator;
; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                              /label= EGF domain
196..257
                                                                                                                                                                                                                    /label=
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                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                          /label=
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                                                                                                                                                                             Cytoplasmic
                                                                                                                                                                                               Transmembrane domain
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                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; DB 17;
. 2.3e-63;
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                                                                                                                                                                                                                                                                                                                                                           inflammation;
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RESULT AAR9811 ID AAR9811 ID AAR9811 ID AAR9811 ID AAR981 ID AAR98
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Best Local S
Matches 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
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                                         Domain
                                                                                                                  Binding-site
                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR98120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin chain comprising the ligand binding situ
transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                    /label=
332..354
                                                                                                                  /label= (
258..316
                                                                                                                                                                                                /label=
196..257
                                                                                                                                                                                                                                                                          38..154
/label- Lectin domain
159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell surface glycoprotein (HuLHR) variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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    Transmembrane domain
                                                                         Complement binding repeat 2
                                                                                                                                                       Complement binding repeat 1.
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Pred. No. 2.3e-63;
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RESULT
AAR98121
ID AAR
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AC AAR
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Hum

01-NOV-1996 AAR98121; AAR98121

(first entry)

Human lymphocyte cell surface glycoprotein (HuLHR) variant.

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standard;

Protein;

371

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immunoglobulin super family, nor a multiple subunit polypeptide
cencoded by discrete genes. The hybrid immunoglobulin chain combines
ceffector functions of a ligand binding partner (LBP) with the
ceffector functions of immunoglobulin and can bind to activate
more than one ligand. It can be used diagnostically for the in
vitro assay of LBP and their targets; or therapeutically to deliver
LBP such as toxins, enzymes, growth factors to particular cells.
Typical applications are as antiviral, neuromodulating and
treating graft rejection; inflammation; metastasis of lymphoma etc.)
The immunoglobulin component increases plasma half life and
ceffective facilitates purification while deletion of the transmembrane region
ceffectilitates recovery, improves aqueous solubility and removes
potentially immunogenic epitopes. Variants of the human lymphocyte
cell surface glycoprotein described in AAR98106 are given in
                                                                                                                    Matches
                                                                                                                                 Query Match
Best Local
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis and treatment e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capon
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding hybrid immunoglobulin comprising the binding site of a receptor fused to Ig constant region - us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1994;
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   98
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                                                       twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                             TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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                                                                                                                                  Similarity
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                                                                                                                    Conservative
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89US-0315015.
91US-0808122.
92US-0986931.
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                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of inflammation
                                                                                                                                 Score 666; DB 17;
Pred. No. 2.3e-63;
                                                                                                                   Mismatches
                                                                                                                    0;
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                                                                                                                                                Length
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Best Local Similarity Matches 117; Conserv

Conservative

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Pred. No. 2.: ; Mismatches

2.3e-63; thes 0;

Indels

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Gaps

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100.0%;

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WTYHYSEKPMNWQRARRFCRDNYTDLVATQNKAEIEYLEKTLPFSRSYYWTGIRKIGGIW 60

wtyhysekpmnwqrarrfordnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 97

Qγ Ъ

61 38

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A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in the used diagnostically for the in LBP such as toxins, enzymes, growth factors to particular cells.
Sequence
                                       Typical applications are as antiviral, neuromodilating and immunomodilating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                       cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Thr282Ser substitution.
                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                          diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capon
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371 AA
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89US-0315015.
91US-0808122.
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258..316
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332..35
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196..257
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1..37
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159..192
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Query Match

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RESULT
AAR9812
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                   Nucleic
binding
                                                                                                                  WPI;
                                                                                                                                     Capon
                                                     Disclosure;
                                                                                                                                                          (GETH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98122 standard; Protein; 371
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                                                                                                                 1996-238773/24.
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                                                                    acid encoding hybrid immunoglobulin comprising site of a receptor fused to Ig constant region is and treatment e.g. of inflammation
                                                                                                                                                         GENENTECH INC
                                                                                                                                    Lasky LA;
                                                     Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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89US-0315015.

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92US-0986931.

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332..354
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1..37
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                                                                                                                                                                                                                                                                                                                         Transmembrane domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Ile288Val substitution.
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                                                                                                          07-MAY-1996
                                                                                                                                                                  US5514582-A
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  22-NOV-1989;
                                                     23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation
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  89US-0440625
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332..354
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196..257
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38..154
/label= Lectin domain.
159..192
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355..371
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Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein (HuLHR) variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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Key

Location/Qualifiers

Homo sapiens metastasis. diagnosis; therapy; drug delivery; antiviral; ne immunomodulator; cell adhesion; graft rejection;

Immunoglobulin; transmembrane receptor; adhesion; targetting;

neuromodulator;

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                                                                                                                                                                                                                            AAR98124
                                                                                                                                                                                                                                         RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.). The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in ARR98106. This variant contains a Lys298-Lys299; Arg-Arg
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A hybrid immunoglobulin chain comprising the ligand binding situations as single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                                                                                        01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region
                                                                                                                       Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                    AAR98124;
                                                                                                                                                                                                             AAR98124 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                        117;
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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91US-0808122.
92US-0986931.
94US-0185670.
                                                                                                                                                                                                              Protein;
                                                                                                                                                     entry)
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Pred. No. 2.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded by discrete genes. The hybrid liminungians. With the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an analysis of the compression of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin constant region. The receptor is not immunoglobulin super family, nor a multiple subunit polypeptide immunoglobulin super family, nor a multiple subunit polypeptide combined by discrete genes. The hybrid immunoglobulin chain combined by discrete genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capon
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                                61
                                                                             38
                                                              TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996-238773/24.
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid encoding hybrid immunoglobulin comprising the site of a receptor fused to Ig constant region - us is and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                              371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lasky LA;
                                                                                                                                                                        Conservative
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91US-0808122.
92US-0986931.
94US-0185670.
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196..257
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/label= Lectin domain.
159..192
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/label= Signal region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                        0;
                                                                                                                                                                Score 666; DB 17;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding repeat 2
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                                                                                                                                                                   Indels
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                                                                                                                                                                                                                   371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ne ligand useful for
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                           metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin;
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                                                                                                                                        1996-238773/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Lymphocyte
                                                                                                                                                                                                                                                                                                   -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                              89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                   /label=
258..315
                                                                                                                                                                                                                                                                                                                              /label
                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane receptor;
                                                                                                                                                                                                                                                                /label= Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                             /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                py; drug delivery; antiviral; neuromodulator;
cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                      /label= EGF
                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                            cell
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                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                           surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                    Lectin domain
                                                                                                                                                                                                                                                                                                        Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                 Signal region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                              adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                            targetting;
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Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation e.g. of inflammation

Disclosure; Page 19; 41pp; English.

a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral parenchinations. A hybrid a single Typical applications are as antiviral, neuromodulating immunoglobulin chain comprising the ligand binding agents, or as modulators of cell (e.g. site ín of

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RESULT 1
AAR37960
ID AAR37960
XX AAR3
AC AAR3
AC AAR3
AC AAR3
XX Hulk
KW Hulk
KW Hurar
XX Home
FT Pro
FT Pro
FT Pro
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Best Local S
Matches 117
              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR37960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR37960 standard; Protein; 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Asn271 deletion mutant.
                                                                                                  Modified-site
                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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                                                                          Modified-site
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                                                                          /note=
311..3
           /note= "stop
356..372
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197..2
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                                                                                                                                                   246..248
                                                                                                                                                                                                    216..218
                                    /label-
                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                        /note-
                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                               note- "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                         'label- Lectin_domain
                                                                                                                                                                                                                                                                                                                                                                  note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homing Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                          .313
                                                   355
                                                                                                                                                                                                                             258
                                                                                                                                                                                                                                                                                193
                                                                                                                                                                                                                                                                                                                                                                 "Trp39 is probable
                                                             "potential
                                                                                     "potential
                                                                                                                                      "potential
                                                                                                                                                               "potential
                                                                                                                                                                                     "potential N-glycosylation site"
                                                                                                                                                                                                                                      "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                         "potential N-glycosylation site"
 Cytoplasmic_Domain
                       "stop transfer sequence"
                                                                                                            Complement_Binding_Repeat_2
                                                                                                                                                                                                                                                                EGF_domain
                                                                                                                                                                                                                Complement_Binding_Repeat_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 666; DB 17;
Pred. No. 2.3e-63;
; Mismatches 0;
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                                                                                     N-glycosylation site'
                                                                                                                                     N-glycosylation site
                                                             N-glycosylation
                                                                                                                                                            N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lymphoma
                                                                                                                                                                                                                                                                                                                                                                   N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastasis;
                                                                                                                                                              site"
                                                                                                                                                                                                                                                                                                                site"
                                                             site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                                                                                                                                   mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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RESULT 2
AAR38908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human peripheral blood lymphocyte cDNA library in lambda gt10 was screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was isolated and sequenced. The ORF codes for 372 amino acids with a mol. wt. of approximately 42.200. Comparison of the HuLHR amino acid sequence with the murine LHR sequence (AAR37961) showed a high degree of amino acid conservation in each of the LHR domains, e.g. 96% in the transmembrane domain and 83% in the carbohydrate binding of lymphocytes to lymphoid tissue to treat inflammation or graft conservation. They could also be used to control lymphoma metastasis
                                                                                      Human; murine; lymphocyte; cell surface glycoprotein; homing receptor; LHR; endothelium; lymphocid tissue; signal; domain; complement binding; carbohydrate binding; epidermal growth factor-like; egf; intracellular transmembrane binding; cytoplasmic; ligand binding partner protein;
                                                                              TMD;
                                                                                                                                                       HuLHR.
                                                                                                                                                                                 11-JAN-1994
                                                                                                                                                                                                                                  AAR38908 standard; Protein; 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermal growth factor and complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ43154
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31-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1993
                                                     Homo sapiens
                                                                                                                                                                                                          AAR38908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to treat conditions involving lymphocyte accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lasky
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              1 WTYHYSEKPMNWQRARRECRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                                                                                              1993-188588/23.
                                                                              LBPP.
                                                                                                                                                                                                                                                                                                                                                wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 1 and Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine lymphocyte homing receptors to treat and inflammation - comprise carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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91US-0786149
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Location/Qualifiers 20..32 /note= "Signal pepti
                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                               Score 666; DB 14;
Pred. No. 2.3e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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ate binding,
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Peptide

"Signal peptide"

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RESULT 2
AAR76506
ID AAR7
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AC AAR7
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                                                                                                                                                                                                                                                         The sequences given in AAR38908-09 represent human and murine lymphocyte cell surface glycoprotein (LHR) respectively. These proteins mediate the binding of lymphocytes to the endothelium of lymphoid tissue. LHR is a glycoprotein which contains a signal domain, a carbohydrate binding domain, an epidermal growth factor-like (egf) domain, at least cone complement binding domain repeat, a transmembrane binding domain (TMD) and a charged intracellular or cytoplasmic domain. The murine and human amino acid sequences show a high degree of overall homology (83%), however degrees of homology between the various domains is variable. These proteins may be fused to a ligand binding partner protein (LBPP) which causes an increase in the half life of the LHR. The fusions may be used therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue. They may be used in organ or graft rejection and for the treatment of inflammation.
                                                                                                                                                                                 Matches
                                                                                                                                                                                             Query Match
Best Local
          AAR76506;
                                AAR76506 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1989;
22-NOV-1989;
16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New lymphocyte homing receptor immunoglobulin fusion polypeptide(s) - used to inhibit binding of lymphocytes therapeutic and diagnostic uses
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1993
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                                                        21
                                                                                         99
                                                                                                               61
                                                                                                                                      39
                                                                                                                              1993-226664/28.
                                                                                                                                                                                 al Similarity
117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ44243
                                                                                                                                                                                                                                          372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lasky LA;
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0315015.
89US-0440625.
91US-0808122.
                                                                                                                                                                                                                                          AA;
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/note= '
39..155
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356..3
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160..193
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                               Protein;
                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cytoplasmic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Transmembrane binding
                               372 AA
                                                                                                                                                                                0;
                                                                                                                                                                                           Score 666; DB 14;
Pred. No. 2.3e-63;
                                                                                                                                                                                Mismatches
                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain"
                                                                                                                                                                               Indels
                                                                                                                                                                                                     Length
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                                                                                                                                                                                                     372;
                                                                                                                                                                              0;
                                                                                                                                                                              Gaps
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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
             A murine Mel 14 antigen cDNA clone was used to screen a lambda gtl cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells. A cDNA clone encoding LHR was isolated.
                                                                       New hybrid ligand binding constant region sequences half-life
                                                    Disclosure; Fig.la-1c; 40pp; English.
                                                                                                                                         Capon
                                                                                                              N-PSDB; AAQ92802
                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                            23-FEB-1989;
                                                                                                                                                                                                                                               27-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human LHR.
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                                                                                                                                        Lasky LA;
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                                                                                                                                                                             89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
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                                                                                                                                                                                                                                                                                                                        /label=
335..357
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311..313
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271..273
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246..248
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
177..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= N-glycosylation-site 104..106
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label= Mat_protein
39..334
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20..32
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                        /Label
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                                                                                                                                                                                                                                                                                                                       el= N-glycosylation_site
.357
                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                 "putative intracellular region'
                                                                                                                                                                                                                                                                                                   "putative stop transfer or membrane anchor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "hydrophobic domain, may act as signal for insertion into the endoplasmic reticulum lumen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "putative
                                                                                                                                                                                                                                                                                                                                                 N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                  N-glycosylation_site
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                                                                               partner molecules - fu
to increase stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular
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                                                                                immunoglobulin
vivo plasma
                                                                               plasma
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Sequence

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RESULT 2
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IDAR 83050
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Best Local
                                           22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human LHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR83050 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocyte cell surface glycoprotein; LHR; transmembrane recepto immunoglobulin; IgG; constant region; receptor-mediated disease; vector; plasma-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1996
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                  89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
                                                94US-0185669
                                                                                                                                                                                 89US-0315015
                                                                                                                                                                                                                                                                                                                                      /label=
311..313
                                                                                                                                                                                                                                                                                                                                                                                  /label
271..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
177..179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Epidermal_growth_factor_domain
97..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                abel=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complement_factor_binding_domain
                                                                                                                                                                                                                                                                                                               N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane_binding_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 666; DB 16;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHR; transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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ARESULT 2
AAR98106
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KW 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was us to screen an oligo-dT primed lambda gtl0 cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells. A 2.2 kb clone (sequence given in AAT05869) was isolated that encoded human LHR protein (AAR83050). LHR-IgG hybrids were constructed for in the targeting of therapeutic moleties to lymphoid tissue.
  23-FEB-1989;
                                             07-MAY-1996
                                                                                                                                                       Domain
                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; thera
immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lymphocyte cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98106 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression vector encoding fusion protein to increase plasma life comprises receptor ligand binding site and Ig constant region, for treatment of receptor mediated disease
                                                                                       US5514582-A.
                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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DB; AATO5869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ďď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasky LA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
  89US-0315015
                                                                                                                                                                                                                                                                                                                                                                           /label= Signal
39..155
                                                                                                                                                                                                                                            /label= Complement binding repeat 1.
259..317
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                        /label-
                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                        /label= Lectin domain
                                                                                                                                     /label=
                                                                                                                                                                            label=
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                                                                                                                                                                                                                   Complement binding repeat
                                                                                                                                                                                                                                                                                                               EGF domain.
                                                                                                                                Cytoplasmic domain
                                                                                                                                                                            Transmembrane domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 666; DB 16;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoprotein (HuLHR).
                                                                                                                                                                                                                                                                                                                                                                                                  region
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RESULT 2
AAR981.33
ID AAR98
XX AAR9
AC AAR9
XX O1-N
XX IUMU
DE HUMA
XX IUMU
KW IIUMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subnit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
9
                                                                                                 Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                         Homo sapiens
                                                                                                                                                                            Human
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a single
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                              AAR98133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potentially immunogenic epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Figure 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                                                                                                                                                    wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw
                                                                                                                                                                         lymphocyte cell surface
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DB; AAR98106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d immunoglobulin chain comprising the ligand bir e transmembrane receptor without an active transfused at its C-terminus with the N-terminus of labeling active.
                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                        (first entry)
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89US-0315015.
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                     glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 666; DB 17;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         active transmembrane
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QΥ 밁

38

61 TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC

117

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Qy
                                                                Matches
                                                                            Query Match
Best Local Similarity
                                                                                                                                                        Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 209-Asn insertion.
                                                                                                                                                                                                                                                                                      immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                           a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member o
                                                                                                                                                                                                                                                                                                                                                                                                                     A hybrid immunoglobulin chain comprising the ligand binding a single transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 19; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capon DJ, Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-1996
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                                    Н
372
                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                    AA;
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92US-0986931.
94US-0185670.
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89US-0315015
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38..154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                               0;
                                                            Score 666; DB 17;
Pred. No. 2.3e-63;
Mismatches 0;
                                                             Indels
                                                                                       Length
                                                                                       372;
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     site
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В

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twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc

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22-NOV-1989;
23-FEB-1989;
19-DEC-1991;
08-DEC-1992;
21-JAN-1994;
26-MAY-1995;
The sequence is that of a human lymphocyte homing receptor (LHR) which may be used in the construction of a chimeric molecule comprising an LHR fused at its C terminus to the N terminus of an immunoglobulin constant region. This can be used for the prevention of lymphocyte attachment to endothelial cells. Such a method may
                                                                        Prevention of lymphocyte attachment to endothelial cells - using chimeric molecule comprising lymphocyte homing receptor and immunoglobulin constant region
                                                                                                                                          Capon
                                                        Disclosure;
                                                                                                                                                                                                                                                                03-FEB-1998
                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                               23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW37781 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                              1998-129805/12.
DB; AAV19012.
                                                                                                                                          ď,
                                                                                                                                         Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homing receptor; LHR; HuLHR; organ; graft; rejection; inflammatory disorders; rheumatoid arthritis; diseases; lymphoma metastasis; control; lymphocyte;
                                                     Fig 1; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                            89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.

95US-0451848.
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177..179
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60..62
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246..2
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216..21
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232..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "potential signal sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homing
                                                        English.
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 r the prevention a method may
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ANATAZGA
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CC Invector
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                                                                                                                                                                                                                                                                                                                                                 23-FEB-1989;
31-OCT-1991;
06-MAY-1993;
           This sequence is the human lymphocyte homing receptor (LHR) of the invention. LHR is a lymphocyte cell-surface glycoprotein that mediates the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble LHR polypeptides, lacking signal peptide (amino acids 1-38), transmembrane domain (amino acids 33-355) and cytoplasmic domain (amino acids 356-372), can be used therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue and are especially useful for organ or graft rejection treatment protocols, for treating inflammations such as arthritis and other autoimmune diseases, for control of lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used for preventing organ or graft rejection, for treating inflammatory disorders, e.g. rheumatoid arthritis or other autoimmune diseases, for controlling lymphoma metastasis and for treating conditions in which there is an accumulation of lymphocytes.
                                                                                                                                                      Claim
                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                           (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lymphocyte homing receptor
                                                                                                                                                                                             Lymphocyte
                                                                                                                                                                                                                                                                 Lasky
                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     24 - NOV - 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lymphocyte
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                                                                                                                                                                                                                                                                                                                                     10-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocyte accumulation; human.
                                                                                                                                                                               lymphocyte
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                                                                                                                                                                                                                                      1999-034122/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                 LA,
                                                                                                                                                                                                                                                                                           GENENTECH INC.
UNIV CALIFORNIA.
                                                                                                                                                                                                                         AAV08321.
                                                                                                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homing receptor; LHR; lymphocyte cell-surface glycoprotein; binding; endothelium; graft rejection; inflammation; therap autoimmune disease; lymphoma metastasis;
                                                                                                                                                                             binding to
                                                                                                                                                                               homing receptor polypeptides - I binding to lymphoid endothelium
                                                                                                                                                                                                                                                                 Rosen SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                   1; 33pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                    89US-0315015.
91US-0786149.
93US-0059029.
95US-0513278.
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                                                                                                                                                   English.
                                                                                                                                                                             lymphoid
                                                                                                                                                                                                                                                              Singer
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                                                                                                                                                                                                                                                                 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 666; DB 19;
Pred. No. 2.3e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                 Stachel SE;
                                                                                                                                                                                             useful
                                                                                                                                                                                             for inhibiting
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treating

autoimmune diseases, conditions involving

Soluble

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Best Local Similarity
               The specification describes a product which antagonizes binding of respiratory synctial virus (RSV) G-protein to annexin II or L-selectin, or causes a decrease in cell surface levels of annexin II or L-selectin. Such products are used in the manufacture of a medicament for use in prevention or treatment of RSV infection.
                                                                            Disclosure; Page 67-69; 74pp; English
                                                                                                   Treatment of respiratory synctial virus II or L-selectin derivatives
                                                                                                                                  WPI;
                                                                                                                                                      Malhotra R,
                                                                                                                                                                         (GLAX )
                                                                                                                                                                                             21-OCT-1999;
                                                                                                                                                                                                                 23-OCT-2000;
                                                                                                                                                                                                                                      26-APR-2001
                                                                                                                                                                                                                                                          WO200129054-A2.
                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory synctial virus; RSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB68334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB68334 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHR polypeptides can also be or competitive inhibitors of I antibodies, and as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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        present sequence represents human L-selectin
                                                                                                                                 2001-316238/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
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                                                                                                                                                                          GLAXO GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                    Bird M;
                                                                                                                                                                                                                 2000WO-GB04084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                             99GB-0024990
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55..15
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                                                                                                                                                                                                                                                                                                            /note=
356..3
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                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            ..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                               "cytoplasmic region"
                                                                                                                                                                                                                                                                                                                   "transmembrane region"
                                                                                                                                                                                                                                                                                                                                       "extracellular domain"
                                                                                                                                                                                                                                                                          "C-type lectin carbohydrate binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                   RSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in assays for LHR, anti-LHR antibodies LHR activity, and for purifying anti-LHR for raising anti-LHR antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein; annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 2.3e-63; matches 0;
                                                                                                             infection
                                                                                                         (RSV) using Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                 II; L-selectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372;
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RESULT 1
AAAR98134
AAAP98134
AAAP981
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                                       22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                   Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidingnosis and treatment e.g. of inflammation
                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                     21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1989;
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immunomodulator;
                                                                                                                                                                                                                               (GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin; transmembrane receptor; adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                               1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                      ρJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 100.0%; al Similarity 100.0%; 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphocyte cell
                                                                                                                                                                                                                             GENENTECH INC
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                                                                                                                                                                                  Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
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89US-0315015.

91US-0808122.

92US-0986931.

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261..319
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159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Transmembrane domain 358..374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Cytoplasmic domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 666; I
Pred. No. 2.3
); Mismatches
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No. 2.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Disclosure;

Page

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41pp;

English

for

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RESULT 2
AAR98135
ID AAR9
XX AAR9
XX AAR9
XX IMM
DT 01-N
XX IMM
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC A hybrid immunoglobulin chain comprising the ligand binding site of CC a single transmembrane receptor without an active transmembrane (CC a single transmembrane receptor without an active transmembrane (CC region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the communoglobulin super family, nor a multiple subunit polypeptide (CC encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in composer than one ligand. It can be used diagnostically for the in composer than one sasay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or administration; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates precious columnities achieved achieves solubility and removes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
  07-MAY-1996
                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                 Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 241-Val-Glu-Asn insertion
                                         US5514582~A
                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                            /label-
258..319
                                                                                                                                                                                                                                                          /label= Lectin domain 159..192
                                                                                                                                                                                                                   /label= EGF domain
196..257
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                                                                                                                     /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                 /label - Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                     oy; drug delivery; antiviral; neuromodulator;
cell adhesion; graft rejection; inflammation;
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                                                                              Cytoplasmic domain
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Pred. No. 2.3e-63;
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Best Local Similarity
Matches 117; Conser
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chalm combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR99106 are glven in AAR99109-R98135. This variant contains a 292-Tyr-Tyr-Tyr insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                        Rapid immunoselection cloning technique; cell surface antigen; murine Mel-14; homing receptor; antigen-presenting cells.
                                                                                                                                                                              T lymphocyte-specific Leu8 Antigen major form
                                                                                                                                                                                                                                                 21-MAY-1992
                                                                                                                                                                                                                                                                                                          AAR20815;
                                                                                                                                                                                                                                                                                                                                                                      AAR20815 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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92US-0986931.
94US-0185670.
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89US-0315015
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                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 666; DB 17; 100.0%; Pred. No. 2.3e-63; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      385
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                                                                                         Matches
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                    Two cDNA clones encoding Leu8 determinants were isolated from a human T cell library using the rapid immunoselection cloning method (see e.g. AAQ21164 for description of method). This protein sequence was deduced from the larger insert. The hydrophobic putative membrane-spanning domain is followed by several positively charged
                                                                                                                                             Sequence
                                                                                                                                                                         residues resembling a cytoplasmic anchor sequence. The protein is closely related to the murine Mel-14 homing receptor. See AAQ22500 for the shorter insert and AAR22551 for the phosp
                                                                                                                                                                                                                                                                                           New CD53 cell surface antigen and DNA encoding immuno-therapy and diagnosis of haematopoietic
                                                                                                                                                                                                                                                                                                                                                              Seed
    112
                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                  (GEHO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-1992
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                                        TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
{\tt twvgtnkslte} eaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                                                                                                                                                                                                                                                                                                                                       1992-056864/07
                                                                                                                                                                                                                                                                       14; Page 106; 160pp; English.
                                                                                                                                                                                                                                                                                                                              AAQ21184.
                                                                                                                                                                                                                                                                                                                                                                                  GEN HOSPITAL CORP
                                                                                                                                                                form
                                                                                                                                                                                                                                                                                                                                                            Aruffo A,
                                                                                     100.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                of Leu8 antigen.
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299..301
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113..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= N-linked_glycosylation /note= "putative" 157...159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-linked_glycosylation
/note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-linked_glycosylation
/note= "putative"
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/note= "putative"
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/note= "putative"
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/note= "putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          " N-linked_glycosylation
"putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane
                                                                                        0;
                                                                                     Score 666; DB 13;
Pred. No. 2.4e-63;
; Mismatches 0;
                                                                                                                                                                                                                                                                                            neoplasms,
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                                                                                   Gaps
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RESULT 31 AAR32707

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3C B cell-specific cDNA was isolated from a human tonsil cDNA library
3C (ATCC #37546) using differential hybridisation with labelled cDNAs
3C from either B cell(RAJI) RNA or T cell (HSB-2) RNA. Positive
3C plaques were isolated and cloned and the cDNA inserts subcloned into
3C pSp65. One of the 261 RAJI+ HSB2- cDNA clones isolated, B125
3C contained a 1.9 kb cDNA insert that hybridised with a 2.4 kb RNA
3C species found in several B cell lines. However B125 did not
3C tybridise with any of the other RAJI+ HSB- clones or with mRNA from
3C several T cell lines. The B125 cDNA clone hybridised with a 2.3 kb
3C cDNA, termed pLAM-1 (prod. shown). The amino acid sequence of
3C cDNA, termed pLAM-1 (prod. shown). The amino acid sequence of
3C cDNA, termed plam-1 (prod. shown). The amino acid sequence of
3C contained antibodies specific for LAM-1 may be prepd. and are useful
3C in the treatment of inflammation, autoimmune disease, shock, tissue
3C damage, organ or tissue transplant rejection and to inhibit the
3C metastasis and homing of malignant cells which express the LAM-1
                                                                                                                                                                                                                                                                    Monoclonal antibodies to leukocyte adhesion molecule-1 useful for treating inflammation, cancer, auto-immune citissue damage and organ or tissue transplant rejection
                                                                                                                                                                                                                                         Disclosure; Fig 2; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue; transplant; metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAM-1 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR32707 standard; Protein; 385
                                                                                                                                                                                                                                                                                                                              1993-076177/09.
DB; AAQ37304.
                                                                                                                                                                                                                                                                                                                                                                                                  ) DANA
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245..247
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259..2
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117..1
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73..75
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346..362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "hydrophobic, possible
                                                                                                                                                                                                                                                                    lammation, cancer, auto-immune diseases or tissue transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-glycosylation
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be used to moniter lamY-1 gene regulation
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RESULT 32
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ID ADA 341
XX AR 341
XX Leukog
XX Leukog
KW LAM-1.
XX Homo 9
FH Key
FT Bindin
FT Bindin
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Best Local S
Matches 117
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  Disclosure;
                                                                                                                                                                                                                                                               03-OCT-1991;
                                                                                                                                                                                                                                                                                                      05-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                   W09306835-A
                                         conditions,
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                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER
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                                                             leukocyte adhesion molecule-1 -
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                                                                                                                                            1993-134119/16.
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117; Conser
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                                                                            of inflammation or disease site - by using
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Fig
                                         auto-immune disorders,
                                                                                                                                                                                 Spertini OG
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245..247
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73..75
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44pp;
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Pred. No. 2.4e-63;
Mismatches 0;
                                                           treats leukocyte-mobilising
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RESULT
AAR56663
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding the LAM-1 protein was isolated from a human tonsil cDNA library (ATCC 37546). The mature LAM-1 protein has an extracellular region of about 294 amino acids containing 7 potential N-linked carbohydrate attachment sites. LAM-1 has a cytoplasmic tail of 17 amino acids containing 8 basic and 1 acidic residues. The processed LAM-1 protein has a Mr of at least 50,000. LAM-1 combines domains homologous to domains found in three distinct families of molecules: animal lectins, growth factors, and C3/C4 binding proteins.
This sequence represents L-selectin. The lectin domain of L-selectin may be used in the construction of the new bifunctional ligand-binding polypeptide of the invention. These peptides have leucocyte mobilising activity for treating tissue damage, autoimmune disease, post-reperfusion injury or organ/tissue transplant rejection. They act by interfering with binding of leucocytes at the site of inflammation and also inhibit platelet and mononulcear cell
                                                                                                                                                           New bifunctional polypeptide contg. binding domains of different selectin - and related DNA useful as leucocyte mobilising agents for treating autoimmune disease, post-reperfusion injury etc., also for targetted drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-selectin; lectin domain; bifunctional; ligand-binding polypeptid leucocyte; mobilising activity; tissue damage; autoimmune disease; post-reperfusion injury; organ/tissue transplant rejection; inflammation; inhibition; platelet; mononulcear cell; aggregation;
                                                                                                                             Disclosure; Page 26-28;
                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09417193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-selectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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117; Conservative
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                                                                                                                             56pp; English
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Pred.
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No. 2.4e-63;
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RESULT 3
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XX AAR9
XX AAR9
XX AAR9
XX Cell
KW Cell
KW Cell
KW Cell
KW Anti
XX Homo
XX US55
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Best Local Similarity
Matches 117; Conserv
                                                                                                                                                   01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
                      N-PSDB;
                                      WPI; 1996-200279/20
                                                                     Aruffo
                                                                                                                                                                                                                                                                       09-APR-1996
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                                                                                                      (GEHO)
                                                                                                                                       18-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR91442;
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                                                                                                                                  92US-0983647.
88US-0160416.
89US-0379076.
90US-0553759.
93US-0139273.
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347..368
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285..287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leu8 antigen; T-lymphocyte;
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Pred. No. 2.4e-63;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385;
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RESULT AAW21657
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Best Local
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                              Modified-site
                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                          Domain
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                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            Lymphocyte-associated antibody; autoimmune (
                                                                                                                                                                                                                                                                                                                                                                                                                       Human lymphocyte-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcript of 2.4 kb was present in peripheral blood mononuclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukaemic T-cell lines. Leuß antigens can be obtd. for diagnostic and therapeutic use. The presence or absence of Leuß on CD4+ T-cells identifies suppressor-inducer and helper-inducer CD4+ T-cell subsets. Soluble forms of Leuß can act as antiinflammatory agents by reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated from a human T-cell library using a novel immunosele cloning method. The longer insert (AAT14723) contained 2,350 residues, while the shorter lacked 436 internal residues. A r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 cDNA clones encoding Leu8 determinants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocyte migration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                               /label=
73..75
                                                                                                                                          /label=
363..385
                             /label= Glycosylation
/note= "putative N-glycosylation
190...192
                                                                    /label= Glycosylation /note= "putative N-glycosylation 117..119
                                                                                                                                                                    /label=
346..362
                                                                                                                                                                                                                                                                               /label=
14..51
                                                                                                                                                                                                                                     /label= Sig_peptide
/note= "signal peptide
N-terminal Met"
               /label=
                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                            d cell sur disease;
                                                                                                                                           385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                    362
               Glycosylation
                                                                                                                          Intracellular_domain
                                                                                                                                                    Transmembrane_domain
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                                                                                                                                                                                                          Mat_protein
                                                                                                                                                                                                                                                                                           Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                        surface protein; LAM-1; B lymphocyte;
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                                                                                                                                                                                                                                                                                                                                                                              cancer
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Pred. No. 2.4e-63;
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N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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site'
                                                                                 site"
                                          site"
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Modified-site

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RESULT 3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 117;
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                           Human Leu8 antigen
                                                                           07-JUN-1999 (first entry)
                                                                                                                                                                                       AAW80452 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies to leukocyte adhesion molecule-1 - used for binding LAM-1, e.g. for treating tissue damage, autoimmune disorders, cancers or organ or tissue transplants
                                                                                                                                     AAW80452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or tissue transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tedder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP770680-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT72270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DAND ) DANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                           112
                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                          TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                                                                                                                                                                                                                                                                                        twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
                                                                                                                                                                                                                                                                                                                                                                                                                               wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-238140/22
                                                                                                                                                                                                                                                                                                                                                 Page 6-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FARBER CANCER INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0313109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90EP-0301884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "putative N-glycosylation site" 288..290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≖ "putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "putative N-glycosylation site"
324..326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "putative N-glycosylation site"
259..261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10pp;
                                                                                                                                                                                       Protein; 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 666; DB 18;
Pred. No. 2.4e-63;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385;
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                                                                                                                           Query Match
Best Local Similarity
Matches 117; Conser
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13-JUL-1990;
21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                               The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. It is useful for the isolation and cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell, and was used to clone genes (see AAV63442-63) encoding cell surface antigens from mammalian lymphocytes (see AAW80440-55). The purifice genes and proteins are useful for immunodiagnostic and
                                                                                                                                                                                                                                    mediates adhesion to specialised endothelial cells of lymph nodes, is quite specific in its recognition of the lectin ligand sulphated galactosyl ceramide (sulfatide). Modification of the specificity of this binding could serve to regulate the homing potential of resting T cells. Soluble forms of Leu8 can act as antiinflammatory agents by reducing lymphocyte migration.
                                                                                                                                                                                                                                                                                                                                   immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders of animals, including humans. The extracellular domain of Leu8, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This polypeptide comprises human Leu8 antigen. Its amino acid sequence was deduced from the nucleotide sequence (see AAV63450) of a cDNA clone isolated from a T lymphocyte cDNA library using a novel method for cloning cDNAs from mammalian expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cloning vector and polylinker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human lymphocyte antigenic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992;
25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Column 67-70; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aruffo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leu8; cell surface antigen; human; T lymphocyte; antiinflammatory;
 112
                               61
                                                             52
             TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC 117
                                                            wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw
                                                                            WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
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twvgtnkslteeaenwgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEN. HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV63460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed
                                                                                                                                                                                                         385
                                                                                                                           Conservative
                                                                                                                                                                                                         ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0983647.
88US-0160416.
89US-0379076.
89US-0553759.
97US-0861205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 347..368
                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane
                                                                                                                           0;
                                                                                                                        Score 666; DB 19;
Pred. No. 2.4e-63;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain"
                                                                                                                           Indels
                                                                                                                                                       Length
                                                                                                                                                           385;
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                                                                                                                                                                                                                                                                                                                                     which
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RESULT

37

Matches

117;

Conservative

0,

Mismatches

0;

Indels

0;

Gaps

0,

60

52

1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW

Db Qγ DЬ QY

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AAW86199
    XX
    AAW8
    AC    A
                                                                                                                                                                                                                   C for the isolation and cloning of any protein which can be expressed CC and transported to the cell surface membrane of a eukaryotic cell, C and was used to clone genes (see AV81198-220) encoding cell surface CC antigens such as CD1a, CD1b, CD1c, CD2, CD5, CD7, CD13, CD13, CD14, CD16, CD2, CD20, CD22, CD26, CD27, CD2, CD6, CD7, CD13, CD33, CD34, CD35, CD37, CD38, CD39, CD40, CD31, CD43, CD40, CD33, CD40, CD31, CD40, CD41, CD31, CD40, CD40,
       Best Local Similarity
                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
07-JUN-1995;
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel method is based on transient expression of an antigen in The method is based on transient expression of cells expressing the eukaryotic cells and physical selection of cells expressing the eukaryotic results and physical selection of cells expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises human Leu8 antigen. Its amino acid sequence was deduced from the nucleotide sequence (see AAV81217) of cDNA clone isolated from a Tlymphocyte cDNA library using a novel method for cloning cDNAs from mammalian expression libraries.
                                                                                                                                                                                                            Lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Column 67-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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25-FEB-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leu8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding human CD40 antigen - useful for cloning cDNA encoding surface antigens, constructing cDNA libraries, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-069813/06.
DB; AAV81217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for expression in eukaryotic cells or their fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEN HOSPITAL CORP.
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                                                                                                                                                                                                        migration.
                                                                                                                                            385
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88US-0160416.
89US-0379076.
99US-0498809.
90US-0553759.
95US-0485447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aruffo A, (
       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385
       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camerini D, I
, Stamenkovic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
666; DB 20;
No. 2.4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lauffer L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stengelin
                               Length 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s
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AAY96138
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the antigen by adhesion to (panning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders in animals, including humans. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases or multiple sclerosis. The ability to interfere with the binding of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
                                                                                                                                                                                                           The present sequence is that of a T-cell specific Leu8 antigen, as predicted from 1 of 2 clones (see AAA50596) isolated from a human T-cell library by the method of the invention. A shorter Leu8 antigen is given in AAY96184. The method, designed to isolate cell surface antigen (CSA) cDNAs, is based upon transient expression of a CSA in eukaryotic cells and physical selection of cells expressing a CSA in eukaryotic cells and physical selection of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                           Example 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stamenkovic I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6111093-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO ) GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T-cell specific Leu8 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amyloidosis; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodiagnosis;
immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leu8; cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-586382/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA50596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                        Column 69-70; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0160416.
89US-0379076.
90US-0498809.
90US-0553759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9205-0983647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0181612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 347..368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; immunotherapy; gene therapy;
infection; asthma; immune-complex disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis; inflammation; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; immunoselection; panning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385
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RESULT 39
AAU02447
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such binding to occur on surfaces other than lymphocyte cells, can be useful in diagnostics and therapy. The level of activated Leu8-T-cells relative to resting Leu8+ cells could serve as a measure of immune response to a particular antigen. Modification of the specificity of the extracellular domain of Leu8, which mediates adhesion to specific endothelial cells of lymph nodes, could serve to regulate the homing potential of resting T cells. Soluble forms of Leu8 could act as antiinflammatory agents by radmain.
                 25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
                                                                                                                                                                                                                                                                                                                              Human; T-lymphocyte specific antigen; immune-mediated disease; Leu8; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus crythematosus; platelet disorder; rheumatoid arthritis;
                                                        01-DEC-1992;
                                                                           17-APR-2001
                                                                                              US6218525-B1
                                                                                                                           Domain
                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                       transplant rejection; asthma
                                                                                                                                                                                                                                                                                                                                                                       Human T-lymphocyte specific antigen Leu8 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                              AAU02447;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02447 standard; Protein; 405 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWVGTNKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKAALC
                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt twvgtnksltee} a en {\tt wgdgepnnkknkedcveiyikrnkdagkwnddachklkaalc}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                 88US-0160416.
89US-0379076.
90US-0553759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA,
                                                       92US-0983647
                                                                                                                                                       /note= "/
                                                                                                                                                                                                                                   /note= "I
                                                                                                                                                                         /note= "1
324..326
                                                                                                                                                                                                                                                     /note= "!
157..159
                                                                                                                                                                                                                                                                        Location/Qualifiers 113..115
                                                                                                                          347..368
                                                                                                                                                                                                                 269..271
                                                                                                                                                                                              285..287
                                                                                                                 /label=
                                                                                                                                                                                                      note-
                                                                                                                                                                                                                         /note=
                                                                                                                                    "These amino acids are proform but are absent in
                                                                                                                                                                                                                        "N-linked glycosylation site"
                                                                                                                                                               "Asn is N-glycosylated"
                                                                                                                                                                                   "N-linked
                                                                                                                                                                                                      "N-linked
                                                                                                                                                                                                                                            "N-linked
                                                                                                                                                                                                                                                              "N-linked glycosylation site"
                                                                                                                 Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 666; DB 21;
Pred. No. 2.4e-63;
Mismatches 0;
                                                                                                                                                                                  glycosylation
                                                                                                                                                                                                      glycosylation
                                                                                                                                                                                                                                           glycosylation
                                                                                                                                    present in the short
                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                     form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                    m of Leu8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                         Вb
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                                                                                                                                                                                                                                                                                          γ
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(GEHO) GEN

HOSPITAL CORP

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RESULT 40
AAR98110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte cell surface antigen polypeptide sequences

(AAU02452-AAU02452) are described in the present invention. The invention

(CAAU02453-AAU02452) are described in the present invention. The invention

(CI can are invention of cloning cDNA encoding cell surface antigens

(CI can efficient construction of cDNA libraries. Also described are 2

(CI caxpression vectors (AAS03171, AAS03174) which provide high level

(CI caxpression in eukaryotic host cells. A genetically engineered cDNA

(CI camino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-134 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144-759 of the CD28 cDNA sequence (AAS03175) is also

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

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(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-144 given in AAU02437) and/or comprising nucleotides

(CI (Amino acids 1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA encoding CD28 useful for diagnosing immune-mediated diseases, infections or disorders, e.g. erythematosus, asthma, transplant rejection, rheumatoid {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents human T-lymphocyte specific antigen Leu8 encoded by a long Leu8 cDNA clone. The shorter cDNA clone lacks 431 bases and consequently lacks residues 344-385 given here. Various human lymphocyte cell surface antigen polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seed
                                                                                                                                                                                                                                                                     diagnosis; therap
immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98110 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation, platelet disorders, plasma and other cell neoplasms, parasitic diseases, multiple sclerosis, Guillain-Barre syndrome an tissue and organ transplant rejection. The sequences can also be uidentify, isolate and purify other antibodies and antigens.
                                                                                                                                                                                                                                            metastasis
                                                                                                                                                                                                                                                                                                                                                                                        Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Column 63-66; 72pp; English.
                               Domain
                                                                                                                      Key
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                   Immunoglobulin;
                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WTYHYSEKPMNWQRARRFCRDNYTDLVAIQNKAEIEYLEKTLPFSRSYYWIGIRKIGGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wtyhysekpmnwqrarrfcrdnytdlvaiqnkaeieylektlpfsrsyywigirkiggiw 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-289848/30.
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                                                                                                                                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
/label=
38..154
/label=
                                                                                                                                                                                                                                                                                                                                   transmembrane
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                        cell adhesion; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; So
100.0%; P:
ative 0;
                                                                                                                                                                                                                                                                                              nsmembrane receptor; adhesion; drug delivery; antiviral; neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simmons
                                                        Signal region
   Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 666; DB 22;
Pred. No. 2.5e-63;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                        inflammation;
                                                                                                                                                                                                                                                                                                                                   targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g and treating systemic lupudarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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c encoded by discrete genes. The hybrid immunoglobulin chain combines
C the adhesion/targetting of a ligand binding partner (LBP) with the
C effector functions of immunoglobulin and can bind to and/or activate
more than one ligand. It can be used diagnostically for the in
Vitro assay of LBP and their targets; or therapeutically to deliver
CLBP such as toxins, enzymes, growth factors to particular cells.
C Typical applications are as antiviral, neuromodulating and
C treating graft rejection; inflammation; metastasis of lymphoma etc.)
C The immunoglobulin component increases plasma half life and
C facilitates purification while deletion of the transmembrane region
C facilitates recovery, improves aqueous solubility and removes
C potentially immunogenic epitopes. Variants of the human lymphocyte
C cell surface glycoprotein described in AAR98106 are given in
C AAR98109-R98135. This variant contains an Ala71Ser substitution.
                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                            Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capon DJ, Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1996
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                                                 61
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                                                                                      371 AA;
                                                                                                                                                                                            Conservative
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94US-0185670.
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332..354
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258..316
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/label= I
196..257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Cytoplasmic domain
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                                                                                                                                                                                          1;
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Pred. No. 4.8e-63;
1; Mismatches 0;
                                                                                                                                                                                          0;
                                                                                                                                                                                                                                    Length 371;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Gapop 10.0 ,
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sp_bacteriap:*
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sp_plant:*
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sp_virus:*
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        Gapext
      Q9U443
Q28624
Q63762
Q9GLF0
Q9GLF0
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Q28657
Q2858
Q95509
Q95508
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063762 rattus norv
099160 canis famil
095192 ovis aries
028657 oryctolagus
028657 oryctolagus
028657 oryctolagus
028509 homo sapien
095509 homo sapien
095508 homo sapien
095191 equus cabal
029097 sus scrofa
095193 odocolleus
028290 canis famil
099ngv4 drosophila
                                                                                                                                                                                                                                                                                               Q9uj43 homo sapien
Q28629 oryctolagus
                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9UJ43
        InterPro; IPR002396; Selectin
InterPro; IPR000436; Sushi_SC
Pfam; PP00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; Sushi; 2.
Pfam; PF00084; Sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UJ43 PRELIMINARY; PRT; 385 AA.
Q9UJ43;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
L-SELECTIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \begin{array}{c} 117 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\ 127 \\
                                                                                                                                                                                                             EMBL; AJ246000; CAB55488.1; ...
HNSP; P14151; 1KJB.
InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                  Fieger C.B.;
Thesis (1998), Freie Universtiaet Berlin, Fachbereich Chemie.
EMBL; AJ246000; CAB55488.1; •.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
    PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS50041; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=HEMATOPOIETIC Fieger C.B.;
                                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEMATOPOIETIC
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-SELECTIN.
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Q9H557
3 P79941
Q9U72
Q9U041
Q9GNU3
Q9GNU3
Q91902
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Q9UA13
Q9GPA5
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L Q99PC6
L Q91WN8
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Q25253
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Q9UPL3
Q9R172
Q9R6L8
Q9UM47
L Q35516
Q9U721
Q04721
Q9H240
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Q9U0E2
Q95YG0
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09557 homo sapien
P79941 xenopus lae
09ujv2 homo sapien
09ujv2 homo sapien
09un41 homo sapien
09un41 homo sapien
09un43 caenorhabdi
09un43 caenorhabdi
09un43 branchiosto
006008 mus musculu
09un13 homo sapien
09r172 rattus norv
09v618 homo sapien
09un47 rattus spien
09un47
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Q91wn8 mus musculu
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RESULT
Q63762
ID Q6
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q28629 PRELIMINARY;
Q28629;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-DEC-2001 (TrEMBLrel. 19, L
L-SELECTIN PRECURSOR.
    Q63762;
Q63762;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qian J., Marks R.M.;
"CDNA for rabbit L-selectin.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; UZ6535; AAA67896.1; -.
HSSP; P14151; 1KJB.
HSSP; P14151; 1KJB.
                                                                                                                                                                                                                                                                                                                                                                        CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
Pfam; PF00084; sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
EGF-like
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGE_1; UKKNOWN_1.
PROSITE; PS01186; EGE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNSP; P14151; 1KJB.
InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-KIDNEY CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
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SM00034; CLECT; 1.
SM00181; EGF; 1.
                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 domain;
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domain; Glycoprotein;
51 P
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376 1
      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.)
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                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Lectin; Selectin;
38 POTENTIAL.
376 L-SELECTIN.
A; 42346 MW; 59F6AD530F490947 C
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97.0%;
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Last annotation update)
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                                                                                                                                                                                                                                                                Score 181; DB 6;
Pred. No. 3.8e-17;
3; Mismatches 2;
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                                                                                    PRT;
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sequence update)
annotation update)
                                                                                  372
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1.8e-20;
0;
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                                                         "Cloning and sequencing of beagle E-selectin ge comparison with other species.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ d EMBL; AF287257; AAG10039.1; -.

EMBL; AF287257; AAG10039.1; -.

InterPro; IPR000361; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR002396; Sushi_SCR_CCP.
Pfam; PF00059; lectin_c; 1.

Pfam; PF00084; sushi; 6.
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Best Local :
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Pfam; PF00008; SGF; 1.

Pfam; PF00008; Sushi; 2.

Pfam; PF00008; Sushi; 2.

Pfam; PF00008; SUBECTIN.

SMART; SM00032; CCP; 2.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00041; GJYCOPTOTEIN.

PROSITE; PS01086; EGF_1; UNKNOWN_1.

EGF-like domain; GJYCOPTOTEIN.

SEQUENCE 372 AA; 42471 MW; 7DFD12
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01-MAR-2001
01-DEC-2001
                         PRINTS; PR00343; SMART; SM00032; (
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                    TISSUE=ENDOTHELIAL CELLS;
Zheng L., Shi Y., Wu H.,
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Sackstein R., Meng L., Xu X.M., Chin Y.H.;
"Evidence of post-transcriptional regulation of L-selectin expression in rat lymphoid cells.";
Immunology 8:198-204(1995).
EMBL; S79523; AAC60710.2; -.
HSSP; P14151; IKJB.
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InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR
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NCBI_TaxID=10116;
[1]
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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  SM00032;
SM00034;
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3; SELECTIN.
; CCP; 6.
; CLECT; 1.
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78.8%;
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16,
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                       G.;
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Canis.
                                                                                                                                                                                                                                                                                                           DNA
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RESULT

QS95LG2

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Q95LG2;
Q95LG2;
Q1-DEC-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
E-SELECTIN.
Qvis aries (Sheep).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Cetar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMOO181; EGF; 4.

SMART; SMOO001; EGF_like; 1.

PROSITE; PS500041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF_l; UNKNOWN_1.

Lectin; Selectin.

SEQUENCE 609 AA; 66073 MW; 41E62D
                                                                                                                                                                                                                                                                                                Q28657; PRELIMINARY; Q28657; O1-NOV-1996 (TrembLrel. CO1-NOV-1996 (TrembLrel. CO1-NOV-1996 (TrembLrel.) (TrembLrel.)
                                                                           SEQUENCE FROM N.A.

Vora D.K., Fang 2., Liva S
Territo M.C., Berliner J.A

"Induction of p-selectin b
atherosclerosis";
                                                                                                                                                                                                                                                               Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of equine E-selectin.
Immunology 103:498-504(2001).
EMBL; AF307971; AAK48711.1; -.
                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                        P-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21421234; PubMed=11529941;
Hedges J.F., Demaula C.D., Moore B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
  SEQUENCE FROM N.A. Warden C.H.;
                                                              Submitted
                                                                                                                                                                                                    NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MacLachlan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTPTSCSSHGECVETINSHTCQCHPGFKGLRCE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTPTSCSGHGECVETVNNYTCKCHPGFRGLRCE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 60.0
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 60.
20; Conservative
                                                            (NOV-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                                                                                     us (Rabbit).
Chordata; Craniata; Vertebrata; Euteleostomi;
Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%;
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                                                              the
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19,
                                                                                                                       S.M.,
                                                                                                  þу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 127; DB Pred. No. 1.5e 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 131; DB Pred. No. 5.4e 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.
                                                            EMBL/GenBank/DDBJ databases
                                                                                                    MM-LDL
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                          Parhami
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..5e-09;
les 9;
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.4e-10;
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on update)
                                                                                                    role
                                                                                                                                          Watson
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                                                                                                                                          A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                            Drake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT
Q28982
                                                                                   A LO CONTRA PROPERTO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DELA
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Best Local S
Matches 19
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROCETTE: DECOCO:
                                                                                                                                                                                              Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 4.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 4.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q28982;
01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS50041; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF_1; UNKNOWN_1. PROSITE; PS01186; EGF_2; 1. EGF-1ike domain; Glycoprotein; Lect SEQUENCE 649 AA; 71755 MW; ECCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                               PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS00614; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF_1; UNKNOWN_1. PROSITE; PS00186; EGF_2; 1. EGF-11ke domain; Glycoprotein; Lect SEQUENCE 482 AA; 52341 MW; 97DC
                                                                                                                                                                                                                                                                                                            Pfam; PF00008; Pfam; PF00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U37521; AAC48680.1;
HSSP; P16581; 1ESL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The intron-exon structure of the Gene 176:67-72(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q28982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bach F.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winkler H., Brostjan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-97075911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 CQDMSCSKQGECIETIGNYTCSCYPGFYGPECE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 59.1%;
Similarity 57.6%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                    IPR001304;
IPR002396;
IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : IPR000561; IPR001304; IPR002396; IPR002396; IPR000436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8918234;
jan C., Csizmadia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                        EGF-like.
lectin_c.
Selectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like.
lectin_c.
Selectin.
  58.1%;
60.6%;
                                                                                                                                                                                                                                                                                                                                                    Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ
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01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
  Score
Pred.
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127; DB 6;
Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                 Lectin; Selectin
97DC5D70BF115944
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ECCD8C847B84BC31
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.
  125; DB 6;
No. 2.9e-09;
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                   Length
                                                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G:,
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anrather
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RESULT
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O955009
ID O96
AC OPC

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Best Local S
Matches 19
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SMART; SM00032; CCP; 6.
SMART; SM00032; CCP; 1.
SMART; SM000181; EGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF 1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin_
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00054; sushi; 6.
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
              Howden
                                     SEQUENCE FROM N.A
                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like domain; Glycoprotein.
NON_TER 616 616
SEQUENCE 616 AA; 67736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O95509 PRELIMINARY; PRT; 616 AA.
O95509;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ780M13.1.3 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1998)
EMBL; AL022146; CAA1E
HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Howden P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD62, GMP140)) (ISOFORM 3) (FRAGMENT). SELP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \perp
                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                      CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTPTSCSGHGECIETINSSTCQCYPGFRGLQCE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 58.1%;
Similarity 57.6%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                  'Atazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [998] to the EMBL/GenBank/DDBJ databases CAA18144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125; DB 4;
Pred. No. 3.7e-09
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35CD4BFADE61D724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                         Vertebrata;
                                                                                               Hominidae;
                                                                                                                                                                                                             n update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                  Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo.
                                                                                                                                                                                                             KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ğ,
                                                                                                                                                                                                             ANTIGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                      RESULT
095508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ОĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 19
       Query Match
                                                                                                                                Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 8.
Pfam; PF00084; sushi; 8.
PFNNTS; PR00343; SELECTIN.
SMART; SM00032; CCP; B.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1
PROSITE; PS00615; C_TYPE_LECTIN_2; 1
PROSITE; PS00041; C_TYPE_LECTIN_2; 1
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; BGF; 1.

Pfam; PF00008; Sushi; 8.

Pfam; PF00084; Sushi; 8.

PFINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 8.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS01186; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 1.

EGF-1ike domain; Glycoprotein.

NON_TER 740 740
                                              PROSITE; PS01186; Esc. PROSITE; PS01186; Glycoprotein.
EGF-like domain; Glycoprotein.
HON_TER 740 740
SECUENCE 740 AA; 81390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001304; 1
InterPro; IPR002396; S.
InterPro; IPR0027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     095508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ780M13.1.2 (SELECTIN P (GRANULE MEMBRANE PROTEIN
CD62, GMP140)) (ISOFORM 2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304;
InterPro; IPR002396;
InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1998)
EMBL; AL022146; CAA18
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL022146; CAA
HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P16109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA18143.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA18142.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81095 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ť
    58.1%;
                                                                                                                                                                                                                                                                                                                                                                                   Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                        Selectin.
                                                                                                                                                                                                                                                                                                                                                                                                                           lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selectin.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                   1D2E35E6D93745CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3B5F70A45B1A3CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
  125;
                                                                                                                                                                                 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740
  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae;
  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                   CRC64;
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIGEN
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Gaps

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RESULT OF THE PROPERTY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q29097 PRELIMINARY;
Q29097;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-JUN-2001 (TrEMBLrel. 1
P-SELECTIA PRECURSOR.
                                                                         EMBL;
                                                                                                                                                                                            MEDLINE-20171534; PubMed-10706724; Stocker C.J., Sugars K.L., Harari O.A., L Haskard D.O.; "TNF-alpha, IL-4, and IFN-gamma regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                       and E-selectin expression by por J. Immunol. 164:3309-3315(2000). EMBL; L39075; AAA79007.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of equine E-selectin.";
Immunology 103:498-504(2001).
EMBL; AF307972; AAK48712.1; -.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-AORTA;
                                                                                                                                                                                                                                                                                                                                                                      Rollins S.A., Johnson Submitted (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-AORTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hedges J.F., Dem MacLachlan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21421234; PubMed=11529941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-SELECTIN
                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95LG1
                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity hes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHTSCSGHGECVETINNYTCQCHPGFTGLRCE 174
                                                                         AF163766; AAF43272.1; -. P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                         IPR000561;
IPR001304;
       IPR002396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Demaula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66191 MW;
                         EGF-like.
lectin_c.
                                                                                                                                                                                                                                                                                                                                                                      n K.K.,
to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
01,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19,
19,
                                                                                                                                                                          by porcine
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6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore
                                                                                                                                                                                                                                                                                                                                                                      Birks C.W., Matis EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB 6;
Pred. No. 6.9e-09;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F9D3DED12C445382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . No. 4.5e-09;
                                                                                                                                                                          aortic endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McLaughlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                               Landis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                 differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                      L.A., Rother R.P.; databases.
                                                                                                                                                                                                                                            R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В.Е.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                            Morley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simon
                                                                                                                                                                                                                                               В. Л.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT
Q28290
ID AC
Q200
AC
Q2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q95LG3
                                                                                                                                                                                                                                                                                                                                                                                   Ş
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                                                                                                                                                                                                                                                                                                                                               144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
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Query Match
Best Local S
Matches 19
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SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; UN

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF_1; UNKNOWN_1.

PROSITE; PS00106; EGF_2; 1.

EGF-like domain; Glycoprotein; Lectin
                                                                         Q28290
Q28290;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95LG3;
Q95LG3;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
OMPIJO.

Canis familiaris (Dog).

Canis familiaris (Chordata; (
Eukaryota; Metazoa; Chordata; (
Mammalia: Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21421234; PubMed-11529941;
MEDLINE-21421234; PubMed-11529941;
MEDLINE-21421234; Demanda C.D., Moore B.D.,
                                                                                                                                                                                                                                                                                                                                                           "Characterization of equine E-selectin.";
Immunology 103:498-504(2001).
EMBL; AF307970; AAK48710.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Odocoileus hemionus (Mule deer) (Black-tailed deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutei
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Cervidae; Odocoileinae; Odocoileus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
                                                GMP140.
                                                            CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin_c; 1. Pfam; PF00084; sushi; 6. PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                   1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
                                                                                                                                                                                                      CTPTPCSSHGECVETINNYTCQCHPGFKGLKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQSTSCSKQGECTETIGNYTCSCYSGFYGPRCE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00008;
                                                                                                                                                                                                                                                           ch 56.3%;
l Similarity 57.6%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                 Selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain; Glycoprotein; Lectin;

4 POTENTIAL

42 646 P-SELECTII

646 AA; 71127 MW; 3863F4AH
                                                          5 (TrEMBLrel. 01, 05 (TrEMBLrel. 01, 10 (TrEMBLrel. 19, 10 (TrEMBLrel. 19, 10 MOLECULE PRECUION MOLECULE PRECUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF;
                                                                                                                                                                                                                                                                                                                                  53247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.7%;
57.6%;
                                                          . 01, Last sequence update)
. 19, Last annotation update)
PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                           Score 121; DB Pred. No. 1e-0 4; Mismatches
                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122; DB v,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
P-SELECTIN.
; 3863F4AFE09F0BB6 CRC64;
    Craniata; Vez; Fissipedia;
                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                  69959199EAFE9980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1
                                                                                                                                 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485
                                                                                                                                                                                                      176
                                                                                                                                                                                                                                 33
                                                                                                                                                                                                                                                                        1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                    McLaughlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selectin; Signal
     Vertebrata;
ia; Canidae;
                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                 ⋧
                                                                                                                                                                                                                                                                                       6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ه</u>
                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
       Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                      Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cervoidea;
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                              Gaps
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Best Local
                    EMBL; AF239608; AAF63500.1; -...
HSSP; P00740; 1EDM.
FlyBase; FB9n0031879; Sp1070.
InterPro; IPR000152; Asx.hydro:
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 8.

SMART; SM00032; CLECT; 1.

SMART; SM00018; EGF; 1.

PR051TE; PS00615; C_TYPE_LECTIN_1; 1.

PR051TE; PS50041; C_TYPE_LECTIN_2; 1.

PR051TE; PS00022; EGF_1; UNKNOWN_1.

PR051TE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                Q9NGV4;
Q9NGV4;
01-OCT-2000
01-OCT-2000
01-DEC-2001
SP1070.
                                                                                                          development.";
Submitted (FEB-2000)
EMBL; AF239608; AAF6
                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=ENDOPLASMIC RETICULUM;
Serano T.L., Pendleton J.D., Rubin G.
                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
            InterPro;
                                                                                                                                             "A reverse genetic screen
                                                                                                                                                                                                                                                                     SP1070 OR CG9138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     model of myocardial ischemia/reperfusion.";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
EMBL; M88170; AAA63789.1; -.
HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin_c; 1. Pfam; PF00084; sushi; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manning A.M., Sanders W.E.Jr. ., Kukie
Rosenbloom C.L., Hawkins H.L., Michael
Beaudet A.L., Anderson D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of canine GMP140 and studies of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       CQDMSCSKQGECIETIGNYTCSCFPGFYGSECE 180
                                                                                                                                                                                                                                                                                                                                                                                                                              CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain; Glycoprotein; Signal.
            IPR003410;
                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                     Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754
82303 MW;
                                                           Asx_hydroxyl.
EGF-like.
                                                                                                                       to the
                                                                                                                                                                                                                                Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.3%;
Laminin_EGF
                                                                                                                                             for genes
                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 119; DB 6;
Pred. No. 3.1e-08;
6; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CELL ADHESION MOLECULE
F0438EEAA521E773 CRC
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kukielka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1551
                                                                                                                                           involved in Drosophila
                                                                                                                                                          ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                               Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entman M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dore M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith C.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Borkova D., Doubley S., Dahlke C., Davenportt L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Meinert K., Reminoton K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Meinert K., Reminoton K.S., Pan S., Polladd J., Puri V., Reese M.G.,
RA Randers R. D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9VM55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSULLU,
PROSITE; PSULLU,
PROSITE; PSULLBY; EGF
Calclum-binding; EGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (Tr
01-MAY-2000 (Tr
01-DEC-2001 (Tr
CG9138 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
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SMART; SM00179; EGF_CA; 6.
SMART; SM00001; EGF_like; 9.
SMART; SM00282; LamG; 1.
SMART; SM00192; LDLa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CENRPCANEGTCVDLVDGYSCNCEPGYTGKNCQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00008; EGF; PF02494; HYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00010;
PS00022;
PS01186;
PS01187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001791; Laminin_G.
IPR002172; LDL_recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; ASX_HYDROXYL; UNKNO
2; EGE_1; UNKNOWN_15.
16; EGE_2; 12.
17; EGE_CA; 5.
17; EGF_Like domain; Gly
AA; 167816 MW; A97E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6%;
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19,
Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Glycoprotein; Repeat A97EA229E9384F31 CRC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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RESULT
Q93563
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DE F2
GN F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 16.
Pfam; PF00754; F5_F8_type_C; 2
Pfam; PF00757; Idl_recept_a; 1
Pfam; PF00087; ushi; 7
PRINTS: nanaa; sushi; 7
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0010; EGFELOOD.
SMART; SM00032; CCP; 8.
SMART; SM00042; CCB; 3.
SMART; SM00179; EGF_CA; 8.
SMART; SM00179; EGF_like; 9.
SMART; SM002031; EA5EC; 2.
SMART; SM00281; LamG; 1.
SMART; SM00282; LamG; 1.
SMART; SM00182; LDLA; 1.
SMART; SM00182; LDLA; 1.
SMART; SM00182; LDLA; 1.
                    093563

093563;

01-FEB-1997 (TrEMBLrel. 0

01-FEB-1997 (TrEMBLrel. 0

01-DEC-2001 (TrEMBLrel. 1

F25D7.5 PROTEIN.
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InterPro; IPR002172; I
InterPro; IPR000436; S
InterPro; IPR001368; T
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                    2092
  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003615; AAF52472.1;
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                         1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
                                                                                                                                                                                                                                                                    CENRPCANEGTCVDLVDGYSCNCEPGYTGKNCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; PS00010; ASX_HYDROXYL; 11.
2; PS01180; CUB; 6.
2; PS00022; EGF_1; 15.
2; PS01186; EGF_2; 13.
3; PS01187; EGF_CA; 7.
3; PS01285; FA58C_1; 1.
3; PS01209; LDLRA_1; 1.
2; PS01209; LDLRA_2; 2.
3; PS01209; LDLRA_2; 2.
4; PS50068; LDLRA_2; 2.
5; PS50068; LDLRA_2; 2.
6; PS50068; LDLRA_2; LDLRA_2; 2.
6; PS50068; LDLRA_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o; IPR000742; EGF_2.
c; IPR001881; EGF_Ca.
c; IPR001438; EGF_II.
c; IPR000421; FA58_C.
c; IPR001092; HLH_dim.
c; IPR003440; HYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000152; Asx_hydroxyl.
IPR000859; CUB.
IPR000561; EGF-like.
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          Conservative
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; Sushi_SCR_CCP.
; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                 45.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP1070
                                                                  02,
19,
                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                       Score 98; DB Pred. No. 0.00 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                            9;
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                                                                                                                                                        PRT;
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                                                                                                                                                        710
                                                                                                                                                                                                                                                                    2124
                                                                                                                                                                                                                                                                                                              33
                                                                                                                                                                                                                                                                                                                                                                              DB 5;
.00012;
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                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                 Length 3396;
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RESULT
Q9H557
ID Q9H557
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Best Local S
Matches 14
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Best Local S
Matches 13
                                                                                                                                                                                                         Submitted (AUG-2000) to the EMBL/Ger EMBL; AL137007; CAC10575.1; -. HSSP; P00749; 1URK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                       Ó9H557;

01-MAR-2001 (TrEMBLrel. 16, C

01-DEC-2001 (TrEMBLrel. 16, L

01-DEC-2001 (TrEMBLrel. 19, L

DJ303E99.1 (SIMILAR TO NOTCH
                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                              SMART; SM00181; EGF; 3.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 3.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                              PRINTS; PRO0010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                              Williams
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      DJ303F19.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9н557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
EGF-11ke domain; Glycoprotein.
SEQUENCE 710 AA; 80783 MW; 4F5D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z78418; CAB01698.1; -. InterPro; IPR000561; EGF-like. SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McMurray A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the
47
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                    CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIPTICNGHGKCYDYVEDVKCDCYWGYEGEHCEV 181
CSSEPCKNNGTCVDLTNRFFCNCEPEYHGPFCEL
                                               l Similarity
14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 38.:
13; Conservative
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                                                                                                           112
112 AA;
                                               Conservative
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12638 MW;
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Primates;
                                                          43.7%;
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H (DROSOPHILA) HOMOLOG)
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                                                          Score 94;
Pred. No.
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Pred.
                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                           4141BD74D9924E7A CRC64;
                                               Mismatches
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                                                           DB 4;
1.3e-05;
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6.2e-05;
80
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                                                                      Length 112;
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RESULT P799411
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Q9UJV2
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Best Local :
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SMART; SM00051; DSL; 1.

SMART; SM00179; EGF_Ck; 3.

SMART; SM00101; EGF_Like; 5.

PROSITE; PS000010; ASX_HYDROXYL; UNKNOWN_2.

PROSITE; PS001186; EGF_1; 7.

PROSITE; PS01186; EGF_2; 7.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS01187; EGF_LA; 2.

Calcium-binding; EGF-like domain; Glycoprotein; Reg SEQUENCE 642 AA; 70667 MW; D7DC31EB9D92820C CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P79941 PRELIMINARY;
P79941;
01-MAY-1997 (TrEMBLrel. 0:
01-MAY-1997 (TrEMBLrel. 0:
01-DEC-2001 (TrEMBLrel. 1:
NOTCH LIGAND X-DELTA-2.
Han W., Ye Q., Moore M.A.S.;

"A Soluble Form of Human Delta-like-1 Inhibits Differentiation Hematopoietic Progenitor Cells.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF196571; AAF05834.1; -.
                                                                                                                                                                                                                                                                                Q9UJV2;
Q9UJV2;
01-MAY-2000 ('
01-MAY-2000 ('
01-DEC-2001 ('
DELTA-LIKE-1')
                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mesoderm in Xenopus embryos.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U70843; AAB37131.1; -.
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01414; DSL; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001774; DSL.
InterPro; IPR001661; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Notch ligand, X-Delta-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
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13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93;
                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
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CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 642;
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ACONO DE PROPERTO 
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Pfam; PF000006; EGF; 8.

PRINTS; PR00010; EGFEDADOD.

PRINTS; PR00011; EGFEDAMININ.

SMART; SM00051; DSL; 1.

SMART; SM000179; EGF-Like; 4.

SMART; SM000179; EGF-Like; 4.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.

PROSITE; PS001186; EGF-2; 8.

PROSITE; PS011187; EGF-CA; 1.

PROSITE; PS011187; EGF-CA; 1.

Calcium-binding; EGF-like domain; Glycoprotein; Ref Calcium-binding; EGF-1; Mark Calcium-binding; Mark Calcium-binding; EGF-1; Mark Calcium-binding; Mark Calcium-binding; Mark Calcium-binding; Mark Calcium-b
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Best Local S
Matches 13
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Pfam: PF000008; EGF; 8.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00011; EGFLAMININ.

SMART; SM00179; EGF_CA; 1.

SMART; SM000179; EGF_Like; 4.

SMART; SM00001; EGF_Like; 4.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.

PROSITE; PS00012; EGF_1; UNKNOWN_8.

PROSITE; PS01186; EGF_2; 7.

R PROSITE; PS01187; EGF-Like domain; Glycoprotein; Rel Calcium-binding; EGF-Like domain; Glycoprotein; Rel SEQUENCE 723 AA; 77985 MW; C7F418DA2265A5F7 CR
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01-OCT-2000
01-DEC-2001
DJ894D12.3 ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL; AL078605; CAB89569.1; HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001438;
InterPro; IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Asx_hydro
InterPro; IPR001774; DSL.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF_Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Almeida
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13; Conser
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) (TrEMBLrel. 15, Last sequence update)
l (TrEMBLrel. 19, Last annotation update)
(DELTA-LIKE 1 (MOUSE) HOMOLOG).
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Primates;
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EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Laminin_EGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
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EGF_Ca.
EGF_II.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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No.
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Best Local
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Q91902;
Q91902;
O1-NOV-1996 (TrEMBLrel. 0
O1-NOV-1996 (TrEMBLrel. 0
O1-DEC-2001 (TrEMBLrel. 1
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O1-MAR-2001 (TrEMBLrel. 1
O1-MAR-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
FIBROSURFIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cluzel C., Lethias C., Humbert F., Garrone R., Exposito J.Y.;

"Characterization of fibrosurfin, an interfibrillar component of
urchin catch connective tissues.";

J. Biol. Chem. 276:18108-18114 (2001).

EMBL; AJ291489; CAC20782.1; -.
HSSP: P00740; 1EDM.
InterPro: IPR000152; Asx.hydroxyl.
InterPro: IPR000151; EGF-like.
InterPro: IPR000742; EGF_Ca.
InterPro: IPR001438; EGF_Ca.
InterPro: IPR001438; EGF_II.
Pfam; PF00008; EGF; 17.
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SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         2556
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                      X-DELTA-1.
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SMART; SM00181; EGF; 17.
SMART; SM00179; EGF_CA; 17.
SMART; SM00001; EGF_like; 5.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; i
    SEQUENCE FROM N.A.
                                                                                                                                             Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-ADULT TEST;
MEDLINE-21264600; PubMed-11259425;
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                                              NCBI_TaxID-8355;
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Pred. No. 0.00
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Echinidae;
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InterPro;
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R PRINTS; PROUDID; EGFBLOOD.
R SMART; SMO010; EGF_CA; 4.

JR SMART; SM00179; EGF_CA; 4.

JR SMART; SM00010; EGF_Like; 4.

JR SMART; SM00010; EGF_Like; 4.

DR PROSITE; PS00010; EAS_HYDROXYL; UNKNOWN_3.

DR PROSITE; PS01186; EGF_1; UNKNOWN_8.

DR PROSITE; PS01186; EGF_CA; 2.

DR PROSITE; PS01187; EGF_CA; 2.

KW Calcium-binding; EGF_like domain; Glycoprotein; Repeat.

KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
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InterPro; IPR001774; DSL.
InterPro; IPR0007561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
Pfam; PF001414; DSL; 1.
Pfam; PF00108; EGF_8.
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O16004;
O1-JAN-1998 (TrEMBLrel. (
01-JAN-1998 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. 1
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Henrique D., Adam J., Myat A., Chitnis A., Lewis J.,
"Expression of a Delta homologue in prospective neurochick.";
                                                                                                                                                                                                                                                                                                                                                         NOTCH HOMOLUG:
Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Eukaryota; Metazoa; Echinacea; Temnopleuroida; Toxopn
                                                                                                                                                          Development 124:3363-3374(1997).
EMBL; AF000634; AAB82088.1; -.
                                                                                                                                                                                                               Sherwood D.R., McClay D.R.;
"Identification and localization of
insights into vegetal plate regiona.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97454256; PubMed=9310331;
                                                                                                                                                                                                                                                                                                                                                     Echinoidea; Euechinoidea; Lytechinus.
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Chitnis A., Henrique D., Lewis J.,
"Primary neurogenesis in Xenopus e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L42229; AAC38017.1; -. HSSP; P00740; 1EDM.
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                                                                                                                      P01132; 1EGF.
Pro; IPR002110; ANK.
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; IPR000561; EGF-1ike.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
; IPR000800; Notch.
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Q9UA13; Q21340;
01-MAY-2000 (TremBLrel. 13, C:
01-MAY-2001 (TremBLrel. 13, L:
01-DEC-2001 (TremBLrel. 19, L:
TRANSMEMBANE CELL ADHESION R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0010; EGFBLOOD.

PRINTS; PRO1452; NOTCH.

SMART; SM00248; ANK; 5.

SMART; SM00179; EGF_CA; 23.

SMART; SM00001; EGF_like; 11.

SMART; SM00004; NL; 3.

PROSITE; PS50088; ANK_REPEAT; 10.

PROSITE; PS50097; ANK_REP_REGION; 2.

PROSITE; PS00010; ASX_HYDROXYL; 21.

PROSITE; PS00022; EGF_1; UKNOWN_33.

PROSITE; PS01186; EGF_2; 25.

PROSITE; PS01187; EGF_CA; 20.

ANK repeat; Calcium_binding; EGF_like do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00023; ank; 6.
Pfam; PF00008; EGF; 3.
Pfam; PF00006; notch; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
                                                               InterPro;
InterPro;
                                                                                                                                                                         EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: investigating biology."; Science 282:2012-2018(1998).
EMBL; AF139060; AAD29428.1; -.
EMBL; Z30974; CAA83226.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Kershaw J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu Z., Vogel B., Hedo
"mua-3 mRNA Splicing
Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu 2.,
"mua-3
                                                                                                            InterPro;
                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1994)
                                                                                                                                                                                                                                                                                                                              none,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FRAGMENT).
MUA-3 OR KO8E5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydroxylation; | SEQUENCE 2531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                  Z30974; CAA83226.2; -. Z30423; CAA83226.2; JOINED P01130; ILDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQSSPCENGGTCIDGVNQFTCLCETGYEGHRCEM 588
               ; IPR000152; Asx_hydroxyl.
IPR001762; Disintegrin.
IPR001561; EGF-Like.
IPR001881; EGF_Ca.
IPR002172; LDL_recept_A.
IPR002035; SEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hedgecock E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pattern to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
RECEPTOR MUA-3 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n Revealed.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90; DB Pred. No. 0.00 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5BF42BEC627CA303
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. 0.0011;
. ~ 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditoidea;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
               InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002060; Notch.
Pfam; PF00008; EGF; 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00289; DISINTEGRIN.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00181; EGF; 51.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_1ike; 45.
                                                                                                                        Notch (AmphiNotch): evolutionary conservation domains in amphioxus and vertebrates."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ EMBL; Y12539; CAC19873.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                    O9GPA5;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                         Holland L.Z., Burgtorf C., Holland N.D., Lehn Abi-Rached L., Pontarotti P., Lardelli M.; "Cloning and developmental expression of the
                                                                                                                                                                                                                                        Eukaryota; Metaz
Branchiostoma.
NCBI_TaxID=7739;
                                                                                                                                                                                                                                                                                                                                                                                                 3380 CNAHGDCVHNTATNNITCVCTDGWTGPQCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                         Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                         TISSUE=LARVA;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            PUTATIVE
                                                                                                                                                                                                                                                                                                                                                Q9GPA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_32.
PROSITE: PS00022; EGF_1; UNKNOWN_1.
PROSITE: PS01186; EGF_2; 6.
PROSITE: PS01187; EGF_CA; 1.
PROSITE: PS50068; LDLRA_2; 2.
PROSITE: PS50024; SEA; 4.
PROSITE: PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                              6 CSGHGECVE--IINNHTCNCDVGYYGPQCQL
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SM00192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00092;
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SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -binding; EGF-like
                                                                                                                                                                                                                                                                                             NOTCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3767
3767
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                            RECEPTOR
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SEA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vwa;
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>3767
        EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3767
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.9%;
51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417284
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. 16, Last sequence upd
. 19, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain; Glycoprotein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
4; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE CELL 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
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                                                                                                                                                                                              Lehrach H.,
                                                                                                                                                                                                                                                                                                                                              ΑA
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                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                amphioxus
n of multip
                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3767;
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                                                                                                                                                                multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                              Tamme
                                                                                                                                                                            homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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Best Local S
Matches 15
                                                                                                                                                                                     wide variety of tissues.";

Exp. Cell Res. 204:364-372(1993).

EMBL; X68279; CAA48340.1; -.

HSSP; p16109; 1FSB

MGD; MGI:97364; Notch2.

InterPro; IPR000152; Asx.hydroxyl.

InterPro; IPR000761; EGF-like.

InterPro; IPR000761; EGF-2.

InterPro; IPR000742; EGF-2.

InterPro; IPR000743; EGF_2.

InterPro; IPR000183; EGF_1.

InterPro; IPR000083; fibronectin_type_1.

InterPro; IPR002049; Laminin_EGF.

InterPro; IPR0000080; Notch.
                                                                                     PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO0011; EGFLAMININ.
PRINTS; PRO0012; FNTYPEI.
SWART; SM00179; EGF_CA; 19.
SMART; SM00001; EGF_like; 7.
SMART; SM00004; NL; 2.
SMART; SM00004; NL; 2.
PROSITE; PS00010; ASX_HYDROXYL; 19.
PROSITE; PS01022; EGF_1; UNKNOWN_27.
PROSITE; PS01186; EGF_2; 22.
PROSITE; PS01187; EGF_CA; 19.
Calcium-binding; EGF-like domain; Glycoprotein;
NON_TER 1 1
SEQUENCE 1203 AA: 138000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q06008
Q06008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1452; NOTCH.
SWART; SM001248; ANK; 6.
SWART; SM00181; EGF; 37.
SWART; SM00179; EGF_Like; 34.
SWART; SM00001; EGF_Like; 13.
SWART; SM00004; NL; 3.
PROSITE; PS50088; ANK_REP_REGION; 1.
PROSITE; PS50089; ANK_REP_REGION; 1.
ANK_REP_REGION; 1.
ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, MOTCH B PROTEIN (FRAGMENT). NOTCH2 OR MOTCH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                 Pfam; PF00008; EGF; 27. Pfam; PF00066; notch; 1.
                                                                                                                                                                                                                                                                                                                                                  Lardelli M., Lendahl U., \begin{tabular}{ll} Motch A and Motch B - two mouse Notch \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-F1 (CBA X C57BL); TISSUE-EMBRYO; MEDLINE-93178563; PubMed-8440332;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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5 . .
6 . .
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6,
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Pred. No. 0.00
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
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      65040843799BCA37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.5;
No. 0.
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                                                                                                                                                                                                                                                                                                                                                     homologues
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                            Hydroxylation;
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     CRC64
                                                                                                                                                                                                                                                                                                                                                      coexpressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
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                             Repeat
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Query Match

41

.48;

Score

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DB

11;

Length 1203

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RESULT
Q9UPL3
ID Q9
                                                                                                                     SOFTWOOD DRADD DRA
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  Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002111; ANK.
Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR0001562; Disintegrin.
Interpro; IPR000761; EGF-11ke.
Interpro; IPR000742; EGF_2.
Interpro; IPR001881; EGF_Ca.
Interpro; IPR001438; EGF_II.
Interpro; IPR001438; EGF_II.
Interpro; IPR000083; fibronectin_type_1.
Interpro; IPR002049; Laminin_EGF.
Interpro; IPR000080; Notch.
                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO0011; EGFLAMININ.
PRINTS; PRO0012; FUTYPEI.
SMART; SM00248; ANK; 5.
SMART; SM000179; EGF_CA; 19.
SMART; SM000179; EGF_Like; 14.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                               PROSITE; PS50088; A
PROSITE; PS50297; A
PROSITE; PS00010; A
PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS01187; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UPL3;
Q9UPL3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 34. Pfam; PF00066; notch; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwage Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwage Phan H., Velasco N., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., And Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                           ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00289; DISINTEGRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC004663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Lamerdin J.E., McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTCH 3 (FRAGMENT).
                                                                                                                                                                  Hydroxylation; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
|| | :|:||: | | | |: || ||:
181 CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of an ~1.5 Mb olfactory receptor (OLFR)
  Local Similarity hes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                     2281
                                                                                                                                                                                           Calcium-binding;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1EDM
                                                                                                                                                                                                          8; ANK_REPEAT; 8.
7; ANK_REP_REGION; 2.
1); ASX_HYDROXYL; 18.
1); EGF_1; UNKNOWN_33.
1; EGF_2; 25.
1; EGF_CA; 16.
                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998) to the AAC15789.1;
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                        41.48;
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                                                                                                                     MW;
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Last sequence update)
Last annotation update)
  4.
                        Score 89;
Pred. No.
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6; Mismatches 14
                                                                                                                                                                                           EGF-like
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  Mismatches
                                                                                                                     DE23B2F129709D75 CRC64
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                                                                                                                                                                                        domain;
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                                                 DB 4;
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                                                                                                                                                                                           Glycoprotein;
                                            Length 2281;
  Indels
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  0;
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  Gaps
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RESULT Q9YGL8
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ID G18
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Best Local S
Matches 15
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R PRINTS; PR00010; EGFBLOOD.

R PRINTS; PR00011; EGFLAMININ.

PRINTS; PR00248; ANK; 5.

R SMART; SM00179; EGF_CA; 20.

R SMART; SM00011; EGF_like; 12.

R SMART; SM00001; EGF_LIKe; 12.

R SMART; SM00001; EGF_REGION; 1.

R PROSITE; PS50088; ANK_REPEAT; 4.

R PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50210; ANK_REP_REGION; 1.

R PROSITE; PS50210; ANK_REP_REGION; 1.
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O9R172;
O1-MAY-2000 (TIEMBLICEL I
01-MAR-2001 (TIEMBLICEL I
01-DEC-2001 (TIEMBLICEL I
                                                                                                                                               NOTCH3.
                                                                                                                                                                                                                                                                Q9Y6L8;
                                                                  Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
    SEQUENCE
                                                                                                                                                                                                                 01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK.hydroxyl.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                             NCBI_TaxID=9606;
[1]
                                                                                                                                                                                        01-DEC-2001
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Submitted (SEP-2000) to t
EMBL; AF164486; AAD46653.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 33.
                                                                                                                                                                                                                                                                                                                                                                                                          930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Haritunians T., Boulter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTCH 3 PROTEIN.
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                        CSPSSCFNGGTCVDGVNSFSCLCRPGYTGTHCQ 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
  FROM N.A
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IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000800;
                                              s (Human).
Metazoa; Chordata; C
--+heria; Primates; (
                                                                                                                                                                                      (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.4%;
45.5%;
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12,
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16,
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for
the
3.2;
                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Last annotation updat
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                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                    2321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                    A
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RESULT
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ID Q9UM47
ID Q9
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Best Local S
Matches 15
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Pfam; PF00008; EGF; 34.

Pfam; PF00008; EGF; 34.

Pfam; PF00006; DGFBLOOD.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00011; EGFLAMININ.

PRINTS; PR00017; EGF_CA; 19.

SMART; SM00179; EGF_CA; 14.

SMART; SM00004; NL; 3.

SMART; SM00004; NL; 3.

SMART; SM00004; NL; 3.

SMART; SM00001; EGF_11ke; 14.

SMART; SM00001; ASX_HYDROXYL; 18.

PROSITE; PS00106; ASX_HYDROXYL; 18.

PROSITE; PS001187; EGF_1; UNKNOWN_33.

PROSITE; PS01187; EGF_2; 25.

PROSITE; PS01187; EGF_CA; 16.

ANK repeat; Calcium-binding; EGF-11ke
                                                                                                        Q9UM47
Q9UM47;
Q9UM47;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
NOTCH3.
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InterPro; IPR000152; A
InterPro; IPR000561; E
InterPro; IPR000742; E
InterPro; IPR001881; E
InterPro; IPR001438; E
InterPro; IPR002049; L
InterPro; IPR000800; N
Pfam; PF00023; ank; 6
Pfam; PF00023; ank; 6
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroxylation; SEQUENCE 232
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HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gunel M.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF058891; AAC14346.1; JAF058881; AAC14346.1; JAF058883; AAC14346.1; JAF058883; AAC14346.1; JAF058885; AAC14346.1; JAF058886; AAC14346.1; JAF058886; AAC14346.1; JAF058888; AAC14346.1; JAF058889; AAC14346.1; JAF058889; AAC14346.1; JAF058891; AAC14346.1; JAF058893; AAC14346.1; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFU5500, AAC. AFU58899; AAC. 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF058897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 41.48;
Similarity 45.58;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artavanis-Tsakonas
                                                                                                                                                                              (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on; Repeat
2321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APR-1998) to the
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC14346.1;
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EGF_Ca.
EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243628 MW;
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EGF-like.
                                                                                                                                                                                  13,
13,
19,
                                                                                                                                                                              Created)
Last sequence
Last annotation
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Pred. No. 0.00
4; Mismatches
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JO
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   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                  annotation
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                                                                                                                                                                                                                                                                                                                               2321
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0.0014;
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                                     Euteleostomi;
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RESULT
O35516
ID O35516
OC DT O1
DT O1
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Best Local S
Matches 15
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Interpro; IPR001881; EGF_Ca.
Interpro; IPR001438; EGF_II.
Interpro; IPR002049; Laminin_EGF.
Interpro; IPR000800; Notch.
Pfam; PF00023
                                                                                                                                                                                                                                                                                                                                                                                      PFAM: PF00066; NOTCH; 3.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00011; EGFLAMININ.

PRINTS; PR00011; EGF_CA; 19.

SMART; SM000179; EGF_CA; 19.

SMART; SM00001; EGF_L1Ke; 14.

SMART; SM00001; NL; 3.

PROSITE; PS50088; ANK_REPEAT; 4

PROSITE; PS50010; ASK_REPEAT; 4

PROSITE; PS00010; ASK_REPEAT; 4

PROSITE; PS000116; ASK_REPEAT; 4

PROSITE; PS00012; EGF_1; UNKNOW
                                                                   O35516 PRELIMINARY;
O35516;
O1-JAN-1998 (TrEMBLrel. (
O1-JAN-1998 (TrEMBLrel. (
O1-DEC-2001 (TrEMBLrel. )
CELL SURFACE PROTEIN.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
                                                        CELL SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE-97032728; PubMed-8878478;
Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P. Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J., Vayssiere C., Cruaud C., Cabanis E.A., Ruchoux M.M., Weissenbach J., Bach J.F., Bousser M.G., Tournier-Lasserve E.;
"Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke and dementia.";
Nature 383:707-710(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDIJINE-98049753; PubMed-9388399;

Joutel A., Vahedi K., Corpechot C., Ti
Vayssiere C., Cruaud C., Maciazek J.,

Bach J.F., Tournier-Lasserve E.;
                                                                                                                                                                                                                                                                                                                                   Hydroxylation; I SEQUENCE 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U97669; AAB91371.1; HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADASIL patients.";
Lancet 350:1511-1515(1997).
                                                                                                                                                                                                                                                                                                                                                            ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Strong clustering and stereotyped nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                    COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                          CSPSSCFNGGTCVDGVNSFSCLCRPGYTGAHCQ
                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                          PS50297; ANK_REP_REGION; 1.
PS00010; ASX_HYDROXYL; 18.
PS00022; EGF_1; UNKNOWN_33.
PS01186; EGF_2; 25.
PS01187; EGF_CA; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002110; ANK.
IPR000152; Asx_hydroxyl.
IPR000561; EGF-11ke.
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK_REPEAT; 4
              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                           41.4%;
45.5%;
                                                                                                                                                                                                                                                                                                                                   243656 MW;
                                                                                  05,
19,
                                                                                                                                                                                                                                                              Pred. No. 0.00
4; Mismatches
                                                                                Created)
Last sequence update)
Last annotation updat
            Craniata; Veri
Sciurognathi;
                                                                                                                                        PRT;
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., Weissenbach J., Bou
                                                                                                                                        2470
                                                                                                                                                                                                          960
                            Vertebrata; Euteleostomi;
                                                                                                                                        AA
                                                                                                                                                                                                                                                                               0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Notch3
                                                                                                                                                                                                                                                                                            4,
                                                                                  update)
              Muridae;
                                                                                                                                                                                                                                                                                        Length 2321;
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              Murinae;
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               Mus
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 4.
SMART; SM000179; EGF_CA; 22.
SMART; SM00001; EGF_like; 12.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00023; Pfam; PF00008; Pfam; PF00066;
MEDLINE-93265135; PubMed-1303260; Stifani S., Blaumueller C.M., Rec Artavanis-Tsakonas S.;
                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia: Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                          Q04721;
01-NOV-1996 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50010; ASX_HYDROXYL; 22.
PROSITE; PS00022; EGF_1; UNKNOWN_33.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_CA; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exp.
                                SEQUENCE OF 1810-2447 TISSUE=BRAIN;
                                                                                                                 NOTCH
                                                                                                                                                                    Q04721
                                                                                                                                                                                                                                                                                                                            ANK repeat; Calcium-binding; EGF-like Hydroxylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single copy of mouse Notch2 gene."; Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lardelli M., Lendahl U.;
"Motch A and Motch B - two mouse
"wide variety of tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57B/6; TISSUE=THYMUS; MEDLINE=93178563; PubMed=8440332;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97364; Notch2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamada Y., Higuchi M., Tsujimoto Y.; "Complete amino acid sequence and mutliform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57B/6;
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                                                                                                                                                                                                                      CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI 529
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P16109; 1FSB.
                                                                                                                                                                                                                                                                14;
                                                                                                                 PRECURSOR
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ); IPR002110; ANK.
); IPR000152; Asx_hydroxyl.
); IPR000561; EGF-1ike.
); IPR000742; EGF_2:
); IPR001481; EGF_Ca.
); IPR001438; EGF_II.
); IPR000800; Notch.
                                                                                                                                                                                                                                                                                                                    2470 AA;
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                     PRELIMINARY;
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EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            notch;
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35.
h; 2.
                                                                                                                                                                                                                                                                         41.4%;
41.2%;
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                                          FROM N.A.
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16,
19,
                                                                                                                           Last sequence up
                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                        Score
Pred.
                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
          Redhead
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                Mismatches
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          z
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0.0015;
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          .J.,
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                                                                                                                                    update)
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Best Local
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                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
COIrea R.G., Camargo A.A., More
"Human Notch2, a novel member o
Submitted (OCT-2000) to the EMB
EMBL; AF315356; AAG37073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   Q9H240 PRELIMINARY;
Q9H240;
Q1-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
NOTCH2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00066; notch; 2.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00248; ANK; 4.
SMART; SM00179; EGF_CA; 22.
SMART; SM00001; EGF_Like; 12.
SMART; SM00001; NL; 2.
                                                                                     InterPro;
InterPro;
                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                    NOTCH2.
NOTCH2.
Homo sapiens (Human).
Homo sapiens (Human).
'~rvota; Metazoa; Chordata;
'~rvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
                           InterPro;
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HSSP; P007
InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blaumueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human homologs
a novel family (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .m., Mann R.S.;

plete Human Notch 2 (hN2) cDNA sequence.";

tted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

AF308601; AAA36377.2; -.

P007-0; 1EDM.
                                                                                                                            P00740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 41.2
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50088; ANK_REPEAT; 4.
PS50297; ANK_REP_REGION; 1.
PS50297; ANK_HYDROXYL; 1.
PS00010; ASX_HYDROXYL; 1.
at: EGF-like domain; Glycoprotein; Hydroxylation; Repeat;
                                           IPR000152;
IPR000561;
IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001438;
IPR002049;
IPR000800;
        IPR001881;
IPR001438;
                                                                                                     IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
IPR000742; EGF_2.
IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
2471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      logs of a Drosophila enhancer of
ily of nuclear proteins.";
2:119-127(1992).
                                                                                                                            1EDM
    Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
265401 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.4%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF_II.
Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANK.
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                                                                                                                                                                                                                                                                                                                                                                                                        16,
19,
                                                                                                                                                           Moreira E.S., Simpson A.J.; ber of cell-fate determining NOTCH to EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89; DB 4;
Pred. No. 0.0015;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB4FD003CCAE5AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMOULDERS, ANK_REPEAL, OF PROSITE; PS50088; ANK_REP_REGION; 1
PROSITE; PS500297; ANK_REP_REGION; 1
PROSITE; PS00010; ASX_HYDROXYL; 1
ANK repeat; EGF-like domain; Glycop 2471 AA; 265429 MW; 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                   InterPro;
InterPro;
InterPro;
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01-MAY-2000
01-MAY-2000
01-DEC-2001
NOTCH2 PROTE:
                                                                                            InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000800; Notch.
                                                                                                                                                                                                                                                                  EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Rattus sp., and Rat; TISSUE=BRAIN; MEDLINE=93202015; PubMed=1295745; Weinmaster G., Roberts V.J., Lemke G.; "Notch2: a second mammalian Notch gene."; Development 116:931-941(1992).
[2]
                                                                                                                                                                                                                                                                               weinmaster G., Lemke G.;
Submitted (APR-1993) to the EMBL/GenBank/DDBJ
EMBL; M93661; AAXI3558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10118, 1
                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                            Weinmaster G.,
                                                                                                                                                                                                                                                                                                                                                  SPECIES=Rat; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp., and Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QW30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00181; EGF; 37.
SMART; SM00179; EGF_CA; 35.
SMART; SM00001; EGF_like; 12.
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
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                                      ; PF00023; ank;
; PF00008; EGF;
; PF00066; notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI
                                                                                                                                                                                                                                                              M93661; AAK13558.1; P00743; 1CCF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 41.4%; l Similarity 41.2%; 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PR01452; NOTCH.
SM00248; ANK; 6.
                                                                                                                                                        ; IPR002110; ANK.
; IPR002113; Asx_hydroxyl.
; IPR000515; Asx_hydroxyl.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00010; EGFBLOOD. PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ن
                                                                                                                                                                                                                                                                                                                                                                                                            (APR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                        notch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α
EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10116;
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Rodentia;
                                                            35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notch.
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13,
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Last sequences
Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Hydroxylation; WW; 7DA7F8FF44589B1C CRC64;
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update) annotation updat
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0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531
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Best Local S
Matches 14
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R SMART; SM001248; ANK; 4.

R SMART; SM00129; EGF_CA; 22.

R SMART; SM00101; EGF_11ke; 10.

R SMART; SM00004; NL; 2.

R SMART; SM00004; NL; 2.

R PROSITE; PS50088; ANK_REP.REGION; 1.

PROSITE; PS00010; ASK_HYDROXYL; 22.

R PROSITE; PS001010; ASK_HYDROXYL; 22.

R PROSITE; PS01186; EGF_1; UNKNOWN_34.

R PROSITE; PS01186; EGF_2; 26.

R PROSITE; PS01187; EGF_CA; 22.

W ANK repeat; Calcium-binding; EGF-11ke domain; Glycoprotein; W Hydroxylation; Repeat.

O SEQUENCE 2471 AA; 265367 MW; 7D5C8E18DDE95FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q25253
Q25253;
                                                                                                   Chen 2., McKenzie J.A., Batterham P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; U58977; AAC36151.; -
EMBL; AF032672; AAC36152.1; -
EMBL; AF032670; AAC36152.1; JOINED.
EMBL; AF032671; AAC36152.1; JOINED.
EMBL; AF032671; AAC36152.1; JOINED.
EMBL; AF032673; AAC36153.1; -
EMBL; AF032673; AAC36153.1; -
EMBL; AF032673; AAC36153.1; -
EMBL; AF032673; AAC36153.1; -
                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                           MEDLINE=96400928; pubMed=8807304; Davies A.G., Game A.Y., Chen Z., Williams T.J. McKenzie J.A., Batterham P.; "Scalloped wings is the Lucilia cuprina Notch candidate for the modifier of fitness and asym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
NOTCH HOMOLOG SCALLOPED
                                                                                                                                                                                                                                                                  Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                               STRAIN-SS SEEKING;
Chen Z., McKenzie
                                                                                                                                                                                                                          SEQUENCE OF 39-265
                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                             STRAIN-SS SEEKING;
                                                                                                                                                                                                                                                                                          SEQUENCE OF 39-265
                                                                                                                                                                                                                                                                                                                    Genetics 143:1321-1337(1996).
                                                                                                                                                                                                                                                                                                                                   resistance
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SS
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                       InterPro;
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      ; IPR002110; ANK.
;; IPR000152; Asx_hydroxyl.
;; IPR000361; EGF_11ke.
;; IPR000742; EGF_2.
;; IPR001881; EGF_11.
;; IPR0001438; EGF_11.
;; IPR000800; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 41.:
14; Conservative
                                                                                                                                                                                                                                                   Newsome T.,
d (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                             SEEKING;
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                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                  McKenzie J.A., Batterham to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                          N.A.
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01, Last sequence update)
19, Last annotation update)
WINGS (SCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 0.00
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Williams T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
.0015;
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                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                         homologue
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diazinon
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RESULT
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Best Local S
Matches 14
                                                                                     Query Match
Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 36.
Pfam; PF00066; notch; 3.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00179; EGF_CA; 24.
SMART; SM00001; NCF_11ke; 11.
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                                                                                                                                                                              093574
093574;
01-NOV-1998
01-NOV-1998
01-DEC-2001
                                            1885
                                                                                                                                         PROSITE; PS00022; EGF_1; UNKNOWN_7
PROSITE; PS01186; EGF_2; 7.
EGF-11ke domain; Glycoprotein.
NON_TER 1 1
SEQUENCE 3209 AA; 361288 MW; 81
                                                                                                                                                                                              Interpro; IPR002860; BNR. Interpro; IPR000561; EGF-11ke. Pfam; PF02012; BNR; 15. Pfam; PF020018; EGF; 4. SMART; SM00181; EGF; 5.
                                                                                                                                                                                                                                                  Bernier B., Goffinet A.M.; "Comparative study of reelin in vertebrates."; "Submitted (SEP-1998) to the EMBL/GenBank/DDBJ EMBL; AF090441; AAC35559.1; -.
                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK repeat; Calcium-binding;
Hydroxylation; Repeat.
SEQUENCE 2653 AA; 285928 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK REPEAT; 5.
PROSITE; PS50297; ANK REP_REGION;
PROSITE; PS00010; ASX HYDROXYL; 2:
PROSITE; PS00022; EGE 1; UNKNOWN_
PROSITE; PS01186; EGF_2; 28.
PROSITE; PS01187; EGF_CA; 21.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
            38
                                                       6 CSGHGECVEIINNHTCNCDVGYYGPQCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNGHGSC---INGTKCICDPGYSGPTCKI 1910
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14; Conserv
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2653 AA; 2
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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45.28;
                                                                                               41.2%;
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; Pred. No. 0.00
7; Mismatches
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Last sequence update)
Last annotation updat
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                                                                                     Score 88.5; In Pred. No. 0.00 as Mismatches
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                                                                                                                                            81A7B6676BCAA3D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain; Glycoprotein;
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0.0016;
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Best Local :
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InterPro; IPR000088; Avidin.
InterPro; IPR000088; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR000083; fibronectin_typ
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VQI2;
01-MAY-2000
01-MAY-2000
01-JUN-2001
MEDLINE-20196006; PubMed-10731132;
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                              CG2991 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VQI2
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PROSITE; PS0057; AVIDIN; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_11.
PROSITE; PS01186; EGF_2; 10.
PROSITE; PS01187; EGF_CA; 7.
Calcium-binding; EGF_CA; 7.
Calcium-binding; EGF_Like domain; Glycoprotein;
NON_TER 1
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Pfam; PF01008; EGF; 10.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
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ProDom; PD016055; Avidin; 1.
SMART; SM00179; EGF_CA; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evolution of the fibropellin gene family and pattern o gene expression in sea urchin phylogeny"; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases EMBL; L33861; AAA39995.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01. 01-NOV-1996 (TrEMBLrel. 01. 01-DEC-2001 (TrEMBLrel. 19. EIBROPELLIN IA (FRAGMENT).
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002049; Laminin_EGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 CASMPCLNGGQCIEMVNGYTCQCAAGFTGVLCE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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Last annotation update)
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Pred. No.
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7; Mismatches
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RESULT COMMENT OF THE PRINCE O
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                             A Tautz D., Lardelli M., Westin "Embryonic expression of Trib. Submitted (APR-1998) to the ENEMBL; AJ005083; CAB65469.1; -. HSSP; P00740; IEDM.
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Best Local :
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01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
SIGNAL RECEPTOR PROTEIN (
                                                                                                                                                                                                                                                                                                          Tribolium castaneum (Red flour beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tribolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9U0E2
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InterPro; IPR000561; EGF-like.
PROSITE; PS00022; EGF_1; UNKNOWN_1
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50.0%;
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of Tribolium
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Pred. No.
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Notch.";
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Result
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Perfect score:
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Biochem. Biophys. Res. Commun. 216:1018-1023(1995).
-!- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96074584; PubMed=7488174;
Bajorath J., Aruffo A.;
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD62L entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62l.htm".
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A TSUTUSHITAN.;

L SUBMILTED (NOV-1996) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: CELL SURFACE ADHESION PROTEEN. MEDIATE THE A
C OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIA
C OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIA
C -!- SUBCELLULAR LOCATION: Type I membrane protein.
C -!- SUBCELLULAR LOCATION: Type I membrane protein.
C -!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
C -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
C -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 32
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CONFLICT
                                                                                                          This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordatá; Ćraniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                            Budman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
01-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                      Johnson C.E.,
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Chordata; Craniata; Vertebrata; Euteleostomi;
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BY
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N-Y (IN REF. 4).
Y > H (IN REF. 4).
Y > F (IN REF. 1 ANI.
P -> F (IN REF. 4).
SFS -> NFN (IN REF. 2).
G -> E (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 205;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372
                                                                                                                              is produced through a collaboration ormatics and the EMBL outstation -
                                                                                       rmatics and the EMBL outst
There are no restrictions
ng as its content is in
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MEDIATE THE
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                                                                                                                                                                                                                                                                                                          ENDOTHELIAL
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tions on its
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use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).

http://www.isb-sib.

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P14151;

IPR000561;

EGF-like.

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Best Local
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                                                                                                                                                 LEMI_PANTR STANDARD; PRT; 372 AA.

Q95237;
Q1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
(LECAM1) (CD62L).
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SEQUENCE
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SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF; 1.
PROSITE; PS001186; EGF; 2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycoprotein;
                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
SEQUENCE FROM N.A
                                          Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                PANTR
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PRINTS;
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IPR000436;
IPR001304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
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sush1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SELECTIN.
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; Sushi_SCR_CCP.
; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.3%;
97.0%;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM).

EGF-LIKE.

SUSHI 1.

BY SIMILARITY.

BY SIMILAR
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BY SIMILARITY.
                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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..8e-18;
les 0;
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                                                                                               Euteleostomi;
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SUBMILLARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

TSURUARITY CONTAINS 2 SUSHI (SCR) DOMAINS.
       DOMAIN
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Cell adhe
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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Pfam; PF00059;
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P14151; 1KJB.
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PS01186; EGF_2; 1.
PS00615; C_TYPE_LECTIN_1;
PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000561; EGF-like.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
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  Sushi;
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         ₩,
CYTOPLASMIC (POTENTIAL).

CTYPE LECTIN (SHORT FORM).

EGF-LIKE.

SUSHI 1.

SUSHI 2.

BY SIMILARITY.

BY SIMILA
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BY SIMILARITY.
L-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thakur A.B., Berg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like domain; Lectin;
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Pfam; PF00084; sushi; 2.
Pfam; PF000843; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
       DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561; EG
InterPro; IPR002396; Se
InterPro; IPR000436; Su
InterPro; IPR001304; leu
Pfam; PF00008; EGF; 1.
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DOMAIN
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DOMAIN
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PROSITE; PS01186; EEF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
101-NOV-1997 (Rel. 35, Last annotation update)
1-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                         Selectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U52074; AAB40903.1;
HSSP; P14151; 1KJB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsurushita N., Fu H., Berg E.L.;
"PCR cloning of the cDNA encoding baboon L-selectin.";
Gene 181:219-220(1996).
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NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papio hamadryas (Hamadryas baboon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEM1_PAPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VENULES IN PERIPHERAL LYMPH NODES.
SUBCELULIAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTALNS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                   adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 192
                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                   Transmembrane;
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                                                                                                                                                                                                                                                                       Sushi;
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; Selectin.
; Sushi_SCR_CCP.
; lectin_c.
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L-SELECTIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM).

EGF-LIKE.

SUSHI 1.

SUSHI 2.

BY SIMILARITY.
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BY SIMILARITY.
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                                                                                             (SHORT FORM)
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Best Local
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                                    InterPro; IPR000561; EGI
InterPro; IPR002396; Se.
InterPro; IPR000436; Sus
InterPro; IPR001304; Lec
InterPro; IPR001304; Lec
Pfam; PF00008; EGF; 1.
                                    Pfam;
                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
(LECAMI) (CD62L).
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                   EMBL; U73729;
HSSP; P14151;
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Budman J.I.,
Tsurushita N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SUBGELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DO
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CELL SURFACE ADHESION PRODOF LYMPHOCYTES TO ENDOTHELIAL CELLS
                                                                                                                                                                                                                                   non-profit institutions as long and this statement is not removed.
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                                                        IPR000436; Sushi_SCR_CCP IPR001304; lectin_c.
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lectin_c; 1.
sushi; 2.
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azoa; Chordata;
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Selectin.
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97.0%;
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امار 1
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P98131;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

01-FEB-1996 (Rel. 33, Last annotation update)

L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1) (LECAM1) (CD62L).
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CARBOHYD
CARBOHYD
receptor:
Eur. J. In
[2]
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CARBOHYD
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DISULFID
                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Cetartioda
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                    SEQUENCE FROM N.A.

MEDLINE-92164727; PubMed=1371468;

Malcheck B., White M., Kurk S., Kishimoto T.K., Jutila

"Characterization of the bovine peripheral lymph node

"Characterization of the bovine peripheral lymph node

receptor: a lectin cell adhesion molecule (LECAM).";
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RT; SM00032; CCECT; 1.

RT; SM00034; CLECT; 1.

STTE; PS000181; EGF 1; 1.

STTE; PS000022; EGF 1; 1.

SSITE; PS01186; EGF 2; 1.

OSITE; PS01186; C_TYPE_LECTIN_1; 1.

OSITE; PS00615; C_TYPE_LECTIN_2; 1.

OSITE; PS50041; C_TYPE_LECTIN_2; 1.
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42118
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: Pred. No. 1.8e
1; Mismatches
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SUSHI 2.

BY SIMILARITY.

BY GILCNAC.

N-LINKED (GLCNAC.

N-LINKED (GL
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CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
EGF-LIKE.
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L-SELECTIN.
EXTRACELLULAR (POTENTIAL).
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1. No. 1.8e-18;
--+ches 0;
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InterPro;
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SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT;
SMART; SM00181; EGF; 1.
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Pfam;
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1. SUBCELLULAR LOCATION: Type I membrane protein.

1. SIMILARITY: TO OTHER SELECTINS/LECAMS.

1. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

1. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

1. SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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-i- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELLAL CELLS OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bosworth B.T., Dowbenko D., Shuster D.E., Harp J.A.; "Bovine L-selectin: a peripheral lymphocyte homing r Vet. Immunol. Immunopathol. 37:201-215(1993).
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ITE: PS001186; EGF_2; 1.

ITE: PS001187; C_TYPE_LECTIN_1; 1.

ITE: PS50041; C_TYPE_LECTIN_2; 1.

adhesion: Transmembrane; Glycoprotein;
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IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
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                                                                                                                                  lectin_c; 1. sushi; 2.
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CYTOPLASMIC (POTENTIAL).
CYTYPE LECTIN (SHORT FOR
EGF-LIKE.
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY 
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Query Match

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                                                                                                                                                                          COTTESPONDENCE DETWEEN PROTEIN domains and coding exons.";
GENOMICS 9:270-277(1991).

1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
VENULES IN PERIPHERAL LYMPH NODES.

1- SUBCELLULAR LOCATION: Type I membrane protein.
1- SIMILARITY: TO OTHER SELECTINS/JECAMS.
1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
1- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 EMBL;
EMBL;
EMBL;
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or send an email t
                                                                                                                  use
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MEDIJNE-9119529; PubMed=2004776;
Dowbenko D.J., Diep A., Taylor B.A., Lu
"Characterization of the murine homing
correspondence between protein domains
                                                                                                    modified and this st
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MEDLIND-89162048; PubMed=2646713;
Siegelman M.H., van de Rijn M., Weissman I.L.;

"Mouse lymph node homing receptor cDNA clone en

revealing tandem interaction domains.";
Science 243:1165-1172(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-89168433; PubMed-2647302;
Lasky L.A., Singer M.S., Yednock T.A., Dowbenko D., Fennie C.,
Rodriguez H., Nguyen T., Stachel S., Rosen S.D.;
ROdriguez H. alymphocyte homing receptor reveals a lectin domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-90263086; PubMed=1693096;
Siegelman M.H., Cheng I.C., Weissman I.L., Wakeland E.K.;

"The mouse lymph node homing receptor is identical with the lymphocyte cell surface marker Ly-22: role of the EGF domain endothelial binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEM1_MOUSE P18337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (LY-22) (Lymphocyte surface MEL-14 antigen)
(Leukocyte-endothelial cell adhesion molecule 1) (LECAM1) (CD62L).
SELL OR LNHR OR LY-22.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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Mammalia; Eutheria;
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                                                                                                            ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
; X14772; CAA32880.1;
; M36005; AAA39722.1;
; M36058; AAA39723.1;
; M25324; AAA39431.1;
                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                            56:1045-1055(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                       equires a license agreement (email to license@isb-sib.ch)
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a license
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Rodentia;
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                                                                                                   not removed.
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                                                                               (See http://www.isb-sib.ch/announce/
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
SMART; SM00201; SG; 1.
LEM1_RAT
P30836;
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PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01615; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
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EMBL; M64440; AAA75651.1;
EMBL; M64545; AAA75651.1;
EMBL; M64548; AAA75651.1;
EMBL; M64548; AAA75651.1;
PIR; A32375; A32375.
HSSP; P14151; 1KJB.
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InterPro;
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27; Conservative
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IPR001212;
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26, Created)
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5.2e-14;
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SMART; SM00032; CCC; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Cell adheaton; Transmembrane; Glycoprotein;
Selectin; Signal; Sushi; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92329548; PubMed-1378303;
Watanabe T., Song Y., Hirayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (LY-22) (Lymphocyte surface MEL-14 antigen) (Leukocyte-endothelial cell adhesion molecule 1) (LECAMI) (CD62L). SELL OR LNHR OR LY-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                        DOMAIN
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; P14151; 1KJB.
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IPR002396;
IPR000436;
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BY SIMILARITY
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C-TYPE LECTIN (SHORT FO
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  (GLCNAC.
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for LECAM-1.";
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                                                                    SMART;
                                                                                                         Pfam; PF00059; lectin_c; 1. Pfam; PF00084; sushi; 6. PRINTS; PR00343; SELECTIN. SMART; SM00032; CCP; 6.
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenbloom C.L., Anderson D.C.; Submitted (XXX-1993) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel.
01-FEB-1994 (Rel.
01-FEB-1996 (Rel.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Jugular vein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED B
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1--3)FUCOSYLATED DERIVATIVES
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
GLYCOLIPIDS).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.
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SM00034; CLECT; 1.
SM00181; EGF; 2.
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  PS00022; EGF_1; 1.
PS01186; EGF_2; 1.
PS00615; C_TYPE_LECTIN_1;
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4 (Rel. 28, Last sequence update)
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precursor (Endothelial leukocyte a
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oa; Chordata; Craniata; Vej
ia; Carnivora; Fissipedia;
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Pred. No. 9e-13;
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ia; Canidae;
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                       Hession C.
Pasek M.,
                                                                                                                                                                                                                                                                                                                           _HUMAN STANDARD; PRT; 610 AA.

LEM2_HUMAN STANDARD; PRT; 610 AA.

P16581; P16111;

01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E-selectin precursor (Endothelial leukocyte ad
(ELAM-1) (Leukocyte-endothelial cell adhesion
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                                                                           SEQUENCE FROM N.A. MEDLINE=90175359;
                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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20; Conservative
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        , E.,
           PubMed=1689848;
n L., Goff D., Chi-Rosso G.,
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Primates;
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5; Mismatches 8;
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GLYCOLIPIDS).

GLYCOLIPIDS).

I SUBCELLULAR LOCATION: Type I membrane protein.

POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIAY
HIGHER RISK OF CORONARY ARPERY DISEASE (CAD). A SIGNIFIV
HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATI
ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED
UNSELECTED POPULATION (SER-149).

SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.

MWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm".
   This
                                                                                                                                                                                                                                                                          MEDLINE=99134508; PubMed=9933738; Ye S.Q., Usher D., Virgil D., Zha
                                                                                                                                                                                                                                                                                                                       WEDLINE=95179107; pubMed=7533025; Wenzel K., Felix S., Kleber F.X., Brachold R., Schulte K.L., Glaser C., Rohde K., Baumann G., "E-selectin polymorphism and atherosclerosis: & Hum. Mol. Genet. 3:1935-1937(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            Graves B.J., Crowther R.L., Chandran C., Run Huang K.-S., Presky D.H., Familletti P.C., W "Insight into E-selectin/ligand interaction structure and mutagenesis of the lec/EGF dom Nature 367:532-538(1994).
                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95179107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) MEDLINE=94150646; PubMed=7509040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
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Phillips M.L., Nudelman E.,
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MEDLINE-91115870; PubMed-1703529;
Collins T., Williams A., Johnston
Gimbrone M.A. Jr., Bevilacqua M.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "ELAM-1 mediates cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and chromosomal location leukocyte adhesion molecule 1."; J. Biol. Chem. 266:2466-2473(1991).
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   SWISS-PROT
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                                                                                                                                                                                                                                                                                                     ARG-149
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250:1130-1132(1990)
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Stengelin S., Gimbrone M.A. Jr., Seed B.;
Stengelin S., Gimbrone M.A. Jr., Seed B.;
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Pfam; PF00084; sushi; 6.

PRINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 6.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00186; EGF_1; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00187; C_TYPE_LECTIN_1; 1.

PROSITE; PS00187; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
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R: A35046; A35046.
R: A35615; A36615.
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R: A3615; A36615.
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EXTRACELLUAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
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N-LINKED
N-LINKED
N-LINKE
NAIMILA
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-LINKED (GLCNAC.
-LINKED (GLCNAC.
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   L25527;
P16581;
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LEM2_RAT STANDARD; PRI,
p98105;
p01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAN-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                            ROSENDLOOM C.L., Auchampach J.A., Anderson D.C., Manning A.M.;
Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.

-I-FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED B
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
GLYCOLIPIDS).

-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-I- SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
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This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
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21; Conservative
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Pred. No. 5.6e
4; Mismatches
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E -> Q (IN DBSNP:5366).
/FTId-VAR_011792
H -> Y (IN DBSNP:5368).
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L -> F (IN DBSNP:5355).
/FTId=VAR_011794.
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/FTId=VAR_004191
E -> K (IN DBSNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7D43E3C0D1229229 CRC64;
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pfam; pF00008; sGF; 1.

pfam; pF00059; lectin_c; 1.

pfam; pF00084; sushi; 5.

sMART; sM00034; CLECT; 1.

sMART; sM00034; CLECT; 1.

sMART; sM00181; EGF; 1.

sMART; sM00181; EGF; 1.

pROSITE; pS00122; EGF_1; 1.

pROSITE; pS00615; C_TYPE_LECTIN_1; 1.

pROSITE; pS00615; C_TYPE_LECTIN_2; 1.

cell adhesion; fransmembrane; Glycoprotein; EG
                           P42201;
01-NOV-1995
01-NOV-1995
15-JUL-1999
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LEM3_BOVIN
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IPR000436; S
IPR001304; I
    95 (Rel. 32,
95 (Rel. 32,
99 (Rel. 38,
precursor (
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62.5%;
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Sushi_SCR_CCP.
lectin_c.
  , Last sequence update)
, Last annotation update)
(Granule membrane protein 140) (GMP-140) (PADGEM)
                         Created)
Last sequence
Last annotation
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CYTOPEASMIC (SHORT FORM).

EGF-LIKE.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 3.

SUSHI 5.

BY SIMILARITY.

BY SIMILARIT
                                                                                                                                                                                                                                                                                                               Score 127; DB 1;
Pred. No. 1.2e-08;
4; Mismatches 8
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                           Length 549;
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RX MEDLINE-93249394; PubMed-7683458;
RX MEDLINE-93249394; PubMed-7683458;
RX MEDLINE-93249394; PubMed-7683458;
RA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;
RA "Isolation and characterization of a bovine cDNA encoding a functional homolog of human p-selectin.";
RL Biochem. Biophys. Res. Commun. 192:338-344(1993).
CC -!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDLATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH CC LEUKOCYTES. THE LICAND RECOGNIZED IS SIALYL-LEWIS X.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND MEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND MEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See I
                                    EMBL; L12041; AAA30743.1; HSSP; P16109; 1FSB.
                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD62P)
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS; BOVINE
THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event European Bioinformatics Institute. There are no restricted the state of the state of the swiss institute.
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IPR000561;
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SMART; SM00032; CCP; 6.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

SMOSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1

PROSITE; PS00614; C_TYPE_LECTIN_2; 1

Cell adhesion; Transmembrane; Glycop

Selectin; Signal; Sushi; Repeat. Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN. InterPro; IPR002396; InterPro; IPR000436; InterPro; IPR001304; 41 646 587 611 646 158 195 258 320 320 320 382 444 444 516 578 158 EGF-like. Selectin. Sushi_SCR_CCP. lectin_c POTENTIAL.
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Matches 19
                                                                                                      Burns S.A., Neufeld E.J., Donady J.J.;

FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS

TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE

INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

-I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-I- SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaila; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
  This SWISS-PROT entry is copyright. It is postween the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p98109;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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                                                                  try is copyright. It is produced through a constitute of Bioinformatics and the EMBL
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SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS001186; EGF_2; 1.

PROSITE; PS00615; C.TYPE_LECTIN_1; 1

PROSITE; PS00615; C.TYPE_LECTIN_2; 1

Cell adhesion; Transmembrane; Glycop

Selectin; Signal; Sushi; Repeat
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                  SMART;
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InterPro; iPR002396; Selectin.
InterPro; iPR000436; Sushi_SCR_CCP.
InterPro; iPR001304; lectin_c.
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EMBL; M87862; AAA37577.1;
HSSP; P16581; 1KJA.
MGD; MGI:98278; Sele.
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-C) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
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μετουθές sushi, 6.

μετουθές proudad; sushi, 6.

μετουθές proudad; sproudad; sproudad
                                                                                                      PF00084;
                                                                                                                                                                                         PF00008; EGF; 1.
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                                                                                                                                           PF00059;
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57.6%;
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Best Local
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SELE.
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P98110;
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01-FEB-1996 (Rel. 33, Last sequ
15-JUL-1998 (Rel. 36, Last anno
E-selectin precursor (Endotheli
(ELAM-1) (Leukocyte-endothelial
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    Eukaryota;
Mammalia; !
                                                Sus scrofa
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SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF; 1; 1.
PROSITE; PS01186; EGF; 1.
PROSITE; PS01186; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                             143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity 19; Conserv
    Eutheria;
                         Metazoa;
                                                                                              i (Rel. 33, Created)
5 (Rel. 33, Last sequence update)
8 (Rel. 36, Last annotation update)
precursor (Endothelial leukocyte ad
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612 AA;
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243
273
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336
3368
3399
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                                                                                                                                                                                                                                                  STANDARD;
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Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.6%;
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C-TYPE LECTIN (SHORT FORM)
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSH
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E-SELECTIN.
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No. 1
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                                                                                                        adhesion molecule
on molecule 2) (LEC
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Interrio,

Pfam; PF00008; EGF; 1.

Pfam; PF00059; lectin_G; 1.

Pfam; PF00084; sushi; 4.

Pfam; PF00084; sushi; 4.

PRINTS; PR00343; SELECTIN.

R SMART; SM00032; CGP; 4.

R SMART; SM00031; EGF; 1.

DR PROSITE; PS00015; EGF_1; 1.

DR PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS00015; C_TYPE_LECTIN_2; 1.

DR PROSITE; PS00015; C_TYPE_LECTIN_2; 1.

CR PROSITE; PS0001; Transmembrane; Glycoprotein; EGF

KW Cell adhesion; Transmembrane; Glycoprotein; EGF

KW Cell shear and Sushi; Repeat.
        DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; EGF-11ke.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE-94271236; PubMed-7516159;
Tsang Y.T.M., Haskard D.O., Robinson M.K.;
"Cloning and expression kinetics of porcine vascular cell adhesion molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matis L.A., Rother R.P.;
"Molecular and functional analysis of porcine E-selectin reveals potential role in xenograft rejection.";
Biochem. Biophys. Res. Commun. 204:763-771(1994).
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TISSUE-Aortic
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[1]
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SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS; PORCINE E-LECTIN THE HUMAN SUSHI-1 AND -4 EQUIVALENTS.
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U08350;
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AAA21541.1; -.
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1391
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM).

EGF-LIKE.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

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BY SIMILARITY.
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P16109;

01-APR-1990 (Rel. 14, Created)

01-AUG-1990 (Rel. 15, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)

(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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                                                                   MEDLINE=93266599; PubMed=7684381;
Fujimoto T., Stroud E., Whatley R.E.
Laposata M., McEver R.P.;
"P-selectin is acylated with palmiti
cysteine 766 through a thioester lin
J. Biol. Chem. 268:11394-11400(1993)
                                                                                                                                                                                                     endothelium: sequence similarity to
adhesion and inflammation.";
Cell 56:1033-1044(1989).
                                                                                                                                                                                                                                                                                                                                         SELP OR GMRP.
Homo sapiens (Human).
Homo sapiens (Homan).
'Troota; Metazoa; Chordata; Metazoa; Primates;
   STRUCTURE BY NMR OF 160-199.
MEDLINE=97057176; PubMed=8901515;
Freedman S.J., Sanford D.G., Back
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-89168432; PubMed-2466574;
Johnston G.I., Cook R.G., McEver R.P.;
"Cloning of GMP-140, a granule membrane
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     ω.w.,
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Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
"The P-selectin gene is highly polymorphic: reduced frequency of t
Pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284(1998).

-1- FUNCTION: CA(2+)-DEDENDENT RECEPTOR FOR MYELOID CELLS THAT BIN
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS STAIAL-LEWIS X.

-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
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"Structure ;
selectin.";
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94093388; PubMed=7505680;
Bajorath J., Stenkamp R., Aruffo A.;
"Knowledge-based model building of proteins: concepts
Protein Sci. 2:1798-1810(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS ASN-331; ASP-603; VAL-640
MEDLINE=98334547; PubMed=9668170;
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                                                                                                                                           ; 1FSB; 01
; 1KJD; 03
; 173610;
1; PF00059; Tectin_c; 1.
1; PF00084; sushi; 9.
1TS; PR00343; SELECTIN.
1TS; SM00034; CELECT; 1.
1T; SM00034; CLECT; 1.
1T; SM000181; EGF; 1.
                                                                                                                                                                                         SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 9 SUSHI (SCR) DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European
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IPR002396;
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Selectin; Signal; §
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E; PS01186; EGF_2; 1.
'E; PS00615; C_TYPE_LECTIN_1; 1.
TE; PS50041; C_TYPE_LECTIN_2; 1.
adhesion; Transmembrane; Glycoprotein; EGF-
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                                  /FTIG=VAR_004194.
T -> P (REDUCED FREQUENCY IN PATIENTS WITH MYOCARDIAL INFARCTION).
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S -> N.
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                                                                                                                                               /FTId=VAR_004192
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Length 830

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Matches 19; Conserv
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J. Biol. Chem.
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BLOOD 80:795-800(1992).

BLOOD 80:795-800(1992).

FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

FUNCTION: TYPE I MEMBERATE POTCHIA.

FUNCTION: TYPE I MEMBERATE OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS OF PALADE BODIES OF ENDOTHELIAL CELLS OF PALADE BODIES OF THE BODIES 
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EMBL; M72332; AAA37712.1;
PIR; A42755; A42755.
HSSP; P16109; IFSB.
MGD; MGI:98280; Selp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
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Q01102;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1993 (Rel. 26, Last sequence update)
Q1-APR-1993 (Rel. 27, Last sequence update)
Q1-APR-1993 (Rel. 28, Last sequence update)
Q2-1994 (Rel. 20, Last sequence update)
Q2-1995 (Leukocyte-endothelial emembrane protein 140) (GMP-140) (PADGEM)
Q2-1995 (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
Q2-1995 (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
Q2-1995 (Rel. 25, Last sequence update)
Q2-1995 (Rel. 25, Last sequence update)
Q3-1995 (GMP-140) (PADGEM)
Q2-1995 (Rel. 25, Last sequence update)
Q3-1995 (GMP-140) (PADGEM)
Q4-1995 
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MEDLINE-92345617; PubMed-1379089;
Sanders W.E. Jr., Wilson R.W., Ba
"Molecular cloning and analysis o
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"Cloning of the mouse endothelial selectins. E
and P-selectin is inducible by tumor necrosis
J. Biol. Chem. 267:15176-15183(1992).
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SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
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                                            PF00008;
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sushi; 8.
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6; Mismatches
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SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE: PS00186; EGF_1; 1.
PROSITE: PS00186; EGF_2; 1.
PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
PROSITE: PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycoprotein;
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C-TYPE LECTIN (SHORT FORM)
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(POTENTIAL).
(POTENTIAL).
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THEFFERENCE OF SOME THE FEET T
                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_C; 1.
Pfam; PF00084; sushi; 4.
Pfam; PF00084; sushi; 4.
PRINTS; PR00343; SELECTIN.
SMARF; SM00032; CCP; 4.
SMARF; SM00034; CLECT; 1.
SMARF; SM00081; EGF; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00022; EGF_2; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
    DISULFID DISULFID
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DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000742; I
InterPro; IPR002396; S
InterPro; IPR000436; S
InterPro; IPR001304; I
                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                            SIGNAL
CHAIN
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                                               DOMAIN
                                                                        DOMAIN
                                                                                                                                                                                                                                                                                       Selectin;
                                                                                                                                                                                                                                                                                                           Cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nguyen M., Strubel N.A., Bischoff J.;
"A role for sialyl Lewis-X/A glycoconjugates morphogenesis.";
Nature 365:267-269(1993).
-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SELE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Adrenal gland;
MEDLINE=93382537; PubMed=7690465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CD62E).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES (POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOLIPIDS).

FUNCTION: INVOLVED IN CAPILLARY MORPHOGENESIS
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een the Swiss Institute of Bioinformatics and the EN
Suropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                Signal;
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                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein;
    Sushi;
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430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Sushi_SCR_CCP.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
SUSHI 4.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                          BY SIMILARITY.
E-SELECTIN.
EXTRACELLULAR (POTENTIAL).
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TARLY). .
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DNA CEÎL BIOL. 11:149-162(1992).

-i--FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL MEDIATES THEIR BINDING TO LEUKOCYTES. THE LICAND REC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DER POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TE
                                                   This
                                                                                                                                                                                                                                                                             Larigan J.D., Tsang T.C., Rumberger J.M., Burns D.K.; "Characterization of cDNA and genomic sequences encoding rabbi ELAM-1: conservation of structure and functional interactions leukocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM
                                  between
                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
MEDLINE=92189729; PubMed=1372169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEM2_RABIT P27113;
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Mammalia; Eutheria;
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                                                                          POLYLACTOSAMINE THAT ARE FOUND AT THE NONREL GLYCOLIPIDS).

SUBGELLULAR LOCATION: Type I membrane protei INDUCTION: BY CYTOKINES.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
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             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                        cuniculus (Rabbit).
Metazoa; Chordata; Craniata;
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Pred. No. 1.4e
4; Mismatches
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.4e-07;
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Query Match
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SMART; SM00032; CCP; 5.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
PROSITE: PS00022; EGF=1; 1.
PROSITE: PS01186; EGF=2; 1.
PROSITE: PS01186; C_TYPE_LEB
PROSITE: PS05041; C_TYPE_LEB
PROSITE: PS05041; C_TYPE_LEB
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EMBL; M91005;
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 5.
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InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
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                    l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00022; EGF_1; 1.
PS01186; EGF_2; 1.
PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equires a license agreement (Some ail to license@isb-sib.ch).
                                                                                                                      Conservative
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X
                                                                                                               EGF-LIKE.

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SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 4.

SUSHI 5.

SUSHI 4.

SUSHI 5.

SUSHI 4.

SUSHI 4.

SUSHI 5.

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SUSHI 5.

BY SIMILARITY.

B
                   Score 116; DE
Pred. No. 2.8e
6; Mismatches
                    6,
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C-TYPE LECTIN (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-SELECTIN.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                   -> A (IN REF. 1;
-> A (IN REF. 1;
-> V (IN REF. 1;
23BC8A883B23240E
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                    .8e-07;
les 9;
                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like
                                                                                                                AAA31244).
AAA31244).
AAA31244).
                                                Length 551;
                    Indels
                                                                                                                                                                     (POTENTIAL)
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                   0,
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LEM3_RAT
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                                                                                            EMBL; L23088; AAA60325.1; -.

HSSP; P16109; 1FSB.

RINTEPTO; IPR000561; EGF-like.

InterPro; IPR002396; Selectin.

InterPro; IPR002396; Selectin.

InterPro; IPR002396; Selectin.

InterPro; IPR002396; Selectin.

InterPro; IPR001304; lectin.c; 1.

Pfam; PF00084; sushi; 8.

PFRNTS; PR00343; SELECTIN.

RART; SM00034; CLECT; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00186; EGF-2; 1.

PROSITE; PS00187; CTYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EGF-1

Selectin; Signal; Sushi; Repeat; Lipoprotein; Pa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **Rachampach J.A., Oliver M.G., Anderson D.C., Manning **Cloning, sequence comparison and in vivo expression encoding rat P-selectin.**; Gene 145:251-255(1994).
 DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LICAND RECOGNIZED IS SIALVI-LEWIS X.

-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN, LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
-!- INDUCTION: BY ACUTE INFLAMATION (PROBABLE).
-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS; RAT P-LECTIN LACKS THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWI
between
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                                                                   CHAIN
                                                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM)
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM)
                                                EXTRACELLULAR
                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathbf{u}
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                                                  (POTENTIAL)
                                                                                                                    EGF-like domain;
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Q04962;
01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
01-NOV-1997 (Rel.
Coagulation factor
(HAF) (Fragment).
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DISULFID
CARBOHYD
             MEDLINE=93003367; PubMed=1390917; Semba U., Yamamoto T., Kunisada T Kambara T., Okabe H.;
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10141;
                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
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16; Conser
                                                                                                                                                                                                                                                                          (Rel. 33, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
factor XII precursor (EC 3.4.21.38)
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48.5%;
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                                                                                                 SEQUENCE
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SUSHI 6.
SUSHI 6.
SUSHI 7.
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BY SIMILARITY.
BY SIMILARI
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Pred. No. 2.
                                                                                                                                                                  Hystri
                                                                                                                                                                                         Craniata;
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                                                                                                   얽
                                  Shibuya
                                                                                                                                                                  cognathi;
                                                                                                 19-37;
                                                                                                                                                                                                                                                                                                                                                                                         603
                                                                                                                                                             Vertebrata; Euteleostomi;
nathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
%.8e-06;
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                                                                                               318-332
                                Υ.,
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                                                                                                                                                                                                                                                                            (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                 AND 359-373
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                                                                                                                                                                                                                                                                            factor)
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      THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                              Pfam; pro0040; fn2; 11.

R pfam; pr00040; fn2; 1.

R pfam; pr00089; trypsin; 1.

R pfam; pr00089; trypsin; 1.

R proDom; p0000995; FN2; 1.

SMART; SM00181; EGF; 2.

SMART; SM00181; EGF; 1.

SMART; SM00130; KR; 1.

SMART; SM00130; KR; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; pS01186; EGF_1; 2.

PROSITE; pS01186; EGF_2; 1.

PROSITE; pS00023; FIBRONECTIN_1; 1.

PROSITE; pS00023; FIBRONECTIN_2: 1.

PROSITE; pS00021; KRINGLE 1; 1.

PROSITE; pS000134; TRYPSIN_DOM; 1.

PROSITE; pS00135; TRYPSIN_SER; 1.
DOMAIN
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NON_TER
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InterPro;
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HSSP; P00750; 1RTF.
MEROPS; S01.211; -.
InterPro; IPR000561; EGF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rPro; IPR000742; I

rPro; IPR001881; I

rPro; IPR000061; I

rPro; IPR000001; I

rPro; IPR001254; T

rPro; IPR000084; EGF; 2:

PF00008; EGF; 2:
    19
359
466
93
132
173
216
312
359
359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF; 2.
fn1; 1.
fn2; 1.
kringle;
  18
358
603
87
130
172
209
294
342
603
398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like.
EGF_2.
EGF_Ca.
FN_Type_II.
Kringle.
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RT "Primary structure of guinea-pig Hageman factor: sequence around the Cleavage site differs from the human molecule.";
RL Biochim. Biophys. Acta 1159:113-121(1992).
CC -!- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE GENERATION OF BRADYKININ AND ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor VII to form factor VIIa and factor XI to form factor XIa.
CC -!- CATALYTIC ACTIVITY: CLEAVES SELECTIVELY ARD HAW KININOGEN FORM A COMPLEX BOUND TO AN ANIONIC SUFFACE. PREKALLIKREIN AND HAW KININOGEN FORM A COMPLEX BOUND TO AN ANIONIC SUFFACE. PREKALLIKREIN IS CLEAVED BY FACTOR XII TO FORM KALLIKREIN, WHICH THEM CLEAVES FACTOR XII FIRST TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR XIIA ACTIVATES FACTOR XI TO FACTOR XIA.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPESIN FAMILY.
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Trypsin. fibronectin_type_1.
ALPHA-FACTOR XIIA HEAVY CALPHA-FACTOR XIIA LIGHT CFIBRONECTIN TYPE-II.
EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
KRINGLE.
PRO-RICH.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SCHARGE RELAY SYSTEM (BY S
                                                                                                                                                                             Plasma; Kringle; e domain; Repeat;
                                                                                                                                                                              Serine pı
Zymogen;
                                                                                                                        CHAIN
  SIMILARITY).
SIMILARITY).
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n; Signal.
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLL1_HUMAN
000548;
This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the European Bioinformatics Institute. use by non-profit institutions as longitude and this statement is not remodified and this statement is
                                                                                                                                                                            Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE INVOLVED IN CELL-TO-CELL COMMUNICATION IN
MAMMALIAN EMBRYOS. MAY HAVE A ROLE IN CELLULAR INTERACTIONS
UNDERLYING SOMITOGENESIS AND DEVELOPMENT OF THE NERVOUS SYSTEM
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99180765; PubMed-10079256;

Gray G.E., Mann R.S., Mitsladis E., Henrique D., Carcangiu M.L.,

Banks A., Leiman J., Ward D., 136-Horowitz D., Artavanis-Tsakonas

"Human ligands of the Notch receptor.";

"Human ligands of the Notch receptor.";

"Am. J. Pathol. 154:785-794(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta (H-Delta-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                            [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                       SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE DELTA/SERRATE/JAGGED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.28;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                  ght. It is produced through a collab
Bioinformatics and the EMBL outst
titute. There are no restrictions
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0.00012;
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; Homo.
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PROSITE; PS001186; EGF_2; 8.
PROSITE; PS011187; EGF_CA; 1.
Signal; EGF-like domain; Repeat; T
Differentiation; Glycoprotein.
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                       CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
CDPSPCKNGGSCTDLENSYSCTCPPGFYGKICEL
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P00740; 1EDM
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SM00179; EGF_CA; 4.
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an email to license@isb-sib.ch).
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                                                                                                                 InterPro; iPR00080; Notch.

Pfam; pF00003; ank; 6.

Pfam; pF00008; EGF; 36.

Pfam; pF00006; notch; 3.

Pfam; pF00066; notch; 3.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00145; NOTCH.

SMART; SM00248; ANK; 5.

SMART; SM00001; EGF_like; 11.

SMART; SM00001; ANK_REPEAT; 4.

PROSITE; PS50088; ANK_REP REGION; 1

PROSITE; PS00010; ASX_HYDROXYL; 23.

PROSITE; PS00010; ASX_HYDROXYL; 23.

PROSITE; PS001186; EGF_2; 29.

PROSITE; PS01186; EGF_2; 29.

PROSITE; PS01187; EGF_CA; 21.

Differentiation; Neurogenesis; Repeator Colored C
                                                                                                      Transmembrane;
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Kintner C.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELDULAR LOCATION: Type I membrane protein.

-!- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY |

-!- SIMILARITY: HIGH, WITH OTHER NOTE: TYPE PROTEINS.

-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
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01-OCT-1996
16-OCT-2001
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MEDLINE-90385285; PubMed=2402639;
MEDLINE-90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Amphibia; I
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Xenopus laevis (African clawed Xenopus laevis (African clawed Chordata)

Tenvarvota; Metazoa; Chordata
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A35844; A35844.
; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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); IPR000152; Asx_hydroxyl.
); IPR000561; EGF_1ke.
); IPR000742; EGF_2.
); IPR001881; EGF_Ca.
); IPR001438; EGF_II.
); IPR000800; Notch.
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Batrachia;
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       1; Glycoprotein.
1; Glycoprotein.
29 POTENTIAL.
24 NEUROGENIC LOCUS N
28 EXTERCELLULAR (POT
20 POTENTIAL.
24 CYTOPLASMIC (POTEN
257 EGF-LIKE 1.
26 EGF-LIKE 2.
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RESULT 24
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ID YNN3_CAEEL
AC 934576;
DT 01-FEB-1994
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     EMBL; Z30423; CAA83007.1; -.
PIR; S42373; S42373.
HSSP; P02468; 1TLE.
WormPep; T20G5.3; CE00478.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002035; yWFA.
InterPro; IPR002035; yWFA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
Berks M., Smith A.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 45 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 SEA DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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PF00092;
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SM00001;
SM00200;
SM00327;
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PS00022; EGF_1; 1.
; PS01186; EGF_2; 5.
; PS01187; EGF_CA; 1.
; PS50024; SEA; 2.
; PS50234; VWFA; 1.
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Caenorhabditis.
POTENTIAL.

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EGF-LIKE 5 .
EGF-LIKE 5 .
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PRIC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vitamin.K dependent protein C precursor (EC 3.4.)
DE (Autoprothrombin IIA) (Anticoagulant protein C)
DE (Autoprothrombin IIA) (Anticoagulant protein C)
DE factor XIV).
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  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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L Similarity 51.1
16; Conservative
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Pred. No. 0.00
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Sciurognathi; Muridae;
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Pfam; PFO0008; Ffam; PF000594; c
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the European Bioinformatics Institute. Their
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modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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"A comparative study of partial primary structures of the catalytic region of mammalian protein C.";

Br. J. Haematol. 86:590-600(1994).

-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THE PROJECT OF CAGULATION BY INACTIVATING FACTORS VA AND VIIIE IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
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"Isolation and characterization of
J. Blochem. 111:491-495(1992).
                                                                                                                                          HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=149/370;
MEDLINE=98152576; PubMed=9493582;
Talbert L.R., Rosen E.D., Lissens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Liver;
MEDLINE-92316897; PubMed-1618739;
                                                                                                                    MEROPS; S01.218; -. MGD; MGI:97771; Proc.
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D43755; BA
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                                       JIPR000152; Asx_hydroxyl.
JIPR001314; Chymotrypsin.
JIPR001561; EGF_1ike.
JIPR001881; EGF_Ca.
JIPR0012383; GIA_blood.
JIPR001254; Trypsin.
JIPR000294; VitK_dep_GLA.
 PR00722;
; EGF; 2.
; gla; 1.
; trypsin; 1.
22; CHYMOTRYPSIN.
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of a mouse protein C cDNA.";
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SMART; SM00001; EGF_11ke; 1.

SMART; SM00009; GLA; 1.

SMART; SM000020; Tryp_SPc; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00118; EGF_L; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001187; EGF_CA; 1.

PROSITE; PS00135; TRYPSIN_HS; 1.

PROSITE; PS00135; TRYPSIN_HS; 1.

PROSITE; PS00135; TRYPSIN_HS; 1.
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EGF-LIKE 1.
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CHARGE RELAY SYSTEM.
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BY SIMILARITY.
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Score 87; DB Pred. No. 0.0066; Mismatches
                                                                     MISSING (IN REF. 2)
N -> D (IN REF. 2);
53FAA0D85B194D6E
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ium-binding; Vitamin K; Hydroxylation;
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DB 1;
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InterPro;
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P97677;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                           Signal; EGF-like Differentiation;
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InterPro;
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Pfam; PF00008; EGF; 7
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE INVOLVED IN CELL-TO-CELL COMMUNICATION IN
MAMMALIAN EMBRYOS. MAY HAVE A ROLE IN CELLULAR INTERACTIONS
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 8 EEF-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE DELTA/SERRATE/JAGGED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                         E; PS00010; ASX_HYDROXYL; 1
F; PS00022; EGF_1; 8.
E; PS01186; EGF_2; 8.
E; PS01187; EGF_CA; 2.
F; EGF-like domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                               SM00051; DSL; 1.
SM000179; EGF_CA; 4.
SM00001; EGF_like;
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IPR001774; DSL.
IPR000561; EGF-like.
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IPR001881;
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EGF_Ca.
EGF_II.
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EXTRACELLULAR (POTENTIAL.
CYTOPLASMIC (POTENT)
EGGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4. CALCIUM-
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7. CALCIUM-
EGF-LIKE 8.
BY SIMILARITY.
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Sciurognathi;
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otation update)
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There are no rest
ng as its content
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thi; Muridae;
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Murinae; Rattus
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MBL outstation -
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FASEB J.
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SEQUENCE FROM N.A.
MEDLINE-90112459; PubMed=2514273;
MeDLINE-90112459; PubMed=2514273;
Medlino-Reynoso M.G., Rollo D.R., Hursh D.A., Raff
"Structural analysis of the uEGF gene in the sea urchi
strongylocentrotus purpuratus reveals more similarity
than to invertebrate genes with EGF-like repeats.";
J. Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P10079;
01-MAR-1989
01-FEB-1996
16-OCT-2001
Fibropellin
                                                                                                                                                      "A sea urchin gene encodes a growth factor ";
Science 237:1487-1490(1987).
[3]
MEDLINE=91285254;
Bisgrove B.W., An
                                                                                                       MEDLINE=89196806; PubMed=2784773; Hunt L.T., Barker W.C.;
                                                                                                                                                                                                                  Hursh
                                                                                                                                                                                                                             SEQUENCE OF 279-476
MEDLINE=87319677; Pu
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EGF1.
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                             CHARACTERIZATION.
                                                                                        Hunt L.T., Ba
"Avidin-like
                                                                                                                                       AVIDIN-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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1 Similarity 35.1
12; Conservative
                                                           3:1760-1764(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
I precursor (Epidermal growth factor-related
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PubMed=2060714;
drews M.E., Raff
                                                                                                                                                                                                                  PubMed=3498216;
/s M.E., Raff R.
                                                                                                                                                                                                                                                                                                                                                                                                                               purpuratus (Purple sea urchin)
; Echinodermata; Eleutherozoa;
noidea; Echinacea; Echinoida; 
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Pred. No. 0.00
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C. I. FUNCTION: FORM THE APICAL LAMINA, A COMPONENT OF THE EXTRACELLIA LAYER THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE OF THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE OF ALTERNATIVE PRODUCTS: 2 ISOFORMS; IA (SHOWN HERE) AND IB; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM (IB) LACKS 8 IF OF THE MERCON OF THE STATE LEVELS IN UNFERTILIZED EGGS AND COMPINE CHAPTE OF THE MATTERNAL FORM (IB) LACKS 8 IN ABUNDANCE BETWOOD THROUGH SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALL COMPINE SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALL COMPINE SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALL COMPINE SUBSEQUENT STAGES. EXPRESSED BOTH MATERNALL CONTAINS 21 EGF-LIKE DOMAIN.

C. I. SIMILARITY: CONTAINS 21 EGF-LIKE DOMAIN.

C. I. SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR CONTAINS 1 CUB DOMAIN.
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PEAM; PEO0431; CUB; 1.

Pfam; PEO0431; CUB; 1.

Pfam; PEO0008; EGF; 21.

PRINTS; PRO0010; EGFLAMININ.

PRINTS; PRO0011; EGFLAMININ.

PRODOM; PDO16055; Avidin; 1.

SMART; SM00042; CUB; 1.

SMART; SM00001; EGF_Like; 3.

SMART; SM00001; EGF_Like; 3.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00180; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; EGF_2; 19.

PROSITE; PS01180; EGF_Z; 19.

PROSITE; PS01187; EGF_CA; 19.

PROSITE; PS01180; EGF_CA; 19.

PROSITE; PS01187; EGF_CA; 19.

PROSI
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EMBL; L08692; AAA62163.1;
EMBL; X17530; CAA35571.1;
EMBL; M17421; AAA30050.1;
EMBL; M17421; AAA30050.1;
EMBL; X17533; CAA35573.1;
PIR; A29316; A29316
HSSP; P07204; 1FGD
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                                  EMBL; M33753; AAA28428.1; EMBL; X05144; CAA28793.1;
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Cell 61:78
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STRAIN-OREGON-R; TISSUB-Embryo;
MEDLINE-90263104; PubMed-2344615;
Tepass U., Theres C., Knust E.;
"Crumbs encodes an EGF-like prote:
Drosophila epithelial cells and re
                                                                                                                entities
                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                Knust E., Dietrich U., Tepass U., Bremer K.A., Vaessin H., Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome melanogaster, and their relation to neurogenic EMBO J. 6:761-766(1987).

-i- FUNCTION: MAY PLAY A ROLE IN THE DEVELOPMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1663-1955 FROM
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                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Emburopean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                           POSSIBLY FOR THE ESTABLISHMENT AND/OR MAINTENA POLARITY. IT MAY ACT AS A SIGNAL.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: PHOSPHORYLATED IN THE CYTOPLASMIC DOMAIN SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
                в26637;
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                                                                               non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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SMART; SM00179; EGF_CA; 11.
SMART; SM00001; EGF_like; 16.
SMART; SM00282; LamG; 3.
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Pfam; PF00054; laminin_G; 3.
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; IPR000561; EGF-like.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
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EGF_1; 26.
EGF_2; 17.
EGF_CA; 15.
        LAM_G_DOMAIN; 3. Repeat; EGF-like
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EGF-LIKE 21.
LAMININ G-LIKE 22.
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Harlis H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawleys S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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NOTC_DROME STANDARD; PRT; 2703 AA.

P07207; P04154; O97458; Q9W4T8;

01-NOV-1986 (Rel. 03, Created)

01-MAR-2002 (Rel. 41, Last sequence update)

01-MAR-2002 (Rel. 41, Last sequence update)

01-MAR-2002 (Rel. 41, Last sequence update)

Neurogenic locus Notch protein precursor.

Neurogenic locus Notch protein precursor.

Neurogenic locus Notch protein precursor.
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STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-66079339; PubMed-393525;
Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
"Nucleotide sequence from the neurogenic locus notch implies product that shares homology with proteins containing EGF-lik repeats.";
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STRAILN-Canton-S, and Oregon-R; TISSUE-Embryo;
MEDLINE-87064624; PubMed-3097517;
Kidd S, Kelley M.R., Young M.W.;
"Sequence of the notch locus of Drosophila me
of the encoded protein to mammalian clotting
Mol. Cell. Biol. 6:3094-3108(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley;
MEDLINE-20196006; Pub
Adams M.D., Celniker
Amanatides P.G., Sche
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscr
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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MAN Mount S.M., Moy M., Murphy B., Murphy L., Musry D.M., Nelson D.L.,
AN Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
AN Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
AN Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
AN Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
AN Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
AN Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
AN Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AN Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
AN Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
AN Yeb R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
AN Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu |

Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova

Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,

Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,

"Form."
EMBL;
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                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Science 287:2220-2222(2000).
[5]
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NEUROGENIC GENES.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECTODERM.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
THE TOTAL THE PROCESS IS UNDER CONTROL OF THE
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                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
    M16152;
M16153;
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Kidd S., Berg R.L., You
of P-element insertions
AAB59220.1;
AAB59220.1;
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PROSITE; PS50297; ANK_REP_REGION; 1

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00022; EGF_1; 34.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_CA; 22.
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InterPro; IPR001881;
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InterPro; IPR000561;
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IBL; M16150; AAB59220.1; JOINED.
IBL; M16151; AAB59220.1; JOINED.
IBL; K03508; AAA28725.1; -
IBL; K03508; AAA28725.1; JOINED.
IBL; K03507; AAA28725.1; JOINED.
IBL; AB030426; AAA48725.1; JOINED.
IBL; AE003426; AAA48848.2; -
IBL; AE035436; CAB37610.1; -
IBL; AL035436; CAB37610.1; -
IBL; AL035436; CAB37610.1; -
IBL; M16025; AAA4496.1; -
IBL; M16025; AAA28728.1; -
IBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S; PR00010; EGFBLOS; PR01452; NOTCH.
S; SM00248; ANK; 4.
SM000179; EGF_CA;
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EGF_like; 13.
NL; 2.
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                                           Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_C1.
EGF_II.
Notch.
  40.0%;
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                                  EGF-LIKE 5, C

EGF-LIKE 6,

EGF-LIKE 9, C

EGF-LIKE 9, C

EGF-LIKE 11,

EGF-LIKE 11,

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EGF-LIKE 11,

EGF-LIKE 11,

EGF-LIKE 15,

EGF-LIKE 16,

EGF-LIKE 17,

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EGF-LIKE 19,

EGF-LIKE 20,

EGF-LIKE 21,

EGF-LIKE 21,

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Score
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EXTRACELLULAR (POTENTIAL).
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6;
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DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FP2_MYTGA STANDARD; PRT; 473 AA. Q25464; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Adhesive plaque matrix protein 2 precursor (Foot MCFB-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: SOME TYROSINES ARE HYDROXYLATED (THUS DIHYDROXYPHENYLALANINE). SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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4; Mismatches
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Pteriomorphia; Mytiloida;
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Best Local
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DISULFID
SEQUENCE FROM N.A., AND SEQUENCE TISSUE-Fetal brain, and Melanoma; MEDLINE-91187670; PubMed-1707164; Siri A., Carnemolla B., Saginati Baralle F., Zardi L.;
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13; Conser
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nilarity 38.2%;
Conservative
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RESULT 31

TENA_HUMAN STANDARD;

ID TENA_HUMAN STANDARD;

AC P24821; Q15567; Q14583;

DT 01-MAR-1992 (Rel. 21, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tenascin precursor (TN) (Hexaborachion) (Cytotactin) (Neuronectin)

TE (GNEM) (JI) (Miotendinous antigen) (Glioma-associated-extracellular (Glioma-associated-extracellular antigen) (GP 150-225) (Tenascin-C) (TN-C).
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Pred. No. 0.00
8; Mismatches
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Leprini A.,
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This SWI
between
the Euro
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PIR;
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Nucleic Aci
[2]
                                                                                                                                                                                                                                                                                                                                                                                              INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROUND INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROUND FEBTAHELIAL TUMORS. IS A LIGAND FOR INTEGRINS ALPHA-8/BETA-ALPHA-9/BETA-1, ALPHA-V/BETA-3 AND ALPHA-V/BETA-6.

SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILLIZED BY DISULFIDE RINGS. HOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LIMITHIN THE CENTRAL GLOBULE.

SUBCELLULAR LOCATION: EXELTACEILLIAR MATIX.

ALTERNATIVE PRODUCTS: FOUR VARLANTS ARE PRODUCED FROM A SINGI GENE IN A TISSUE- AND TIME-SPECIFIC MANNER DURING DEVELOPMENT: INDUCTION: BY TGF-BETA.

SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93068293; PubMed=1279805;
Leahy D.J., Hendrickson W.A., Aukhil I., Erickson "Structure of a fibronectin type III domain from MAD analysis of the selenomethionyl protein.";
Science 258:987-991(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An alternatively spliced region of the human hexabrachion repeat of potential N-glycosylation sites.";
"Proc. Natl. Acad. Sci. U.S.A. 86:1588-1592(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marton L.S., Stefansson K.; "Structure of the human hexabr Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gherzi R., Carnemolla B., Siri A., Pon "Human tenasoin gene. Structure of the characterization of the transcription J. Biol. Chem. 270:3429-3434(1995).
                                                                                                                                                                                                                                         entities
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Gulcher To
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antibodies.";
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L; X78565; CAA55309.1
L; M55618; AAA88083.1
L; M24630; AAA52703.1
; S14015; S14015.
                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the February Buropean Bioinformatics Institute. There are no rest by non-profit institutions as long as its content by non-profit institutions as long as its content.
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                                                                                                                                                                                                              non-profit institutions as lon and this statement is not remove requires a license agreement (san email to license@isb-sib.ch).
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         IPR000561;
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olla B., Siri A.,
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       Pfam; PF00008; EGF; 14.
Pfam; PF00041; fibrinogen_C; 1
Pfam; PF00041; fia; 15.
Pfam; PF00041; EGF; 9.
SMART; SM00181; EGF; 9.
SMART; SM00186; FBG; 1.
SMART; SM00186; FBG; 1.
SMART; SM00060; FN3; 12.
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Mech. Nev. 46:123-136(1994).

-I FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DUI-
VARIOUS CELL FATE DECISIONS AND MORPHOLOGICAL MOVEMENTS
DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO-
-I- TISSUE SPECIFICITY: PROLIFERATING NEUROEPITHELIUM.
-I- DEVELOPMENTAL STAGE: CNS DEVELOPMENTAL.
-I- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.
                                                                                                                                        SEQUENCE FROM N.A.
STRALN=ICR X SWISS WEBSTER;
MEDLINE-95001556; PubMed-7918097;
Lardelli M., Dalstrand J., Lendahl U.;
"The novel Notch homologue mouse Notch
growth factor-repeats and is expressed
neuroepithelium.";
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                           NTC3_MOUSE STANDARD; PRT; 23 061982; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation Neurogenic locus notch 3 protein.
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JTCH3.

us musculus (Mouse).

""+Paryota; Metazoa; Chordata; Cr

""+Paryota; Rodentia; S
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    PRINTS: PRODOID: EGFBLOOD.

PRINTS: PRO1452; NOTCH.

SMART; SM00248; ANK; 5.

SMART; SM00248; ANK; 5.

SMART; SM00001; EGF_Like; 13.

SMART; SM00004; NL; 3.

SMART; SM00004; NL; 3.

PROSITE; PS50088; ANK_REP_REGION; 1

PROSITE; PS50297; ANK_REP_REGION; 1

PROSITE; PS0010; ASX_HYDROXYL; 18.

PROSITE; PS001186; EGF_1; 3.

PROSITE; PS01187; EGF_CA; 17.

Differentiation; Neurogenesis; Repertiferences.
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HSSP;
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P00740; 1IXA.
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IPR001881;
IPR001438;
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IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000800;
470
508
543
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696
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EGF;
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iGF; 34.

iotch; 3.

EGFBLOOD.
  EGF_Ca.
EGF_II.
Notch.
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5 ANK REPEATS.
POEST.

POEST-LIKE

BOF-LIKE

BOF-LI
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CYTOPLASMIC
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CALCIUM-BINDING
CALCIUM-BINDING
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                   CALCIUM-BINDING CALCIUM-BINDING
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(POTENTIAL).
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EGGF-LIKE 3
EGGF-L
                               Y SIMILARITY
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-WISTAR; TISSUE-Liver;
RX MEDLINE-92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nava K., Marumoto Y.;
RT "The CDNA cloning and mrNA expression of rat protein C.";
RI Biochim. Biophys. Acta 1131:329-332(1992).

CC :- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT C.

IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLLPIDS.

C :- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

C: CATALYTIC STUTIESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS STRONGLY PROMOTED BY THROMBOMODULIN.

-i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE VITAMIN K-DEPENDENT.
                                  A LOCAL COCCACA CARA RARA COCCACA COCACA COCCACA COCCA
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRTC_RAT STANDARD; PRT; 461 AA. 193194; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Vitamin-K dependent protein C precursor (EC 3 (Autoprothrombin IIA) (Anticoagulant protein C
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14; Conservative
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Da; Chordata;
ia; Rodentia;
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Pred. No. 0.00
5; Mismatches
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Pfam; pF00Uvu,

Pfam; pF00594; gla; 1.

Pfam; pF00089; trypsin; 1.

DR Pfam; pF000089; trypsin; 1.

DR PINTS; PR000722; CIYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00001; GEF_Like; 1.

DR SMART; SM00006; GLA: 1.

DR SMART; SM00006; GLA: 1.

DR SMART; SM00006; GLA: 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00118; EGF_C: 2.

DR PROSITE; PS00114; EGF_C: 2.

DR PROSITE; PS00114; TRYPSIN_DOM; 1.

DR PROSITE; PS00113; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_SRR; 1.

DR PROSITE; PS00135; TRYPSIN_SRR; 1.

DR PROSITE; PS00135; TRYPSIN_SRR; 1.

DR PROSITE; PS00135; TRYPSIN_SRR; 1.

DR PROSITE; PS00136; TRYPSIN_SRR; 1.

DR PROSITE; PS00137; TRYPSIN_SRR; 1.

DR PROSITE; PS00138; TRYPSIN_SRR; 1.

BY SIMILARITY

BY SIMILARITY

PROFIEN C LIGHT CHAIN (BY SIMILARITY).

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"TRY SIMILARITY.

"TRY CHAIN (BY SIMILARITY).

"TRY SIMILARITY).
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DOMAIN
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InterPro;
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MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT
SITE IS NECESSARY FOR THE RECOGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
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$24312; $24312.
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en the Swiss Institute of Bioinformatics and the El
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FR001314; Chymotrypsin.
FR000561; EGF-like.
FPR001881; EGF_Ca.
FR002383; GLA_blood.
FR000254; Trypsin.
FR000294; VitK_dep_GLA.
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196
461
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47
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Trypsin.
VitK_dep_GLA.
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                                                                            (BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC

(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC
(BY SIMILARITY).
                                 GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
                                                      GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
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                                                                                                                          GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
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                                            MATRIX.

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR.

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR.

C -!- DEVELOPMENTAL STAGE: LOW LEVELS IN UNFERTILIZED EGGS AND EARLY CLEAVAGE, THEN RAPIDLY INCREASES IN ABUNDANCE BETW.

MORULA AND MESENCHYME BLASTULA STAGES TO MAXIMAL LEVELS?

THROUGH SUBSEQUENT STAGES.

-!- MISCELLANEOUS: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.

-!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.

-!- SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN TO CONTAINS 1 CUB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                  embryo.";
Dev. Biol. 157:526-538(1993).
--- FUNCTION: FORM THE APICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PBP3_STRPU STANDARD; PRT; 570 AA P49013; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update. Fibropellin C precursor (Epidermal growth f. (EGF III) (Fibropellin III).
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_STRPU
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CARBOHYD
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ACT_SITE
ACT_SITE
                   This
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MEDLINE-93273088; PubMed-8500658;

Bisgrove B.W., Raff R.A.;

"The SpEGF III gene encodes a mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                    containing
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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12; Conservative
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the apical lamina of the sea urchin
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growth factor-related
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PRINTS; PR00010; Eu.

R ProDom; PD016055; Avidin; _

SMART; SM00042; CUB; 1.

PR SMART; SM000179; EGF_CA; 7.

PR SMART; SM00001; EGF_Like; 1.

PR PS00010; ASX_HDROXYL; 8.

PS00010; ASX_HDROXYL; 8.

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PE; PS00577; AVIDIN; 1.
PE; PS01180; CUB; 1.
PS; PS01186; EGF_2; 7.
PS; PS01187; EGF_CA; 6.
PS; EGF_like domain; Repeating the service of the servic
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PF00431; CUB; 1.
PF00008; EGF; 8.
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IPR000742;
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IPR000088; Avidin.
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       ĀΑ;
  Avidin.
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EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
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       MW.;
AVIDIN-LIKE.

BY SIMILARITY.
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EGF-LIKE
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     GLCNAC. . GLCNAC. . GLCNAC. . GLCNAC. . GLCNAC. .
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       CRC64;
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                                                                                                                                                                                                                                                  exudative vasculopathy are associated with mutations in the crumb homologue 1 (CRB1) gene.";

L Am. J. Hum. Genet. 69:198-203(2001).

Am. J. Hum. Genet. 109:198-203(2001).

C -!- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTION IN NEURONA DEVELOPMENT OF THE RETINA.

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR (Potential).

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR (Potential).

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR (Potential).

C -!- SUBCELLULAR LOCATION: EXTRACELLULAR PRESSION IN RETINA, ALSO EXPRESSED IN BRAIN AND FETAL BRAIN.

C -!- TISSUE SPECIFICITY: PREFERENTIAL BRAIN.

C -!- DISEASE: DEPECTS IN CRB1 ARE THE CAUSE OF RETINITIS PIGMENTOS C CHARACTERIZED BY NIGHT BLINDNESS FROM EARLY CHILDOOD AND PROGRESSIVE VISUAL FIELD LOSS. THERE IS GENERAL LOSS OF RETIN PROGRESSIVE VISUAL FIELD LOSS. THERE IS GENERAL LOSS OF RETINA AND PATIENTS EXPERIE
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16-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21303018; PubMed=11389483;
den Hollander A.I., Heckenlively Jr., van den Born L.I.,
de Kok Y.J.M., van der Velde-Visser S.D., Kellner U., Jurklies B.,
van Schooneveld M.J., Blankenagel A., Rohrschneider K., Wissinger
Cruysberg J.R.M., Deutman A.F., Brunner H.G., Apfelstedt-Sylla E.,
                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99438399; PubMed=10508521; der Noble 18.1., ten Brink U.B., de Kok Y.J.M., var den Hollander A.I., ten Brink U.B., van de Pol D.J.R., van den Born L.I., van Driel M.A., van de Pol D.J.R., Bhattacharya S.S., Kellner U., Hoyng C.B., Westerveld Brunner H.G., Bleeker Wagemakers E.M., Deutman A.F., Heckenlively J.R., Cremers F.P.M., Bergen A.B.B., "Mutations in a human homologue of drosophila crumbs o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pigmentosa (RP12).";
Nat. Genet. 23:217-221(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANTS Y-948; T-1041 AND P-1071.
TISSUE=Retina, and Fetal brain;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoyng C.B., Cremers F.P.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT LCA
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                                                                                                                                        amaurosis (LCA).
SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
DATABASE: NAME-Mutations of the CRB1 gene;
NOTE-Retina International's Scientific Newsletter;
                                           ween the swiss institute. The European Bioinformatics Institute. The institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Н
                                                                                                                                                                                                                          SEVERE VISUAL IMPAIRMENT DISEASE: Defects in CRB1
                                                                                                                          WWW="http://www.retina-international.com/sci-news/crb1mut.htm".
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13; Conser
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Pred. No. 0.00
5; Mismatches
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EMBL; HSSP; MIM; (

; AF154671; AAF01361.1; ; P08709; 1BF9. 604210; -. 600105; -.

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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR0007481; EGF_Ca.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_II.
InterPro; IPR001791; Laminin_G.
Pfam; PF00008; EGF; 16.
Pfam; PF00008; EGF_1AMININ.
PRINTS; PR00010; EGFELAMININ.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00079; EGF_CA; 8.
SMART; SM00079; EGF_1Ke; 8.
SMART; SM000282; LamG; 3.
PROSITE; PS00110; ASX_HYDROXYL; 10.
PROSITE; PS001186; EGF_2; 11.
PROSITE; PS00125; LAMG, G_DOMAIN; 3.
EGF-11ke domain; Glycoprotein; Repea Retinitis plymentosa; Vision.
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POTENTIAL.

CCRUMES PROTEIN HOMOLOG 1.

EGF-LIKE 2.

EGF-LIKE 3, CALCIUM-BINDING (PREF-LIKE 4, CALCIUM-BINDING (PREF-LIKE 5, CALCIUM-BINDING (PREF-LIKE 6, CALCIUM-BINDING (PREF-LIKE 7, CALCIUM-BINDING (PREF-LIKE 1, C
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Dodson K.A., Doup L.E., Downes M., Dugan-Rocha S., Dlukov B.C., Dunn P.,
RA Chill K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Menklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Munt S.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Mang Z.-Y., Wassarman D.A., Walshoon M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Welson M., Strong R., Sun E.,
RA Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang S.H., Wang F.N., Ehong W., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Wang S., Pan S., Pan S., Pan S., Pan S., Dan S., Shao Q., Zheng L.,
RA Gibbs R.A., Wayers E.W., Rubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.";
              CURT. Biol. 8:622-632(1998).
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
                                                                              "Roles of Armadillo, system development."
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Neural-cadherin precursor (Cadherin-N protein)
                                                                                                                                        MEDLINE=98298928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Axon patterning requires DN-cadherin, a novel neuronal adhesion receptor, in the Drosophila embryonic CNS.";
Neuron 19:77-89(1997).
                                                                                                                                                            INTERACTION WITH
                                                                                                                      Loureiro J., Peifer M.;
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MEDLINE=97388431; PubMed=9247265;
Iwai Y., Usui T., Hirano S., Stew
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Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
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Transmembrane; Calcium-binding; Repeat;

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or send an email to
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SUBCELLULAR LOCATION: Type I membrane protein (Potential).

TISSUE SPECIFICITY: IN THE EMBRYO, THE PROTEIN FIRST APPEARS IN THE MESODERM AT STAGE 9 AND IS PRESENT IN THE MYOBLASTS AND MUSC FIBERS BY STAGE 12 AND STAGE 14, RESPECTIVELY. AT STAGE 12 THE PROTEIN IS ALSO LOCATED IN THE AXONS OF THE ENTIRE CNS, BUT NOT THE GLIAL CELLS. IN THERD INSTAR LARVAE PROTEIN IS EXPRESSED IN THE CNS NEUROPILE, PHOTORECEPTOR AXONS AND PRECURSORS OF ADULT
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AE003656;
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                                                                                                                                                           Pro; IPR001791; Laminin_G. PF00028; cadherin; 14.
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an email to license@isb-sib.ch).
                                                                     PR00205; CADHERIN.
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AAF53635.1; -.
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-! SUBCELULIAR IOCATION: Type I membrane protein.
-! DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE AND ENTERIOR PREDOMINANTLY IN THE DEVELOPING NEURAL PLATE AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING BRAIN AND HEAD REGIONS.
-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

MCBI_TaxID=7955;
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      This
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"A zebrafish homologue of the Drosophila neurogenic gene its pattern of transcription during early embryogenesis."
Mech. Dev. 43:87-100(1993).
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Pfam; PF00066; notch; 3.
PFINTS; PR000610; EGFBLOOD.
PRINTS; PR00119; EGFEA; 19.
SMART; SM002148; ANK; 5.
SMART; SM00001; EGF_like; 16.
SMART; SM00001; EGF_like; 16.
SMART; SM00001; EGF_Like; 17.
SMART; PS50098; ANK_REPEAT; 4.
PROSITE; PS500297; ANK_REP_REGION; 1
PROSITE; PS00110; ASX_HYDROXYL; 23.
PROSITE; PS001186; EGF_2; 28.
PROSITE; PS01186; EGF_2; 28.
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MEDIJINE-86176794; PubMed-3754331;

Tripodi M., Citarella F., Guida S., Galeffi P.,

Cortese R.;

"CDNA sequence coding for human coagulation fact
Nucleic Acids Res. 14:3146-3146(1986).

[3]

SEQUENCE OF 14-615 FROM N.A.

MEDIJINE-86033830; PubMed-3877053;

CCOl D.E., Edgell C.-J.S., Louie G.V., Zoller M.,

MCGillivray R.T.A.;

MCGillivray R.T.A.;

Prediction of the primary structure of factor XI:

structure of beta-factor XIIa.";

J. Biol. Chem. 260:13666-13676(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-88007593; PubMed-2888762;
COOl D.E., McGillivray R.T.A.;
"Characterization of the human bloc"
"htron/exon gene organization and
                                                                       structure of beta-factor XIIa.";
J. Biol. Chem. 260:13666-13676(1985)
[4]
SEQUENCE OF 146-615 FROM N.A.
MEDLINE=86216049; PubMed=3011063;
Que B.G., Davie E.W.;
"Characterization of a cDNA coding for the second se
factor).";
Biochemistry
[5]
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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(Rel. 12, Last sequence up
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factor XII precursor (EC 3
                            25:1525-1528(1986)
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Saito H.;
"Coagulation
factor XIIa r
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"O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C.";

J. Biol. Chem. 267:5102-5107(1992).

-I- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATI THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE GENERATION OF BRADYKININ AND ANGIOTENSIN.

-I- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor XII to form factor XIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                              the amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
[7]
           between the Swiss Institute of Bioinformat, the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                    This
                                                                                                        -II- PTM: O- AND N-GLYCOSYLATED.
-II- DISEASE: DEFECTS IN F12 DO NOT CAUSE ANY CLINICAL SYMPTOMS. THE SOLE EFFECT IS THAT WHOLE-BLOOD CLOTTING TIME IS PROLONGED.
-II- MISCELLANEOUS: FACTOR XII, PREKALLIKREIN, AND HMW KININOGEN FOR COMPLEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BE FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XII FI TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR XIIA ACTIVATES FACTOR XI TO FACTOR XIA.
-II- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-II- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
-II- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE II DOMAIN.
-II- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
-II- SIMILARITY: TOMAIN 1 KRINGLE DOMAIN.
-II- SIMILARITY: TOMAIN 1 KRINGLE DOMAIN.
-II- SIMILARITY: TOMAIN 1 KRINGLE DOMAIN.
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"The novel acceptor splice site mutation :
XII gene causes a truncated transcript in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujikawa K., McMullen B.A.;
"Amino acid sequence of human beta-factor
J. Biol. Chem. 258:10924-10933(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hovinga J.K.,
Laemmle B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94325559; PubMed-8049433;
Hovinga J.K., Schaller J., Stricker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT WASHINGTON DC.
MEDLINE=90046788; PubMed=2510163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Amino acid sequence of the heavy (activated Hageman factor).";
J. Biol. Chem. 260:5328-5341(1985)
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                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYDRATE-LINKAGE SITE THR-109.
MEDLINE=92184750; PubMed=1544894;
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likrein cleavage site.";
od 84:1173-1181(1994).
                                                                        SWISS-PROT entry is copeen the Swiss Institute
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PubMed=6604055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XII (Hageman factor) Washington D.C.: inactive from Cys-571-->Ser substitution."; c1. U.S.A. 86:8319-8322(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A
                                                                      copyright. It is produced tute of Bioinformatics and
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PRINTS; PR00722; CHYMOTRY
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PRINTS; PR00018; KRINGLE.
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M11723; AAA51986.1;
M17466; AAB59490.1;
M17464; AAB59490.1;
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M17465; AAB59490.1;
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SM00181; EGF; 2.
SM00058; FN1; 1.
SM00059; FN2; 1.
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3; PS00023; FIBRONECTIN_2; 1

2; PS00021; KRINGLE_1; 1.

3; PS50070; KRINGLE_1; 1.

3; PS50240; TRYPSIN_DOM: 1.

3; PS00134; TRYPSIN_HIS; 1.

3; PS00135; TRYPSIN_HER; 1.
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); IPR000562; FN_Type_II.
); IPR000001; Kringle.*
); IPR001254; Trypsin.
); IPR0000083; fibronectin_ty
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PS00022; EGF_1; 2.
PS01186; EGF_2; 1.
PS011253; FIBRONECTIN_1;
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BETA-FACTOR XIIA LIGHT CHAIN.
BETA-FACTOR XIIA PART 1.
BETA-FACTOR XIIA PART 2.
FIBRONECTIN TYPE-II.
EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
KRINGLE.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Walson C., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Ghorey J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., M.,
RA Ghodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gloden S., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., IDegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., IDegwam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Houth S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman
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Q27591; Q9VIG7;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 118:845-858(1993).
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MEDLINE=94357079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

-I. FUNCTION: PROBABLY PLAYS A ROLE IN CELL ADHESION.
-I. SUBURIT: HETERODIMER OF AN AND A BETA CHAIN FAMILY.
-I. SUBURIT: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
-I. SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
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PROSITE; PS01286; EGF_2; UNKNOWN_4.
PROSITE; PS00243; INTEGRIN_BETA; 1.
Integrin PS50234; VWFA; 1.
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  518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom;
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QPFSDKSTSELVCSNHGDC
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SM00187;
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                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics Institute. The profit institutions as long
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VWA;
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-DCGTCLCDPGYTGPFCE
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                                                                                                                                                                                                                                                                                                                                                                                                             INTEGRIN BETA-NU EXTRACELLULAR (POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       VWFA.
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RESULT 40 NTC1_HUMAN

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SEQUENCE FROM N.A.

MEDLINE=91347367; PubMed=1831692;

A Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,

A Smith S.D., Sklar J.;

T "TAN-1, the human homolog of the Drosophila notch gene, is brochromosomal translocations in T lymphoblastic neoplasms.";

Cell 66:649-661(1991).

C -!- FUNCTION: MAY BE IMPORTANT FOR NORMAL LYMPHOCYTE FUNCTION.

ALTERED FORM, MAY CONTRIBUTE TO TRANSFORMATION OR PROGRESS.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SIBLIN STEM AND LUMG. ALSO RRESENT IN MOST ABULT TISSUES WH

IS FOUND MAINLY IN LYMPHOID TISSUES MOST ABULT TISSUES WH

C -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

C -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

C -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                     pfam; pF00008; EGF; 36.

pfam; pF00006; notch; 3.

pfam; pF00066; notch; 3.

SMART; SM00248; ANK; 52.

SMART; SM00001; EGF_CA; 22.

SMART; SM00001; EGF_Like; 13.

SMART; SM00001; EGF_Like; 13.

SMART; SM00001; EGF_Like; 13.

SMART; SM00001; ANK_REPEAT; 4.

PROSITE; pS0008; ANK_REP_REGION; 1.

PROSITE; PS00010; ASK_HYDROXYL; 20.

PROSITE; PS00102; EGF_L; 34.

PROSITE; PS01186; EGF_2; 26.

PROSITE; PS01187; EGF_CA; 18.

Differentiation; Neurogenesis; Repeat; AN

Transmembrane; Signal; Glycoprotein.
                                                                                Transmembrane;
SIGNAL 19
CHAIN 19
DOMAIN 19
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01-NOV-1995
01-NOV-1995
16-OCT-2001
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InterPro;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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LIGNMENTS

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A; Description: binds with low affinity to oligosaccarides like heparan sulfate and siment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr C; Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homolog; C; Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammat F;1-51/Domain: signal sequence #status predicted <SIG>F;42-168/Domain: C-type lectin homology <LCH>F;52-332/Product: L-selectin #status predicted <MAT>F;52-330/Domain: extracellular #status predicted <MAT>F;52-300/Domain: EGF homology <EGF>F;173-204/Domain: complement factor H repeat homology #status atypical <FH1>F;272-323/Domain: complement factor H repeat homology #status atypical <FH2>F;301-318/Domain: intracellular #status predicted <INT>F;319-323/Domain: intracellular #status predicted <INT>F;319-323/Domain: intracellular #status predicted <INT>F;319-323/Domain: intracellular #status predicted <INT>F;319-323/Domain: intracellular #status predicted <INT>F;319-329/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Cross-references: GDB:120157; GDB:118834; OMIM:153240
A;Map position: 1922-1923
A;Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 303/2
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: this translation is not annotated in GenBank entry HSLEU8, release 111.0 C; Comment: For an alternative splice form, see PIR: A34015. C; Genetics:
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Nature 342, 78-82, 1989
A;Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor.
A;Reference number: S06798; MUID:90044046
A;Accession: S09702
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A; Residues: 1-323 <CAM>
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-selectin precursor, short splice form - human
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Best Local S
Matches 32
173
                                   1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 205
                                                                                                                                Similarity 97.
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                                                                                                                                                             95.3%;
97.0%;
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                                                                                                                             Score 205; DB 1
Pred. No. 7e-16;
1; Mismatches
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A;Cross-references: GB:M32414; NID:g187259; PIDN:AAB60700.1; PID:g386860 R;Camerini, D.; James, S.P.; Stamenkovic, I.; Seed, B. Nature 342, 78-82, 1989 A;Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing A;Reference number: S06798; MUID:90044046 A;Accession: S06798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: 155333; S06798; JL0104; A34015; A33912
R;Ord, D.C.; Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertini, O.; Griffin, J.; Tedder, J. Biol. Chem. 265, 7760-7767, 1990
A;Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1, A;Reference number: 155333; MUID:90243637
A;Accession: 155333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JC5377
L-selectin precursor - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 02-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 21-Jan-2000
C;Accession: JC5377; PC4315
C;Accession: JC5377; PC4315
A; Molecule type: mRNA
A; Residues: 1-230,'N',232,'N',234-254,'E',256-385
                                                                                                                                                                                              A;Cross-references: EMBL:X17519; NID:g34344; PIDN:CAB43536.1; PID:g4902829 A;Note: this translation is not annotated in GenBank entry H5LEU8, release 111.0 R;Tedder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Disteche, J. Exp. Med. 170, 123-133, 1989
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                                                                                                                                     oteins.
                                                                                                                                                                 A; Title: Isolation and chromosomal localization of
                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-225, 'S', 227-385 < CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 14-385 < ORD>
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F;39-157/Domain: calcium-binding *status predicted <CAB>
F;160-191/Domain: EGF homology <EGF>
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C; Comment: This receptor is
                                                                     A; Accession:
                                                                                                  A; Reference number: JL0104; MUID: 89310350
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A; Residues: 37-43;142-148 <TSU2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ral lymph node homing receptor Leu-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A34015
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A;Accession: PC4315
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A; Residues: 1-372 <TSU1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sites of inflammation
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                                                                     JL0104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 205; DB 2; Pred. No. 7.9e-16;
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cell adhesion molecule-1 (LECAM-1, LAM-1); leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                              cDNAs encoding
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A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-370 <BOS> A; Residues: 1-370 <BOS> A; Residues: 1-370 <BOS> A; Residues: 1-370 <BOS> A; Residues: Data A; Rishimoto, T.K.; Jutila, M.A. Bur. J. Immunol. 22, 469-476, 1992 Bur. J. Immunol. 22, 469-476, 1992 A; Title: Characterization of the bovine peripheral lymph node homing receptor: A; Reference number: A46531; MUID: 92164727 A; Accession: A46531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)
C;Species: Bos primigenius taurus (cattle)
C;Datte: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;369-385/Domain: intracellular #status predicted <INI'>
F;73,117,190,245,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;377,380/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: binds with low affinity to oligosaccarides like heparan sulfate and siment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr C; Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology C; Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammat
                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S22124
                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data
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A; Residues: 14-49,'Y',51-190,'H',192-205,'L',207-226,'F',228-385
A; Cross-references: GB:X16070; NID:g38092; PIDN:CAA34203.1; PID:g
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A;Note: the translated sequence in GenBank entry HSLYAM1, release 111.0, differs from R;Bowen, B.R.; Mguyen, T.; Lasky, L.A.
J. Cell Biol. 109, 421-427, 1989
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A;Map position: 1q22-1q23
A;Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2
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Pred. No. 8.1e-16;
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PID:g38093
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L-selectin precursor - mouse
N;Alternate names: lymph node homing receptor MEL-14; lymphocyte surface antigen
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A32375; A35102; A40107; A60906
R;Lasky, L.A.; Singer, M.S.; Yednock, T.A.; Dowbenko, D.; Fennie, C.; Rodriguez,
Cell 56, 1045-1055, 1999
A;Title: Cloning of a lymphocyte homing receptor reveals a lectin domain.
A;Reference number: A32375; MUID:89168433
A;Accession: A32375
A;Molecule type: mRNA
A;Residues: 1-372 <LAS>
A;Cross-references: GB:M25324; NID:g198803; PIDN:AAA39431.1; PID:g198804
R;Siegelman, M.H.; Cheng, I.C.; Weissman, I.L.; Wakeland, E.K.
Cell 61, 611-622, 1990
A;Title: The mouse lymph node homing receptor is identical with the lymphocyte c.
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
C;Accession: JC4892
R;Qlan, J; Huang, X; Marks, R.M.
Blochem. Blophys. Res. Commun. 225, 406-412, 1996
A;Title: Cloning of the cDNA for rabbit L-selectin and expression of recombin A;Reference number: JC4892; MUID:96354800
A;Reference number: JC4892; MUID:96354800
A;Reference number: JC4892; MUID:96354800
A;Residues: J-376 cOIA>
A;Residues: 1-376 cOIA>
A;Cross-references: GB:U26535; NID:g847787; PIDN:AAA67896.1; PID:g847788
C;Comment: This protein involved in leukocyte-endothelial adhesion; it medial C;Superfamily: L-selectin; C-type lectin homology; complement factor H repeat F;29-155,Domain: Signal sequence #status predicted <SIG>
F;39-376/Product: L-selectin #status predicted <MAT>
F:197-254/Nomain: EGF homology <EGF>
F:197-254/Nomain: EGF homology <EGFP
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 39-79,'Q',81-151,'K' <WAL>
A;Residues: 39-79,'Q',81-151,'K' <WAL>
A;Rote: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:85686, NCBIP:85687)
C;Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
F;29-155/Domain: C-type lectin homology <LCH>
F;160-191/Domain: EGF homology <EGF>
F;160-191/Domain: complement factor H repeat homology <FH1>
F;259-316/Domain: complement factor H repeat homology <FH2>
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27; Conser
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81.8%;
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Pred. No. 2.9e
6; Mismatches
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Pred. No. 3.9e-13;
""smatches 2;
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N;Alternate Fammes: leucocyte cell adhesion molecule 1 (LECAM-1)
C;Species; Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C;Accession: S33936
R;Watanabe, T.; Song, Y.; Hirayama, Y.; Tamatani, T.; Kuida, K.; Miyasaka, M.
Biochim. Biophys. Acta 1131, 321-324, 1992
A;Title: Sequence and expression of a rat cDNA for LECAM-1.
A;Reference number: S23936; MUID:92329548
A;Retersion: S23936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-372 <WAT>
A;Residues: 1-372 <WAT>
A;Residues: 1-372 <WAT>
A;Cross-references: GB:D10831; NID:9220801; PIDN:BAA01613.1; PID:9220802
C;Superfamily: L-selectin; C-type lectin homology; complement factor H repeat
C;Keywords: transmembrane protein
F;29-155/Domain: Complement factor H repeat homology <FH1>
F;150-9316/Domain: complement factor H repeat homology <FH1>
F;259-316/Domain: complement factor H repeat homology <FH2>
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F;364/Binding site: phosphate (Ser) (covalent) #status predicted
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A; Residues: 1-372 <SIE2>
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A;Accession: A35102
A;Status: not compared with conceptual tr
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81.8%;
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Pred. No. 8
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F:12-138/Domain: C-type lectin homology <LCH>
F:22-610/Product: endothelial leukocyte adhesion molecule 1 #status F:143-174/Domain: EGF homology <EGF>
F:180-237/Domain: EGF homology <EGF>
F:242-299/Domain: complement factor H repeat homology <FH02>
F:242-299/Domain: complement factor H repeat homology <FH03>
F:304-362/Domain: complement factor H repeat homology <FH03>
F:367-425/Domain: complement factor H repeat homology <FH05>
F:430-488/Domain: complement factor H repeat homology <FH05>
F:430-488/Domain: complement factor H repeat homology <FH05>
F:439-547/Domain: complement factor H repeat homology <FH06>
F:439-547/Domain: complement factor H repeat homology <FH06>
F:439-547/Domain: complement factor H repeat homology <FH06>
F:459-578/Domain: transmembrane #status predicted <TMM>
RESULT
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C;Superfamily: unassigned EGF-related p
C;Keywords: duplication: 91ycoprotein;
F;1-21/Domain: signal sequence #status
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A; Residues: 1-467, 'Y', 469-610
A; Cross-references: GB:M24736;
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C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: A38615; A35046; A35606
R;Collins, T.; Williams, A.; Johnston, G.I.; Kim, J.; Eddy, R.; Shows, T.; G. Biol. Chem. 266, 2466-2473, 1991
A;Title: Structure and chromosomal location of the gene for endothelial-leuk A;Reference number: A38615; MUID:91115870
A;Accession: A38615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Endothelial leukocyte adhesion molecule A; Reference number: A32606; MUID:89162047
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A; Residues: 1-610 <HE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement; Keywords: duplication; glycoprotein; tandem repeat; transmembrane protein; 1-21/Domain: signal sequence #status predicted <SIG>
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          9
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                                                                                    CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
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78.8%;
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Pred. No. 3e-07;
4; Mismatches
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No. 1.1e-10;
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B.
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       F;1-21/Domain: signal sequence F;12-138/Domain: C-type lectin
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F;588-611/Domain:
F;612-646/Domain:
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A; Residues: 1-646 <ST
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57.6%;
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A; Note: sequence extracted from NCBI backbone (NCBIP:109470)
A; Note: the sequence in GenBank entry MUSESELEC, release 117.0,
A; Note: it is uncertain whether the initiator is met-1 or the At
C; Superfamily: unassigned EGF-related proteins; C-type lectin ho
                                                                                                                                                                                          A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
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A; Residues: 1-612 <BEC>
A; Cross-references: GB:M80778; NID:g193014;
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A;Accession: S23174
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A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000
C;Accession: S23174; B42755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JN04/3
R;Strubel, N.A.; Nguyen, M.; Kansas, G.S.; Transcohom Biophys. Res. Commun. 192, 338-344,
                                 C; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 'MKATAGV', 1-389, 391-612 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:42-646/Product: P-selectin #status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology
F:262-319/Domain: complement factor H repeat homology
F:362-319/Domain: complement factor H repeat homology
F:324-311/Domain: complement factor H repeat homology
F:386-443/Domain: complement factor H repeat homology
F:458-515/Domain: complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L12041; NID:g304246; PIDN:AAA30743.1; PID:g304247 C;Comment: This protein is a Ca2+ dependent receptor for myeloid cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: granule membrane protein-140 C;Species: Bos primigenius taurus (cattle) C;Date: 30-Sep-193 #sequence_revision 30-Sep-1 C;Accession: JN0473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Isolation and characterization of a bovine cDNA encoding a functional homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 CQDMSCSKQGECIETIGNYTCSCYPGFYGPECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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complement factor H repeat homology <FH2>
complement factor H repeat homology <FH3>
complement factor H repeat homology <FH3>
complement factor H repeat homology <FH4>
complement factor H repeat homology <FH5>
complement factor H repeat homology <FH6>
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intracellular #status
                                                                                                                                                                                                                                                                                                                                                                                        A42755; MUID:92340571
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#status predicted <SIG
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14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAA37547.1; PID:g193015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; L. o.9e-07; 8;
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                                                                                                                              (PIDN:AAA37577.1; PID
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RESULT 11
JC5092
E-selectin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 19-May-2000
C:Accession: JC5092
R:Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Bach, F Gene 176, 67-72, 1996
A:Title: The intron-exon structure of the porcine E-selectin-encoding gene. A; Title: The intron-exon structure of the porcine E-selectin-encoding gene. A; Contents: endothelial cells
A; Contents: endothelial cells
A; Accession: JC5092
A; MUID:97075911
A; Contents: endothelial cells
C:Genetics: 1-482 <WIN>
A; Residues: 1-482 <WIN>
A; Residues: 1-482 <WIN>
A; Cross-references: GB:U37521; NID:g1052974; PIDN:AAC48680.1; PID:g1052975
C:Comment: This protein is a member of the selectin family of adhesion mojecul
C:Genetics:
A; Introns: 13/1; 1421; 178/1; 237/1; 300/1; 363/1; 422/1; 459/1; 466/1.
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology: compl
F:13-139/Domain: complement factor H repeat homology <FH1>
F:240-998/Domain: complement factor H repeat homology <FH1>
F:240-998/Domain: complement factor H repeat homology <FH3>
F:303-361/Domain: complement factor H repeat homology <FH3>
F:303-361/D
P-selectin precursor - human
N; Alternate names: CD62 antigen; granule membrane protein 140
C; Species: Homo sapiens (man)
C; Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 19-May-2000
C; Accession: A30359
R; Jöhnston, G.I.; Cook, R.G.; McEver, R.P.
Cell 56, 1033-1044, 1989
A; Title: Cloning of GMP-140, a granule membrane protein of platelets and endother as a sequence number: A30359; MUID: 89168432
A; Reference number: A30359; MUID: 89168432
A; Accession: A30359
A; Molecule type: mRNA
A; Residues: 1-830 < JOH>
A; Cross-references: GB: M25322
A; Note: parts of this sequence, including the amino end of the mature protein, value of the sequence of t
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F;143-174/Domain: EGF homology <EGF>
F;143-174/Domain: complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;305-363/Domain: complement factor H repeat homology <FH3>
F;368-426/Domain: complement factor H repeat homology <FH5>
F;468-426/Domain: complement factor H repeat homology <FH5>
F;464-548/Domain: complement factor H repeat homology <FH5>
F;494-548/Domain: complement factor H repeat homology <FH6>
F;25,391,528/Binding site: carbohydrate (Asn) (covalent) #st
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5; Mismatche
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Pred. No. 9.1e-07;
4; Mismatches 9;
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3.5e-07;
9;
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A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-723, E',725-768 <SAN>
A; Residues: 1-723, E',725-768 <SAN>
A; Cross references: GB:M72332; NID:g193565; PIDN:AAA37712.1; PID:g193566
A; Mote: sequence extracted from NCBI backbone (NCBIP:109900)
C; Superfamily: unassigned EGF-related proteins; complement factor H repeat horizontal repeat notes in the sequence status predicted <SIG>F:1-41/Domain: signal sequence status predicted <MAT>F:163-194/Domain: EGF homology <EGF>F:262-319/Domain: complement factor H repeat homology <FH02>F:262-319/Domain: complement factor H repeat homology <FH02>F:324-381/Domain: complement factor H repeat homology <FH05>F:486-443/Domain: complement factor H repeat homology <FH05>F:510-567/Domain: complement factor H repeat homology <FH06>F:510-567/Domain: complement factor H repeat homology <FH06>F:510-567/Domain: complement factor H repeat homology <FH07>F:642-699/Domain: complement factor H repeat homology <FH06>F:510-567/Domain: complement factor H repeat homology <FH06>F:710-733/Domain: complement factor H repea
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F;163-194/Domain: EGF homology <EGF>
F;200-257/Domain: complement factor H repeat homology <FH0:
F;202-319/Domain: complement factor H repeat homology <FH0:
F;324-381/Domain: complement factor H repeat homology <FH0:
F;386-443/Domain: complement factor H repeat homology <FH0:
F;386-443/Domain: complement factor H repeat homology <FH0:
F;448-505/Domain: complement factor H repeat homology <FH0:
F;510-567/Domain: complement factor H repeat homology <FH0:
F;572-629/Domain: complement factor H repeat homology <FH0:
F;642-699/Domain: complement factor H repeat homology <FH0:
F;704-761/Domain: complement factor H repeat homology <FH0:
F;772-7765/Domain: complement factor H repeat homology <FH0:
F;770-7765/Domain: complement factor H repeat homology <FH0:
F;770-7765/
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A;Map position: 1q22-1q25
C;Superfamily: unassigned EGF-related proteins; complement factor H repeat homology;
C;Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; surface an F;1-41/Domain: signal sequence #status predicted <SIG>
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A; Residues: 1-768 <WEL>
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Best Local
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Pred. No. 1.4e-06;
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t homology <FH06>
t homology <FH07>
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t homology <FH08>
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dicted <TMN>
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homology <FH02>
homology <FH03>
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F;45,54,107,212,347,398,456,467,603,654,661,679/Binding site: carbohydrate (Asn) (covale

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A;Introns: 13/1; 143/1; 179/1; 241/1; 303/1; 366/1; 429/1; 488/1; C;Superfamily: unassigned EGF-related proteins; C-type lectin homo: C;Keywords: duplication; glycoprotein; tandem repeat F;14-140/Domain: C-type lectin homology <LCH>
F;182-239/Domain: complement factor H repeat homology
                                                                                                                                                                             endothelial leukocyte adhesion molecule 1 - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
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A;Molecule type: mRNA
A;Rosidues: 1-485 <NGU>
A;Rossidues: 1-485 <NGU>
A;Cross-references: GB:L12039; NID:g402913; PIDN:AAA02991.1; PID:g402914
A;Cross-references: GB:L12039; NID:g402913; PIDN:AAA02991.1; PID:g402914
C;Superfamily: unassigned EGF-related proteins; C-type lectin homology; cF;13-139/Domain: C-type lectin homology <LCH>
F;13-139/Domain: C-type lectin homology <LCH>
F;181-237/Domain: complement factor H repeat homology <FH1>
F;242-399/Domain: complement factor H repeat homology <FH2>
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146709
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Nature 365, 267-269, 1993
A;Title: A role for sialyl Lewis-X/A glycoconjugates
A;Reference number: S36772; MUID:93382537
A;Accession: S36772
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36772
E-selectin - bovine
C.Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change
C:Accession: S36772
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                                                                                                                                                                                                                                                                               A; Accession: I46708
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A; Residues: 1-551 <LA
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F;367-421/Domain:
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54.5%;
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4; Mismatches
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Pred. No. 1
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5.6e-06;
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L.7e-06;
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A;Cross-references: EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579 C;Superfamily: coagulation factor XII; ESF homology; fibronectin type I of C;Keywords: hydrolase; serine proteinase F;46-87/Domain: fibronectin type II repeat homology <1F2> F;134-169/Domain: fibronectin type II repeat homology <FB1>
F;177-208/Domain:
F;216-294/Domain:
F;359-597/Domain:
                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-603 <SE
                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1159, 113-121, 1992
A; Title: Primary structure of guinea-pig Hageman
A; Reference number: S28941; MUID:93003367
                                                                                                                                                                                                                                                                                                   C;Accession: S28941
R;Semba, U.; Yamamoto,
                                                                                                                                                                                                                                                                                                                                       coagulation factor XIIa (EC 3.4.21.38)
N,Alternate names: Hageman factor
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb_1994 #sequence_revision
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A;Title: Cloning, sequence comparison and A:Paference number: I53821; MUID:94333817
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                                                                                                                                                                                                                     A; Accession: S28941
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C;Accession: I53821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-768 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:306-364/Domain: complement factor H F;369-427/Domain: complement factor H F;432-486/Domain: complement factor H F;432-485,201,314,321,466/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;580-637/Domain:
F;642-699/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;262-319/Domain:
F;510-567/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L23088; NID:g349552; PIDN:AAA60325.1; PID:g349553 C;Superfamily: unassigned EGF-related proteins; C-type lectin homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: I53821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-selectin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ach, J.A.; Oliver, M.G.;
251-255, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPWSCSGHGECVEIINNHTCNCDVGYYGPOCO
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18; Conserv
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                                   EGF homology <EGF>
                                                                                                                                                           <SEM>
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98 #sequence_revision 29-May-1998 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                                     T.; Kunisada,
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54.5%;
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Pred. No. 8.2e-05;
8; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 116; DB 2
Pred. No. 1e-05;
6; Mismatches
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repeat homology <FH4>
repeat homology <FH5>
                                                                                                                                                                                                                                                                                                                                       03-Aug-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                               Shibuya,
                                                                                                                                                                                                                                                                                                                                                                                                      guinea
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kringle

homology

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F:1025-1056/Domain: EGF homology <EGX3>
F:1924-1956/Domain: ankyrin repeat homology
F:1957-1989/Domain: ankyrin repeat homology
F:1991-2023/Domain: ankyrin repeat homology
F:2024-2056/Domain: ankyrin repeat homology
F:2057-2089/Domain: ankyrin repeat homology
                                                                                                                                                                                                                        F:146-177/Domain: EGF homology <EGX1>
F:184-215/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF2>
F:456-487/Domain: EGF homology <EGX2>
F:757-788/Domain: EGF homology <EGF3>
                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRNA A;Residues: 1-2524 <COF>
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Xotch, the Xenopus homolog of Drosophila A;Reference number: A35844; MUID:90385285 A;Accession: A35844
                                                                                                                                                                                                                                                                                                                                                                                                                                         Xotch protein - African clawed frog C;Specles: Xenopus laevis (African clawed frog) C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F25D7.5
A; Map position: 1
A; Introns: 20/1; 56/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F25D7.5 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Accession: T21339 R:MCMUITAY, A.
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A;Residues: 1-710 <WIL>
A;Cross-references: EMBL:Z78418; PIDN:CAB01698.1; GSPDB:GN00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library
A;Reference number: Z19409
A;Accession: T21339
A;Status: preliminary; translated
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Best Local S
                                      Matches
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Best Local
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                                    Local Similarity
nes 15; Conserv
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   CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
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                                                    43.3%;
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                                   Score 93; DB
Pred. No. 0.01
4; Mismatches
                                    4.
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Pred.
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Pred.
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                                                    93;
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0.0029;
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<AN2>
<AN3>
<AN4>
<AN5>
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                                                  DB 2;
0.013;
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                                    14;
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                                                                  Length 2524;
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                                    Indels
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R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch
A;Reference number: A49175; MUID:93178563
A;Accession: A49175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Accession: T31070
R:Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 19
A:Title: Identification and lo
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A; Residues: 1-3051 <SMI>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          41.9%;
51.6%;
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Motch B protein - mouse (fragment)
N;Alternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision
C;Accession: A49175; PH1570; S32113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146 C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronecti F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1> F;754-793/Domain: fibronectin type II repeat homology <2FI> F;1201-1244/Domain: EGF homology <EGF>
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A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN
A;Cross-references: EMBB:AF000634; NID:g2570350; PID:g2570350; PID:g2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL;Z30423; NID:g458479; PID:g458485
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2664 CNAHGDCVHNTATNNITCVCTDGWTGPQCQV 2694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGHGECVE--IINNHTCNCDVGYYGPQCQL 34
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Lytechinus variegatus (variegated urchin)
-Oct-1999 #sequence_revision 22-Oct-1999 #
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Pred. No. 0
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Pred. No. 0
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0.034;
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0.029;
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coexpressed in a wide variet
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A;Status: preimmin,
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1203 <LAR>
A;Cross-references: EMBI:X68279; NID:9287989; PIDN:CAA48340.1; PID:9287990
A;Cross-references: EMBI:X68279; NID:9287981;
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision between commentation of the neurogenic proteins; ankyrin repeat homology; EGF homology
F;143-174/Domain: EGF homology <EGX1>
F;647-705/Domain: EGF homology <EGX2>
F;712-743/Domain: EGF homology <EGX3>
F;836-867/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                       A;Map position: 19p13.1

C;Function:
A;Description: may be involved in pathogenesis of CADASIL, cau C;Superfamily: unassigned ankyrin repeat proteins; ankyrin rep;Superfamily: unassigned ankyrin repeat protein
C;Superfamily: unassigned ankyrin repeat protein
C;Keywords: tandem repeat; transmembrane protein
F;123-155/Domain: EGF homology <EGX1>
F;162-194/Domain: EGF homology <EGX2>
F;318-349/Domain: EGF homology <EGX3>
F;318-349/Domain: EGF homology <EGX3>
F;473-504/Domain: EGF homology <EGX3>
F;928-959/Domain: EGF homology <EGF3
F;1070-1126/Domain: EGF homology <EGF4
F;1070-1126/Domain: Laminin-type EGF-like homology <LEG>
F;1070-1126/Domain: Laminin-type EGF-like homology <LEG>
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                                                                                                                                                       F;1838-1870/Domain:
F;1871-1903/Domain:
F;1905-1937/Domain:
                                                                                                         F;1938-1970/Domain:
F;1971-2003/Domain:
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A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing A;Reference number: $71825; MUID:97032728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #text_change 20-Sep-1999
C:Accession: S78549; S78525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: notch3
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A; Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 < JOU
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A; Residues: 1-2321 <JOU1>
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A; Accession: S78549
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Matches 14; Conservative
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Local
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ankyrin repeat homology <AN1>
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Library,
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Pred. No. 0.02
6; Mismatches
     Score
Pred.
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homology <AN3>
homology <AN4>
homology <AN5>
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DB 2;
0.035;
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0.021;
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F;1029-1060/Domain: EGF homology <EGFS>
F;1087-1098/Domain: EGF homology <EGFS>
F;1153-1184/Comain: EGF homology <EGFS>
F;1151-1222/Domain: EGF homology <EGFS>
F;1191-1222/Domain: EGF homology <EGSX4>
F;1876-1908/Domain: ankyrin repeat homology <A
F;1909-1941/Domain: ankyrin repeat homology <A
F;1943-1975/Domain: ankyrin repeat homology <A
F;1943-1975/Domain: ankyrin repeat homology <A
F;1943-1975/Domain: ankyrin repeat homology <A
F:27-85/Domain: Gia domain homology <GLA>
F:34-41/Domain: propeptide #status predicted <PRO>
F:42-196,199-461/Product: protein C #status predicted <PRC>
F:42-196/Domain: light chain #status predicted <PCL>
F:91-130/Domain: EGF homology <EG1>
                                                                                                                                                    C; Superfamily: coagulation factor X;
C; Keywords: beta-hydroxyaspartic acid
                                                                                                                                                                                                                         A; Experimental source: lives C; Comment: Protein C is the
                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-461 <TAD>
A;Cross-references: GB:D10445; NID:g220385; PIDN:BAA01235.1; PID:g220386
                                                                                                                                                                                                                                                                                                                                         A; Title: Isolation and characterization of A; Reference number: JX0210; MUID:92316897 A; Accession: JX0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JX0210
                                                                                                                           F;1-33/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                              R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, J. Biochem. 111, 491-495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein C (activated) (EC 3.4.21.69) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI back
C;Superfamily: unassigned ankyrin repeat
F;264-295/Domain: EGF homology <EGX1>
F;799-830/Domain: EGF homology <EGF1>
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A;Title: Notch2: a second mammalian Notch
A;Reference number: A49128; MUID:93202015
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C; Date: 21-Jan-1994 #sequence_revision
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A; Residues: 1-2471 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSPSSCFNGGTCVDGVNSFSCLCRPGYTGAHCQ
                                                                                                                                               ly: coagulation factor X; EGF homology; Gla domain homology; beta-hydroxyaspartic acid; blood coagulation; calcium bindir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.48;
                                                                                                                                                                                                                     zymogen of the vitamin K-dependent serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-Nov-1994 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins;
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<AN3>
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<AN5>
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                                                                                                                                                                                                                                                                                                                                                                                      mouse protein C cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
0.037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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A40136
A40136
A40136
Ribropellin Ia - sea urchin (Strongylocentrotus purpuratus)
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: epidermal growth factor homolog precursor
N;Contains: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: A40136; B40136; C40136; A29316; A43131
R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu A;Reference number: A40136; MUID:90112459
A;Accession: A40136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114 <DEL>
A;Cross-references: GB:X17530; NID:g10225; PID:g667061
A;Accession: B40136
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26

C-Delta-1 - chicken
C-Delta-1 - chicken
C-Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50719
R;Henrique, D; Adam, J; Myat, A; Chitnis, A; Lewis, J; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A;Henrique, D; Adam, J; Myat, A; Chitnis, A; Lewis, J; Ish-Horowicz, D.
A;Title: Expression of a Delta homologue in prospective neurons in the chick.
A;Reference number: I50719; MUID:95319507
A;Reference number: I50719; MUID:95319507
A;Reference number: 150719
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-728 <HEN>
A;Cross-references: EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g882412
C;Superfamily: unassigned EGF-related proteins; EGF homology
F;299-332/Domain: EGF homology <EGF1>
F;39-332/Domain: EGF homology <EGF1>
F;416-447/Domain: EGF homology <EGF1>
F;454-485/Domain: EGF homology <EGF3>
F;492-523/Domain: EGF homology <EGF3>
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F;199-461/Domain: heavy chain #status predicted <PCH>
F;199-461/Domain: activation peptide #status predicted <ACT>
F;199-211/Domain: activation peptide #status predicted <ACT>
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F;212-445/Domain: trypsin homology <TRY>
F;212-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat
F;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGHGTCIDGIGSFSCSCDKGWEGKFCQ 131
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13; Conserv
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Pred. No. 0.02
7; Mismatches
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Pred. No.
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0.023;
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0.016;
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F;180-211/Domain: EGF hr
F;286-287/Domain: EGF hr
F;256-287/Domain: EGF hr
F;294-325/Domain: EGF hr
F;394-325/Domain: EGF hr
F;370-401/Domain: EGF hr
F;370-401/Domain: EGF hr
F;408-439/Domain: EGF hr
F;448-4515/Domain: EGF hr
F;484-515/Domain: EGF hr
F;522-553/Jomain: EGF hr
F;598-629/Domain: EGF hr
F;598-629/Domain: EGF hr
F;636-667/Jomain: EGF hr
F;636-667/Jomain: EGF hr
F;637-713/Domain: EGF hr
F;637-713/Domain: EGF hr
F;638-819/Domain: EGF hr
F;780-781/Domain: EGF hr
F;780-851/Domain: EGF hr
F;864-895/Domain: EGF hr
F;866-857/Domain: EGF hr
F;866-857/Domain: EGF hr
F;866-857/Domain: EGF hr
F;866-857/Domain: EGF hr
F;902-933/Domain: EGF hr
F;902-933/Domain: EGF hr
F;902-933/Domain: EGF hr
                                                            C;Species: Drosophila melanogaster C;Date: 21-Sep-1990 #sequence_revision C;Accession: A35672 R;Tepass, U; Theres, C; Knust, E. Cell 61, 787-799, 1990
A;Title: crumbs encodes an : A;Reference number: A35672; A;Accession: A35672
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57,451-466,468-477,484-495/Disulfide bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: EGF homology repeats 10-17 are spliced out in C;Superfamily: C1r/C1s repeat homology; EGF homology F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1064/Product: fibropellin I #status predicted <FIB>
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F;57-175/Domain: Clr/Cls repeat homology <Clr>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Avidin-like domain in an epidermal growth factor A;Reference number: A43131; MUID:89196806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Hunt, L.T.; Barker, W. FASEB J. 3, 1760-1764, 1
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A; Residues: 'S', 280-481, 786-1064
A; Cross-references: GB:M17421; N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A sea urchin gene encodes a polypeptide A;Reference number: A29316; MUID:87319677 A;Accession: A29316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Hursh, D.A.; Andrews, M.E.
Science 237, 1487-1490, 1987
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A; Residues: 'K', 747-821, 898-978
                                                                                                                                                                            crumbs protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                      A35672
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                     Matches
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homology <EG03>
homology <EG04>
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                       EGF-like protein expressed; MUID:90263104
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<EG20>
<EG21>
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<EG06>
<EG07>
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                                                                                                                                                                                                                                                                                                                                                                                Score 87; DB
Pred. No. 0.03
5; Mismatches
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0.031;
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A;Gene: FlyBase:crb
A;Cross-references: FlyBase:FBgn0000368
C;Superfemily: unassigned EGF-related prot
C;Keywords: transmembrane protein
F;352-385/Domain: EGF homology <EGX1>
F;392-42/Domain: EGF homology <EGF1>
F;691-722/Domain: EGF homology <EGF5>
F;67-799/Domain: EGF homology <EGF3>
                              C;Superfamily: notch protein; ankyrin repeat homology; EGF C;Keywords: differentiation; tandem repeat; transmembrane F;27-43/Domain: transmembrane #status predicted <fmM1> F;297-328/Domain: EGF homology <EGX1> F;530-561/Domain: EGF homology <EGF1> F;568-599/Domain: EGF homology <EGF2> F;988-1019/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 2505-2551, 'QQQ', 'AJL. TRESIDUES: 2505-2551, 'QQQ', 'AJL. TRESIDUES: 2505-2551, 'QQQ', 'AJL. TRESIDUES: VAN PRINCIPLES: VAN PRIN
                                                                                                                                                                                                                                                                          A;Gene: notcu; vya
A;Gross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
    F;1064-1095/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>
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C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #squence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624
A;Accession: A24420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: notch; opa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A05267; A; Accession: A05267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA A;Reference number: S09358; MUID:89385974
A;Accession: S09358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-48, I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Tautz, D
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A; Residues: 1-2139 < TEP>
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Best Local :
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13; Conserv
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Pred. No.
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A) Arcangelo, G.
Submitted to the EMBL Data
submitted to number: S71844
A;Reference number: S71844
A;Accession: S71844
A;Molecule type: mRNA
A;Residues: 1-215,'T',217-1905,'S',1907-3355,'V',3357-3391,'N',3393-3461 <DA2>
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F;1746-1762/Domain: t
F;1950-1982/Domain: a
F;1983-2015/Domain: a
F;1983-2014/Domain: t
F;1988-2004/Domain: t
F;2017-2049/Domain: a
F;2050-2082/Domain: a
F;2083-2115/Domain: a
                                                                                                                                                            A;Status: nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-3461 <DAR>
                                                                                                                                                                                                                          A; Reference number: A; Accession: S58870
                                                                                                                                                                                                                                                                                  R;D'Arcangelo, G.; Mi
Nature 374, 719-723,
                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Datc: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 11-Jan-2000
C;Accession: S58870; S71844; 149297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-473 <INO>
A; Cross-references: GB:D43794; NID:g602767; PIDN:BAA07852.1;
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Keywords: duplication
F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                  A;Cross-references: EMBL:U24703; NID:g902486; PID:g902487
                                                                                                                                                                                                                                             A; Title: A protein related to extracellular A; Reference number: I49297; MUID:95231649
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F;387-419/Domain: EGF homology <EGFF1>
F;429-460/Domain: EGF homology <EGF>
F;23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr
                                                                                                                                                                                                                                                                                                                                                                                      reelin precursor - mouse
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A;Title: Mussel adhesive plaque protein gene
A;Reference number: A56175; MUID:95204464
A;Accession: A56175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adhesive plaque protein Mgfp2 precursor - Mediterranean mussel
C:Species: Mytilus galloprovincialis (Mediterranean mussel)
C:Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_chang
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Best Local Similarity
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ses 14; Conserv
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m. 270, 6698-6701, 1995
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n: ankyrin repeat homology <AN2>
n: transmembrane #status predicted <
n: transmembrane bratatus predicted <
n: ankyrin repeat homology <AN3>
n: ankyrin repeat homology <AN4>
n: ankyrin repeat homology <AN5>
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38.2%;
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42.4%;
                                                                                             Library, April 1995
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Pred. No. 0.08
4; Mismatches
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Pred. No. 0.024;
8; Mismatches
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protein F11C7.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: E89753
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wusti.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: E89753
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1722 <STO>
A;Cross-references: GB:chr_X; PIDN:AAC69012.1; PID:g1125776; GSPDB:GN00028; CESP:F11C7.4
A;Genetics:
A;Gene: F11C7.4
A;Map position: X
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                                                                                                                                                         A;Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1 C;Genetics: A;Gene: Notch
                                                                                                                                                                                                                                                                         Dev. Genes Evol. 20/, J.A. A. Title: Notch homologue from A. Title: Notch homologue from Der: 220775
                                                                                                                                                                                                                                                                                                                      R; Hor1, S.; Saltoh, T.; Matsumoto, M.;
Dev. Genes Evol. 207, 371-380, 1997
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C:Date: 02-Sep-2000 #sequence_revision
C:Accession: T30201
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                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-2352 < H
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                    CQPWSCSGHGECVEIINNHTCNCDVGYYGPQC 32
CSPNPCSNGAGCEELSNSFKCTCTSGYYGDTC 144
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A; Reference number:
A; Accession: A37936
                                                A; Reference number: A; Accession: S14571
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-201,'E',203-317,'S',319-1018,'S',1020-1024,'H',1026-1305,'S',1307-2019
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R;Weller, A.; Beck, S.; Ekblom, P.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X56304
A;Accession: B37936
A;Status: preliminary; nucleic acid sequence
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A;Molecule type: mRNA
A;Molecule type: mrNA
A;Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-2019 <SAG>
A;Residues: 1-2019 <SAG>
A;Cross references: GB:D90343; NID:g220609; PIDN:BAA14355.1; PID:g220610
A;Experimental source: cell line 2H6GR
A;Note: the authors translated the codon ATG for residue 60 as Trp
R;Weller, A; Beck, S; Ekblom, P
J. Cell Biol. 112, 355-362, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 104, 177-185, 1991
A; Title: Murine tenascin: cDNA cloning, structure and temporal expression of isoforms A; Reference number: JQ1322; MUID:92009211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JQ1322; A37936; B37936; S14571; S50209
R;Saga, Y; Tsukamoto, T; Jing, N; Kusakabe, M; Sakakura, T.
Gene 104, 177-185, 1991
                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-201,'E',203-317,'S',319-620,622-1010,'N',1012-1018,'S',1020-1024,'H',10
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submitted to the Embata Library, May 1996
A;Description: The sequence of C. elegans cosmid R05G6
A;Reference number: Z20612
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C;Accession: T29359
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                                                                                                                                                   A; Description: Aminoacid
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A; Residues: 1-372 <MUR>
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Pred. No. 0.029;
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A;Status: p
A;Molecule
                                         A; Molecule type: mRNA A; Residues: 431-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'L' < CA; Cross-references: GB:M24630; NID:g514363; PIDN:AAA52703.1; PID:g553348 R.Siri, A.; Carnemolla, B.; Saginati, M.; Leprini, A.; Casari, G.; Baralle, Nucleic Acids Res. 19, 525-531, 1991
A; Title: Human tenascin: primary structure, pre-mRNA splicing patterns and A; Reference number: S14015; MUID:91187670
A; A; Cccession: $14015
                                                                                                                                                                                                                                                                                                                                                                                                                                      tenascin-C - human
N;Alternate names: hexabrachion
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (pan)
C;Date: 31-Jul-1998 #sequence_revision 12-Apr-1996 #text_change:
C;Accession: I38337; A32100; S14015; S16166; S50208; S49354
C;Accession: I38337; A32100; S14015; S16166; S50208; S49354
R;Gherzi, R.; Carnemolla, B.; Siri, A.; Ponassi, M.; Balza, E.; '
J. Biol. Chem. 270, 3429-3434, 1995
A;Title: Human tenascin gene. Structure of the 5'-region, identii
A;Reference number: A55974; MUID:95155442
A;Accession: I38337
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A;Title: Analysis of aggrecan and tenascin gene expression in A;Reference number: S50206; MUID:95035091
                                                                                                                                                                                                                                        R;Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989
A;Title: An alternatively spliced region of the human hexabrachion contains A;Reference number: A32160; MUID:89160821
A;Accession: A32160
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A; Residues: 46-146 <GLU>
A; Cross-references: EMBL: X80281
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A;Accession: S50209
A;Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-2201 <RES>
A; Cross-references: EMBL:X78565; NID:g556844; PIDN:CAA55309.1;
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16; Conserv
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                                    F;1972-2004/Domain: ankyrin
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F;622-703/Domain: fibronectin type III repeat homology <FN3A>F;711-794/Domain: fibronectin type III repeat homology <FN3B>F;892-976/Domain: fibronectin type III repeat homology <FN3B>F;892-976/Domain: fibronectin type III repeat homology <FN3D>F;1437-1519/Domain: fibronectin type III repeat homology <FN3D>F;1619-1701/Domain: fibronectin type III repeat homology <FN3E>F;1709-1790/Domain: fibronectin type III repeat homology <FN3F>F;1798-1878/Domain: fibronectin type III repeat homology <FN3F>F;1886-1966/Domain: fibronectin type III repeat homology <FN3H>F;1981-2189/Domain: fibronectin type III repeat homology <FN3H
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A;Residues: 1-538/R/,540-1065,'H',1067-1599,'LWLHPRASN',1609-2054,'LH',2055-2201
A;Cross-references: EMBL:M55618; NID:g184483; PIDN:AAA88083.1; PID:g184484
R;Glumoff, V:, Savontaus, M:, Vehanen, J:; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissu A;Reference number: S00206; MUID:95035091
A;Reference number: S0208
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Accession: S16166
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A;Cross-references: EMBL:X56160; NID:g37226; PIDN:CAA39628.1; PID:g37227
R;Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.
J. Biol. Chem. 266, 2818-2823, 1991
                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-2318 <LAR>
A; Cross-references: EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g483581
A; Cross-references: EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g483581
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
F; 163-195/Domain: EGF homology <EGF1>
F;163-195/Domain: EGF homology <EGFI>F;474-505/Domain: EGF homology <EGF2>F;474-505/Domain: EGF homology <EGF2>F;1839-1871/Domain: Ankyrin repeat homology F;1872-1904/Domain: ankyrin repeat homology F;1906-1938/Domain: Ankyrin repeat homology F;1939-1971/Domain: Ankyrin repeat homology F;1939-1971/Domain: Ankyrin repeat homology
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S45306
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C;Superfamily: tenascin: EGF homology; fibrinogen beta/gamma C:Keywords: alternative splicing; extracellular matrix F:408-434/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lardelli, M.; Dahlstrand, J.; Lendahl, U. Mech. Dev. 46, 123-136, 1994
A;Title: The novel Notch homologue mouse Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  notch 3 protein - mouse
C; Species: Mus musculus (house mouse)
C; Date: 20-Feb-1995 #sequence_revision
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A; Map position: 9q33-9q33____
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A; Residues: 46-125 <GLU>
A; Cross-references: EMBL: X80280
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16; Conser
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repeat homology

<AN5> <AN4>

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A; Nolecule type: mRNA
A; Residues: 1-870;871-1069 <AAA>
A; Residues: 1-870;871-1069 <AAA>
A; Cross-references: EMBL:AL133021
A; Experimental source: adult testis; clone DKF2p434E0321
A; Experimental source contains a +1 frameshift near codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Map position: 10p12
A;Map position: 10p12
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: receptor; vitamin B12 uptake
C;Keywords: regretor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted
F;436-467/Domain: EGF homology <EGF>
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74.2681

C; Accession: T42681

C; Accession: T42681

C; Accession: T42681

C; Accession: T42681

C; Accession: T42681
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A; Note: DKFZp434E0321.1
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A; Accession: T42681
A; Status: preliminary
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A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
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Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin Bl2 receptor, cubilin: Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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Best Local S
Matches 14
                                                                         Query Match 38.8
Best Local Similarity 42.4
Matches 14; Conservative
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Best Local Similarity 43.3
Matches 13; Conservative
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CLPCGCSDHGQCDDGITGSGQCLCETGWTGPSC 595
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5; Mis
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Pred. No. 0
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Search completed: September Job time: 206 sec

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2002, 10:15:28

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N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13953
R;Nakayama, M; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like moti
A;Reference number: Z14126; MUID:98360089
A;Reference number: Z14126; MUID:98360089
A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
A;Residues: 1-1523 <NAK>
A;Residues: 1-1523 <NAKA
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C;Genetics:
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Matches 16
1372 CLGHSCS-HGTCVATGNSYVCKCAEGYEGPLC 1402
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16; Conserv
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Pred. No. 0.1;
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      Match
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| Cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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Gapop 10.0 ,
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Listing first 45 summaries
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Copyright (c) 1993 - 2000
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      7, 2002, 10:22:08; Search time 85.16 Seconds (without alignments) 100.974 Million cell updates/sec
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US-10-212-778-1158
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US-09-791-537-53844
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Compugen Ltd
Sequence 152667, A Sequence 53485, A Sequence 1171, Ap Sequence 1171, Ap Sequence 1158, Ap Sequence 12816, A Sequence 42657, A Sequence 42657, A Sequence 42658, A Sequence 53844, A Sequence 5384, A Sequence 53844, A Sequence 50403, A Sequence 50503, A Sequence 60503, A Sequence 60503, A Sequence 81233, Ap Sequence 37750, A Sequence 377, App Sequence 228813, A
                                                                                                                                                                                                                                                                                                                                                                                                         Description
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                                                                                                                                                                                               RESULT 2
US-09-791-537-84593
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US-09-791-537-152667
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Best Local
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TYPE: PRT
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	Sequence 20989, A	Sequence 35618, A	Sequence 22819, A	Sequence 32024, A	Sequence 32023, A	Sequence 32025, A	Sequence 50405, A	Sequence 111285,	Sequence 41672, A	Sequence 86308, A	Sequence 37749, A	Sequence 81892, A	Sequence 73416, A	Sequence 50409, A	Sequence 93873, A	Sequence 84829, A	Sequence 50406, A	Sequence 357, App	Sequence 121834,

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-152667
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; GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 84593
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY |
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CUGRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 153667
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US-09-791-537-53485
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                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/211,364
CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THERBOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
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TYPE: PRT
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TYPE: PRT
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les 33; Conserv
                                                                APPLICATION NUMBER: 60/220,963 FILING DATE: 2000-07-26
                                                                                                                                                                                               APPLICATION NUMBER: 60/180,628 FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/760,486 FILING DATE: 2001-01-16
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                              APPLICATION NUMBER: 60/217,496 FILING DATE: 2000-07-11
                                                                                                             FILING DATE: 2000-07-11 APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                             APPLICATION NUMBER: 60/179,065 FILING DATE: 2000-01-31
APPLICATION NUMBER: 60/225,447 FILING DATE: 2000-08-14
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No. 1.8e-15;
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Best Local Similarity
"hes 32; Conserv:
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SEQ ID NO 1171

: LENGTH: 341

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                                                                              Sequence 1158, Appli GENERAL INFORMATION:
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Best Local S
Matches 32
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Prior application removed -
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1328, Appli GENERAL INFORMATION:
              PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
                                                                                 CURRENT APPLICATION NUMBER: US/10/212,778
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 09/758,449
PRIOR FILING DATE: 2001-01-11
                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PM026ClN
                                                                                                                                                                                            APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
 NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PJZ12C1N CURRENT APPLICATION NUMBER: US/10/212,054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (215)
OTHER INFORMATION: Xaa equals any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                    182 CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 214
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32; Conserv
SEQ ID NOS:
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97.0%;
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Pred. No. 4.7e-15;
1; Mismatches (
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                                                                                                                                                                           and Antibodies
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US-09-791-537-58446
Sequence 58446, Application US/09791537
GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-212-778-1158
                                                                  ; ORGANISM: Homo sapiens US-09-791-537-22816
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APPLICANT: Danzer JOSeph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT TILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 58446
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                Sequence 22816, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Best Local Similarity 9/...
Thes 32; Conservative
                                                                                               SOFTWARE: PatentIn version 3.0
SEQ ID NO 22816
LENGTH: 372
TYPE: PRT
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Best Local Similarity 97.0
Matches 32; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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Pred. No. 4.9e-15;
1; Mismatches 0;
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Pred. No. 4.7e-15;
 Score 205; DB 5; Pred. No. 5e-15;
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RESULT 11
US-09-791-537-42658
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Best Local Similarity
Thehes 32; Conserv:
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                        Best
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SEQ ID NO 42655
LENGTH: 372
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bionomix, Inc.
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                                                                                                                        Local Similarity 97.0
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Pred. No. 5e-15;
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Sequence 42658, Application US/09791537 GENERAL INFORMATION:

APPLICANT:

Bionomix, Inc Debe, Derek

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                                           NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 69658
LENGTH: 372
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 69658, Application US/09791537
ORGANISM: Homo sapiens -09-791-537-69658
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APPLICANT: Bionomix, Inc.
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42658
LENGTH: 372
TYPE: PRT
                                                                                                                                                           APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                               CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBH
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 372
TYPE: PRT
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nes 32; Conserv
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32; Conservative
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Pred. No. 5e-15;
1; Mismatches
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Pred. No. 5e-15;
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RESULT 16
US-09-791-537-113060
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53844
LENGTH: 385
TYPE: PRT
                                                                                                                                  Query Match
Best Local Similarity
Matches 32; Conserv
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 51391
LENGTH: 385
TYPE: PRT
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
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Best Local
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
                                                              173 CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 205
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Pred. No. 5.2e-15;
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Pred. No. 5.2e-15;
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Pred. No. 5e-15;
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TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 113060
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PAtentin version 3.0
SEQ ID NO 50403
LENGTH: 370
TYPE: PRT
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Best Local Similarity
Matches 32; Conserv
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Best Local Similarity
Matches 27; Conserv
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                              APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBH
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                  SOFTWARE:
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TYPE: PRT
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Pred. No. 1.8e-13;
Pred. No. 1.8e-13;
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Pred. No. 5.2e-15;
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APPLICANT: Dobe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37750
LENGTH: 372
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                                                                              ; ORGANISM: Mus musculus US-09-791-537-37750
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Query Match
Best Local S
Matches 27
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Best Local Similarity 84.8
Conservative
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APPLICANT: Bionomix, Inc.
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Best Local Similarity 81.8
Matches 27; Conservative
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 153055
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Local Similarity les 27; Conserv
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Pred. No. 4.7e-11
               Score 169; DB 5;
Pred. No. 4.8e-11;
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Pred. No. 2.3e-12;
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160 CQPGSCNGRGECVETINNHTCICDAGYYGPQCQ 192

1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33

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; SEQ ID NO 6693
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Rattus sp
US-09-791-537-6693
                                                                                                                                              US-09-791-537-118878; Sequence 118878, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO 81233
LENGTH: 372
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-81233
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                                                                                                                                                                                                                    RESULT 23
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Best Local s
Matches 26
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Best Local Similarity
Matches 26; Conserv
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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APPLICANT: Debe, Derek
APPLICANT: Danzer, JOSeph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                             160 CQPESCNRHGECVETINNNTCICDPGYYGPQCQ 192
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Pred. No. 6.2e-10;
2; Mismatches 5
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Pred. No. 6.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                              Length 372;
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PCT-US02-23913-357; Sequence 357, Apr
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Best Local Similarity
"-+ches 21; Conserv:
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                                                                           PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
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; Sequence 23269, Application US/09791537
; GENERAL INFORMATION:
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILLING DATE: 2001-02-22
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 23269
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044PC
CURRENT APPLICATION NUMBER: PCT/US02/23913
CURRENT FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 357
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Best Local Similarity
Matches 20; Conserv
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SEQ ID NO 118878
LENGTH: 611
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/307,982 PRIOR FILING DATE: 2001-07-25
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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NUMBER OF SEQ ID NOS: 153055
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Pred. No. 4.9e-07;
"""" amatches 8;
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Pred. No. 1.2e-06;
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LENGTH: 610

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US-09-791-537-121834
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                                                                                                                                                                                                           Sequence 121834, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Dabe, Derek
APPLICANT: Dabe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0

TYPE: PATE
TITLE: 610
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 22813
LENGTH: 6510
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                                                                            Query Match
Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
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143
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                    CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
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63.6%;
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Pred. No. 1.5e-06;
                                                                         Score 130; DB 5;
Pred. No. 1.5e-06;
4; Mismatches 8
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Pred. No. 1.5e-06;
4; Mismatches 8
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                                                                                                              Length 610;
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                                                                         Gaps
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                                                          ; ORGANISM: Rattus
US-09-791-537-50406
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US-10-205-823-357
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CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR APPLICATION NUMBER: 60/321,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
                                                                                                                        APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50406
                                                                                                                                                                                                                                                                                                                                                               Sequence 50406, Application US/09791537 GENERAL INFORMATION:
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LENGTH: 610
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  Query Match
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Best Local :
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APPLICANT:
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MRI-044
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                                                                                                LENGTH: 549
TYPE: PRT
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21; Conserv
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Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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  59.1%;
  Score 127;
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Pred. No. 1.5e-06;
4; Mismatches 8
  DB 5;
Length 549;
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RESULT 32
US-09-791-537-50409
Sequence 50409, Application US/09791537
GENERAL INFORMATION:
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Best Local Similarity
Matches 19; Conserva
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Best Local Similarity 57.6
Matches 19; Conservative
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 93873
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         APPLICANT: Bionomix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                       LENGTH: 649
TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
                                                                                                                                    163 CQDMSCSKQGECIETIGNYTCSCYPGFYGPECE 195
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                                                                                                                                                                  1 COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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Pred. No. 3.4e-06;
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Pred. No. 3.4e-06;
6; Mismatches 8;
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4; Mismatches
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ORGANISM: Mus musculus
                     TYPE: PRT
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RESULT 34
US-09-791-537-81892
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                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 81892
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 73416
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50409
LENGTH: 769
TYPE: PAT
ORGANISM: Ovis aries
                                                                                                                APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
EILE REFERENCE: 261/210
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Best Local Similarity
Matches 19; Conserv
                                                  CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT:
LENGTH: 618
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57.6%;
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Pred. No. 4.2e-06;
- wismatches 9;
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Pred. No. 3.9e-06;
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US-09-791-537-37749
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RESULT
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                                                                                                              Query Match
Best Local S
Matches 19
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 86308
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Best Local Similarity
Matches 19: Conserv
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                               LENGTH: 40
TYPE: PRT
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TYPE: PRT
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37
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                                               CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 36
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                                                                                                             Score 125; DB
Pred. No. 5.3e
6; Mismatches
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Pred. No. 4
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Pred. No. 4.2e-06;
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                                                                                                              DB 5;
5.3e-07;
nes 8;
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; ORGANISM: Sus scrofa domestica US-09-791-537-41672
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US-09-791-537-111285
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY METHOLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 111285
LENGTH: 482
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Best Local
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 15365
SOFTWARE: PatentIn version 3.0
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bionomix, Inc.
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60.6%;
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Pred. No. 4.4e-06;
4; Mismatches
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RESULT 40
US-09-791-537-32025
(Sequence 32025, Application US/09791537
(Sequence 32025, Application US/09791537
(GENERAL INFORMATION:
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
(CURRENT APPLICATION NUMBER: US/09/791,537
(CURRENT APPLICATION SECONDAMEN: US/09/791,537
(CURRENT FILING DATE: 2001-02-22
(NUMBER OF SEQ ID NOS: 153055
(SOFTWARE: Patentin version 3.0)
(SEQ ID NO 32025
(LENGTH: 616
(TYDE: PRT
(ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 50405
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-791-537-50405
Search completed: September 7, 2002, 10:22:09 Job time: 557 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.1%; Score 125; DB 5; Length 484; Best Local Similarity 60.6%; Pred. No. 4.4e-06; Matches 20; Conservative 4; Mismatches 9; Indels
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1751, Appli Sequence 1751, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 36, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5155, Appli Sequence 5155, Appli Sequence 529, Appli Sequence 194120, Sequence 19313, Appli Sequence 19513, Appli Sequence 19513, Appli Sequence 19513, Appli

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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           1004DD
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                                                                                                                                    Score
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Match
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/cgn2_6/ptcodata/2/paa/USO6_COMB.pep:*
/cgn2_6/ptcodata/2/paa/USO8_COMB.pep:*
/cgn2_6/ptcodata/2/paa/USO80_COMB.pep:*
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/cgn2_6/ptcodata/2/paa/USO86_COMB.pep:*
/cgn2_6/ptcodata/2/paa/USO80_COMB.pep:*
/cgn2_6/ptcodata/2/paa/USO90_COMB.pep:*
/c
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                                                                                                                                    Length
     372
382
1078
341
341
372
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39.284 Million cell updates/sec
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   5 US-09-119-209-2
1 US-09-760-475-2123
6 US-60-211-659-523
1 US-09-758-449-1158
1 US-09-760-443-1328
PCT-US01-26675-3
PCT-US02-03970-2
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                                                                                                                                                                                      SUMMARIES
                                                                                                                                      Description
   Sequence
Sequence
 Sequence 2, Appli
Sequence 2123, App
Sequence 523, App
Sequence 1158, Ap
Sequence 3, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-119-209-2
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application GENERAL INFORMATION:
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/119,209

FILING DATE: 20-Jul-1998

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/513278

FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09119209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
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4 US-08-340-539-2
7 US-08-340-539-2
8 US-08-410-569-2
8 US-08-410-569-2
8 US-08-410-569-2
10 US-08-657-753-2
11 US-08-657-753-2
11 US-08-770-435-3
16 US-09-266-091-2
12 US-09-266-091-2
13 US-09-266-091-2
14 US-10-021-660-12
15 US-09-802-440-36
16 US-60-160-189-8885-6
16 US-60-160-189-8885-6
16 US-60-160-189-8885-6
16 US-60-160-189-8885-6
16 US-60-160-189-8885-6
17 US-09-270-767-48979-5
18 US-09-270-767-48979-5
18 US-09-270-767-48979-5
18 US-60-142-895-1034-6
18 US-60-141-338-711-19715-6
18 US-60-167-217-19715-6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
FILING DATE: 6-MAY-1993 PRIOR APPLICATION DATA:

08/059027

APPLICATION NUMBER:

31-OCT-1991

07/786149

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US-09-119-209-2
                                                                                                                                    Sequence 523, Application:
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2123
LENGTH: 382
                                               APPLICANT: Beasley, Ellen TITLE OF INVENTION: ISOLATITLE OF INVENTION: USES: TITLE OF INVENTION: USES: FILE REFERENCE: CL000674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                  CURRENT APPLICATION NUMBER: US/60/212,659
CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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LENGTH: 372 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         170 COPWSCSGHGECVEIINNYTCNCDVGYYGPQCQL 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Love, Richard B.
                                                                                                                                                        Application US/60212659
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                                                                 ISOLATED HUMAN PROTEASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING IUSES THEREOF
2000-06-19
879
                                                                                                                                                                                                                                                                                                                              97.2%;
97.1%;
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                                                                                                                                                                                                                                                                                                        Score 209; DB 21;
Pred. No. 2.4e-16;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                             Length 382;
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                                                                               HUMAN PROTEASE PROTEINS,
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; LENGTH: 1078
; TYPE: PRT
; ORGANISM: HUMAN
US-60-212-659-523
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-760-443-1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-760-443-1328
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; COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-449-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
watches 33; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1328, Application US/09760443
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJ712
CURRENT APPLICATION NUMBER: US/09/760,443
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2164
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1328
LENGTH: 341
TYPE: PRT
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Best Local :
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SEQ ID NO 523
                                                                  NAME/KEY:
LOCATION:
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER: CCC. TO THE STATE OF TH
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                                                                                                                                        FEATURE:
                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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32; Conserv
                                                                  (215)
                                                                                                       SITE
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97.0%;
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97.1%;
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Pred. No. 6.3e-16;
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Pred. No. 6e-16;
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Similarity

Length 341;

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RESULT 7
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Best Local
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PRIOR TILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bieglecki, Karyn M
APPLICANT: Kliem, Stefanie E
APPLICANT: Koshy, Beena
APPLICANT: Kumar, Anant Madan
TITLE OF INVENTION: HAPLOTYPES OF
FILE REFERENCE: SELL MWH1116-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: PCT/US01/26675
CURRENT FILING DATE: 2001-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 372
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dana-Farber Cancer Institute, TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED TITLE OF INVENTION: PROTEIN
              ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 COPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 192
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                                                                 CLASSIFICATION:
                                                                                 APPLICATION NUMBER: POFILING DATE: 19920513
                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                   CITY: Boston
REFERENCE/DOCKET NUMBER:
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Bieglecki, Karyn M
Kliem, Stefanie E
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97.0%;
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97.0%;
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DFCI-152Bq9
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Pred. No. 6.3e-16;
1; Mismatches 0
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Pred. No. 6.9e-16;
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                                                                                                         PCT-US94-00909-2
Query Match
Best Local Similarity 97.2
Best Conservative
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Best Local (
                                                                                                                                                                                                        FILING DATE: 21-FEB-1989 INFORMATION FOR SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/737,092
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730,503
FILING DATE: 08-JUL-1991
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/962,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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APPLICATION NUMBER: US 07/983,606
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LENGTH: 385 amino acid
                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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TELEFAX: 940675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 97.0 hes 32; Conservative
                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01
FILING DATE: 25-JAN-1993
                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER
                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 542-22: TELEFAX: (617) 451-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
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AMINO ACID
                                                                                                                                                        amino acid
                                                                                                                                                                       385 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                       protein
                                                                                                                                                                                                                                                                          15-MAY-1991
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97.0%;
                                       95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                          us 07/700,773
                                                                                                                                                                                                                                           US 07/313,109
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                      Score 205; DB 1;
Pred. No. 7.1e-16;
1; Mismatches 0;
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Pred. No. 7.
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                                                       Length 385;
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Indels

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Gaps

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-008-459-2
Query Match
Best Local Similarity 97.0
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                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 2, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/31
FILING DATE: 21-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 15-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US 07/983,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,459
FILING DATE: 25-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tedder, Thomas F.

APPLICANT: Kansas, Geoffrey S.

TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM FC
OPERATING SYSTEM:
                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 08-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 29-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                : 385 amino acids
amino acid
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USA
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 07/700,773
15-MAY-1991
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08-JUL-1991
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                                95.3%;
97.0%;
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                           Score 205; DB 4;
Pred. No. 7.1e-16;
              Mismatches
                                             Length 385;
              Indels
            0;
          Gaps
          0;
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; MOLECULE TYPE: US-08-340-539-2
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/
FILING DATE: 21-FEB-199
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.

NAME: Heine, Holliday C.

NAME: Heine, Holliday C.

NAME: Heine, Holliday C.

NAME: Heine, Holliday C.
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                 REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEPAX: (617) 451-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tedder, TAPPLICANT: Kansas, GITITLE OF INVENTION: TITLE OF INVENTION:
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-JUL-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/983,606
FILING DATE: 30-NOV-1992
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                  LENGTH: 385 amino acids
TYPE: amino acid
                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 205
                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 02-APF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                      linear
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29-JUL-1991
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16-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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                                                                                                                                                                                                                                                                                                        US 07/313,109
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                                                                                                                                                                                                                           34,346
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Query Match Best Local Similarity

95.3%; 97.0%;

Score 205; DB 7; Pred. No. 7.1e-16;

Length 385;

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US-60-207-315-428
; Sequence 428, Application US/60207315
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: USCLATED HUMAN E
; TITLE OF INVENTION: USCLATED MOI
; TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 32; Conserv:
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   CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
ATTORNEY/REET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tedder, Thomas F.
APPLICANT: Spertini, Oliviar G.
TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
TITLE OF INVENTION: AND LIGAND THEREOF
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 02109
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                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                               385 amino acids
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                                                                                                                                                                                                                                                                                                                                                               protein
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 NUMBER: US/60/207,315
                                ISOLATED HUMAN PROTEASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING FUSES THEREOF
                                                                                                                                                                                                                                                                                  95.38;
97.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/410,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2:
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                                                                                                                                                                                                                                                                   1; Mismatches
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Pred. No. 7.1e-16;
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                                                                                                                                                                                                                                                                                              Length 385;
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                                                HUMAN PROTEASE PROTEINS, AND
                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                 US-09-119-209-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: HUMAN US-60-230-435-1751
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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SOFTWARE: FastSEQ fo:
SEQ ID NO 1751
LENGTH: 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1751, Application US/60230435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09119209 GENERAL INFORMATION:
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/230,435 CURRENT FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLA:
TITLE OF INVENTION: NUCLE:
TITLE OF INVENTION: USES:
TITLE OF INVENTION: USES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                            APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
                                                                                                                                              ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                              SINGER, MARK S.
YEDNOCK, TED A.
NVENTION: LYMPHOCYTE HOMING RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.3%;
97.0%;
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97.0%;
us/09/119,209
                                                                              1.44 Mb floppy disk
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Pred. No. 1.8e-15;
1; Mismatches 0;
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L.8e-15;
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Length 1078;
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AND
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ENCODING HUMAN PROTEASE PROTEINS,
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Gaps

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/5 FILING DATE: 10-AUG-1995

08/513278

FILING DATE: 2 CLASSIFICATION:

20-Jul-1998

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RESULT 16
US-08-657-753-2
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PCT-US99-28965-19
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   Sequence
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GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0424
                                                                                                                                                                 Matches
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LENGTH: 610
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EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US99/28965
CURRENT FILING DATE: 1999-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                     143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650/225-5530
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|| || ||:| ||:|| ||:|| || ||:|| ||:||
160 CQPGSCNGRGECVETINNHTCICDAGYYGPQCQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/3:
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
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APPLICATION NUMBER: 08/0
FILING DATE: 6-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Love, Richard B. REGISTRATION NUMBER: 3
2, Application US/08657753
                                                                                                                                                                              Similarity
                                                                                                                                                           Conservative
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                                                                                                                                                                          60.5%;
63.6%;
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                                                                                                                                                          Score 130; DB Pred. No. 8.6e
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Pred. No. 1.3e-11;
1; Mismatches 5;
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                                                                                                                                                                        130; DB 1;
No. 8.6e-07;
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                                                                                                                                                                                         Length 610;
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RESULT 17
US-08-770-435-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acid
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,435
FILING DATE: herewith
CLASSIFICATION: 424
                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            APPLICANT: Gimbrone, Jr., Michael A.
APPLICANT: Bevilacqua, Michael P.
TITLE OF INVENTION: Antibodies Speci
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
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APPLICANT:
APPLICANT:
                                                                                                                                                        COUNTRY: US
ZIP: 20005
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ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 CINTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hope, Michael J.
TITLE OF INVENTION: Enhance
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                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Not ye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                             1100 New York Ave.,
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Two Embarcadero Center, Eighth Floor
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Semple, Sean C.
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Pred. No. 8.6e-07
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 610
; TYPB: PRT
; ORGANISM: Homo sapiens
US-09-266-091-2
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US-09-266-091A-2
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Sequence 2, Application US/09266091A
GENERAL INFORMATION:
APPLICANT: KIlmuk, Sandra K.
Semple, Sean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09266091 GENERAL INFORMATION:
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                             Matches
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 08/657,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/850,802
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MAIKOWICZ, KAIEN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 0627.1350004
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hope, Michael J.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: ENHANCED EFFICACY OF LIPOSOMAL ANTISENSE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1996-05-30 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Semple, Sean C
APPLICANT: Scherrer, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Klimuk, Sandra K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ISPH-0342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08 FILING DATE: 05-AUG-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                        143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
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                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
                                                                                                                                                                                                                           60.5%; Score 130; DB 16; 63.6%; Pred. No. 8.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130; DB 11;
Pred. No. 8.6e-07;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                         Length 610;
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; ORGANISM: Homo sapiens US-09-784-356-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 122, Application US/09784356 GENERAL INFORMATION:
                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                CURRENT APPLICATION NUMBER: US/09/784,356
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 60/148,425
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
                                                                                                                                                                                                                                                                                         APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: EOS Blotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-000710US
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2:
                                             TYPE:
                                                                  LENGTH: 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 16303-003600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/657,753
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                          PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hope, Michael J.
TITLE OF INVENTION: Enhanced Efficacy of Liposomal Antisense NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 610 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kezer, William B. REGISTRATION NUMBER: 37,369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/266,091A FILING DATE: 10-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, Eighth Floor
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63.6%;
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Pred. No. 8.6e-07;
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APPLICANT: Braun, Andreas

APPLICANT: Bonsal Aruna

APPLICANT: Bonsal Aruna

APPLICANT: Kleyn Patrick

TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE

FILE REFERENCE: 24736-2048

CURRENT APPLICATION NUMBER: US/09/802,640

CURRENT FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 122

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

LENGTH: 610

TVPE: DRT
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                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-857-670-19
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US-09-857-670-19
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                                                                                                                                                                                                                               APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: Alpha-INDUCED EXPRESSION OF CELL ADHESION METHODS
TILE REFERENCE: ISPH-0424
CURRENT FILING ISPH-0424
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US/09/857,670
PRIOR APPLICATION NUMBER: US 09/209,668
PRIOR FILING DATE: 198-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                         Matches
                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09857670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.5%;
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Monia, Brett P. APPLICANT: Xu, Xiaoxing S APPLICANT: Isis Pharmaceu
                                                                                                                                                                                                                  LENGTH:
143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
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                    1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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                                                                                                                                                                                                                  610
                                                                       21;
                                                                   Similarity 63.6
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                      60.5%;
63.6%;
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                                                                   Score 130; DB 22;
Pred. No. 8.6e-07;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 130; DB 22;
Pred. No. 8.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 130; DB 21; Pred. No. 8.6e-07;
                                                                                                                                                                                                                                                                                                                                                                            OF CELL ADHESION MOLECULES
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                                                                                                       Length 610;
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                                                                     Indels
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RESULT 24
US-60-207-315-467
IS-60-207-315-467
Sequence 467, Application US/60207315
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITILE OF INVENTION: ISOLATED HUMAN PROTEASE
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES
ITITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000601
CURRENT APPLICATION NUMBER: US/60/207,315
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 528
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 467
LENGTH: 700
                                                                                                                                   밁
                                       RESULT 25
PCT-US94-09395-4
                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: VARIANT
; LOCATION: (1)...(700)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-207-315-467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
US-10-021-660-122
                                                                                                                                                                                                 Query Match
Best Local Similarity 57.6
Sequence 4, Application PC/TUS9409395 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: MUTTAY, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 122
LENGTH: 610
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/021,660
CURRENT FILLING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR PPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                            155 CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                                                                                                     1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOLATED HUMAN PROTEASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                        58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.5%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                             Score 125; DB 26; Pred. No. 3.8e-06; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130; DB 24; Pred. No. 8.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                             DB 26;
                                                                                                                                                                                                                                                        Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US94-09395-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.1
Best Local Similarity 57.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (404)-815-65
INFORMATION FOR SEQ ID NO:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,158
FILING DATE: 20-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McEver, Rodger P.
APPLICANT: Pan, Juniliang
TITLE OF INVENTION: Expression Control Sequences of the
TITLE OF INVENTION: P-Selectin Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19-AUG-19
CLASSIFICATION:
                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1'CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PABST, PATTOR L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 30309-4530
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Board of Regents of the University of Oklahoma TITLE OF INVENTION: Expression Control Sequences of the p-Selectin Gene NUMBER OF SEQUENCE: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 195
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                       APPLICATION NUMBER: FILING DATE: 24-MA
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08449687B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 amino acids
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(404)-815-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-1994
                                                                                 24-MAY-1995
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                                                                                                     US/08/449,687B
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Pred. No. 4.5e-06;
Pred. No. 4.5e-8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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В
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Best Local S
Matches 19
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
             CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 10162
                                                                 TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McCarthy, Jeanette
APPLICANT: Ableson, Allen
TITLE OF INVENTION: DIGNOSIS AND TREATMENT OF VASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: MMI-002
CURRENT APPLICATION NUMBER: US/10/020,141
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 21 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/313,097
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/327,485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 830
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LENGTH: 830 amino acids
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE
                                                                                                                                                                                                                                                                   163 CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 195
                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 57.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                          Mismatches
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US-60-160-203-6335, Application US/60160203

Sequence 6335, Application US/60160203

GENERAL INFORMATION:

APPLICANT: BONAZZI, VIVIEN

TITLE OF INVENTION: USCLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING FITTLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(37)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-189-10134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-60-160-189-10134, Application US/60160189; Sequence 10134, Application US/60160189; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000112
US-60-160-203-6335
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; ÓRGANISM: HUMAN
US-60-160-189-8885
                                                                                  SEQ ID NO 6335
LENGTH: 37
TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 10162
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10134
LENGTH: 37
TYPE: PRT
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Best Local
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LENGTH: 36
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Best Local S
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/160,203
CURRENT FILLING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 6374
SOFTWARE: FastSEQ for Windows Version 4.0
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             FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(37)
OTHER INFORMATION: Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HUMAN
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60.6%;
               Any Amino Acid
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Pred. No. le-06;
4; Mismatches
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Pred. No. 1.1e-06;
4; Mismatches 9;
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                                                                                                                                                                                                                                                                   ENCODING HUMAN SECRETED PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-60-169-867-5901
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US-60-169-840-6794
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; ORGANISM: HUMAN
US-60-160-203-5155
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                 Sequence 5901, Application US/60169867 GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 9628
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6794
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5155
LENGTH: 38
                                                                                                                                                                                                        Matches
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Best Local Similarity
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACLD MOLECULES ENCODING H
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000116
CURRENT APPLICATION NUMBER: US/60/160,203
CURRENT FILING DATE: 1999-10-19
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/60/169,840 CURRENT FILING DATE: 1999.12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000164
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                  3 CTNTSCSGPGECVETINNYTCKCDPGFSGLKCE 35
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                                                                                                                                                                                                      Conservative
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Vivien ISOLATED HUMAN DRUG TARGET PROTEINS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                    Score 120; DB 26;
Pred. No. 1.1e-06;
4; Mismatches 9;
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Pred. No. 1.1e-06;
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Pred. No. 1.1e-06;
4; Mismatches 9;
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APPLICANT: Kerlavage, Anthony
INFILE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USE
FILE REFERENCE: CL000036
CURRENT APPLICATION NUMBER: US/60/139,669
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 686
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 665
SEQ ID NO 665
TYPE: PRT
ORGANISM: Drosophila
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; TYPE: PRT
; ORGANISM: Human
US-60-169-867-5901
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US-60-146-055-529
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CURRENT FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 938
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 529
LENGTH: 34
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000067
 Query Match 45.6%;
Best Local Similarity 39.4%;
Matches 13; Conservative
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5901
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Best Local Similarity
Matches 20; Conserv
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Pred. No. 0.0004;
3; Mismatches 12
 Score 98; DB 26;
Pred. No. 0.0017;
9; Mismatches 11
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GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 33762

LENGTH: 321

TYPE: PRT

ORGANISM: Drosophila melanogaster

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US-09-270-767-33762
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
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Best Local Similarity 39.4
Matches 13; Conservative
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SEQ ID NO 596
LENGTH: 183
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Best Local Similarity 39.4
Matches 13; Conservative
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CURRENT FILING DATE: 1999-06-17
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Pred. No. 0.00
9; Mismatches
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Pred. No. 0.0018;
9; Mismatches 1
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CURRENT FILING DATE: 1999-03-17

NUMBER OF SEO ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 48979

LENGTH: 321

TYPE: PRT

ORGANISM: Drosophila melanogaster
US-09-270-767-48979
                                                                      ; FEATURE:

NAME/KEY: VARIANT

; LOCATION: (1)...(427)

; OTHER INFORMATION: Xaa = Any

US-60-142-896-1034
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Sequence 194120, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
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CURRENT FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 1584
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1034
LENGTH: 427
TYPE: PRT
ORGANISM: Drosophila
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GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
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Best Local S
Matches 13
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SEO ID NO 194120
LENGTH: 321
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Query Match
Best Local Similarity
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Best Local Similarity 39.4%;
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
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 45.6%;
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Pred. No. 0.003; 
9; Mismatches 11; Indels
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Pred.
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98;
No.
 DB 26;
0.0039;
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PROTEINS, AND USES THEREOF
                 Length 427;
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                                                               CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                              13;
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         7, 2002, 10:20:38
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Result
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Perfect score:
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-340-539A-24

US-08-340-539A-26

US-08-252-493C-9

US-09-276-197-9

US-09-276-197-9

US-09-10-158-4

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US-09-068-740A-3

US-08-872-855-10
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US-08-340-539A-23

US-08-365-470-3

US-09-209-668-19

US-09-009-490A-89

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US-08-461-592B-2

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(without alignments)
29.007 Million cell updates/sec
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Patent No. 5514...
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appl
Sequence 22, Appl
Patent No.
Sequence 2
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Sequence 3
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Sequence 9
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Patent No.
Sequence
           Sequence 21, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 27, Appli
Sequence 33, Appli
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Sequence
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atent No. 5514582
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4, Appli
5514582
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Sequence 4, A	Sequence 4, A	Sequence 2, A	Sequence 2, A	Sequence 9, A	Sequence 19,	55	ω,	Sequence 2, A	Sequence 5, A	-	Sequence 19,	Sequence 16,	Sequence 5, A	Sequence 7, A	Sequence 18,	Sequence 9, A	Sequence 4, A
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ALIGNMENTS

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US-08-513-278-2
                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-3216
TELEFAX: 415/925-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08513278 Patent No. 5840844 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
ANAME: DATE: C16727 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: STACHELL, STEVEN D.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: YEDNOCK, TED A.
APPLICANT: YEDNOCK, TED A.
APPLICANT: YEDNOCK, TED A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0: FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
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RESULT 2
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US-08-340-539A-2
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Best Local Similarity
                                                                                                                        ZIP: 100000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/340,539A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tedder, APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 193
                                                                APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE:
                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-DEC-1992 APPLICATION NUMBER: 808,122
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 986,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
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 25-JAN-1993
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                 US 08/008,459
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Pred. No. 5.6e-17;
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Best Local Similarity 97.0
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
             TOPOLOGY: 1: MOLECULE TYPE:
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acid
                                                                                                                                                            REFERENCE/DOCKET NUMBER: CG TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                        FILING DATE: 16-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tedder, APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                               TELEFAX: (***
TELEFAX: 14-8367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: ACTIVE BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                       NAME: James F. Haley, Jr. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                           TELEPHONE:
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                                            amino acid
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                                                             385 amino acids
                                                                                                                           (212) 596-9000
(212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Geoffrey S.

CHIMERIC SELECTINS AS SIMULTANEOUS

BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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Pred. No. 7.6e-16;
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RESULT 6
5514582-21
;Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
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                                                                                                                                                                                                                                                                                              US-08-340-539A-22
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; IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
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Best Local S
Matches 32
                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5808025
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-596-900
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·08-340-539A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tedder, Thomas F. APPLICANT: Kansas, Geoffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CQPWSCSGHGECVEIINNYTCNCDVGYYGPQCQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                         CKPWSCSGHGQCVEVINNYTCNCDLGYYGPECQ 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                        36 amino acids
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BLOCKING
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81.8%;
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97.0%;
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                                                                                                                                                                                                                                 Score 191; DB 1;
Pred. No. 2.7e-15;
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Pred. No. 7
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7.6e-16;
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TOPOLOGY: 13;

MOLECULE TYPE:
US-08-340-539A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5808025
Query Match
Best Local Similarity
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APPLICANT: Tedder,
APPLICANT: Kansas,
                                                                                                                                                       TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      FILING DATE: 25-JAN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                       TELEPHONE: 212-596-9090
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
                                                                                                STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 808,122 FILING DATE: 16-DEC-1991
                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                         36 amino acids
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                                                                                     linear
                                                                                                                                                                                    212-596-9000
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                                                                   protein
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas F.
Geoffrey S.
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81.8%;
78.6%;
81.8%;
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Score
Pred.
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169; DB 1;
No. 7.9e-13;
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             Length 36;
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RESULT 9
5514582-4
;Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                    В
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                                                                                                                                                                                                                                                                   US-08-513-278-4
                                                                                                                                                                                                                                                                                           TELEFAX: 415/3/1-7168
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
**ENGTH: 372 amino acids
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APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/786
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/059027

FILING DATE: 06-MAY-1993

FILING DATE: 07/786149
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROSEN, STEVEN D
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                  TOPOLOGY:
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N: 5530
                                                                                                                                                                                                  78.6%;
81.8%;
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                                                                                                                                                                                                  Score 169; DB 2; Pred. No. 7.9e-12;
                                                                                                                                                                                   Mismatches
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                    US-08-340-539A-21
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Best Local
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                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
                                  MOLECULE TYPE:
                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                 TELEPHONE: 212-596-9090
                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                   TOPOLOGY:
                                                                STRANDEDNESS:
                                                                                                                                                                                                                NAME: Gunnison, Jane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 16-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-NOV-1989 APPLICATION NUMBER: 315,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-DEC-1991 APPLICATION NUMBER: 440,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-DEC-1992
                                                                                               CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 808,122 FILING DATE: 16-DEC-1991
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27; Conservative
                                                                                amino acid
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16-NOV-1994
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81.8%;
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Version #1.30

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ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                              Application US/08340539A
                                                           Thomas F.
Geoffrey S.
CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/185,670
                                                                                                                                                                                                                                                                Score 169; DB 6;
Pred. No. 7.9e-12;
1; Mismatches 5
                                                                                                                                                                                                                                                                                         Length 372;
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US-08-365-470-3
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                                                       Sequence 3, Application US/08365470 Patent No. 5632991
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Best Local Similarity
Matches 26; Conserv
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Best Local
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GENERAL INFORMATION:
APPLICANT: Gimbrone,
TITLE OF INVENTION: 1
TITLE OF INVENTION: 7
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/008,459 FILING DATE: 25-JAN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                      TENGTH: 36 L...
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: Z12-596-9090
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
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                                                                                                                                                   CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 35
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21; Conserv
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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, Jr., Michael A. Antibodies Specific For Thereof
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Pred. No. 1.8e-08;
4; Mismatches {
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Pred. No. le-11;
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Best Local Similarity
Matches 21; Conser
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                                 Matches
                                                 Query Match
Best Local
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                                                                                                                                                                                                                  APPLICANT: MONIA, Brett P.
APPLICANT: Xu, Xiaoxing S.
APPLICANT: Xu, Xiaoxing S.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: ALpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
TILE REFERENCE: ISPH-0336
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                      LENGTH: 610
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
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FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 05-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 New CITY: Washington
                               Local Similarity
les 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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SYSTEM: PC-DOS/MS-DOS
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                                             60.5%;
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Pred. No. 3e-07;
4; Mismatches
                                               Score 130; DB 3
Pred. No. 3e-07;
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                                 Mismatches
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143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175

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; ANTI-SENSE:
US-09-009-490A-89
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                                                                   Matches
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                                                                                                   Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                      TELEPHONE: (609) 810-1515
TELEFAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 89
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 440,740
FILING DATE: May 12, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 063,167
FILING DATE: May 17, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: January CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: January 20, 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Februar
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APPLICATION NUMBER: 007,997
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TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 95
 143
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                                                                 Local Similarity
mes 21; Conserv
                                                                                                                                                                                                    TYPE: Amino Acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM:
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CITY: Marlton
STATE: NJ
                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                      LENGTH:
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CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
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                                                                                                                                                                                                                                         610
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                                                                   Conservative
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WORDPERFECT 6.0
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                                                                                                                                                                                                    Single
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                                                                                 60.5%;
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                                                                                                                                                                                                                                                                                                                                                       32,257
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                                                                               Score 130; DB 4
Pred. No. 3e-07;
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                                                                                                 DB 4;
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US-08-340-539A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Patent No. 5217870;
APPLICANT: HESSION, CATHERINE A.;LOBB, ROY R.;GOELZ, SUSAN E.;
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/08340539A Patent No. 5808025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
            TOPOLOGY: 1;
MOLECULE TYPE:
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: LALL STREET: New York CITY: New York
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          FILING DATE: 16-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CHARTITLE OF INVENTION: BINDMER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tedder, APPLICANT: Kansas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 CTNTSCSGHGECVETINNYTCKCDPGFSGLKCE 175
                                                                  TYPE:
                                              STRANDEDNESS:
                                                                                                                                                                               REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                LENGTH:
                                                                                                                                                                                                            NAME: Gunnison, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-APR-1989
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                                                            amino acid
                                                                                36 amino acids
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                                linear
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             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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63.6%;
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                                                                                                                                                                               38,479
ER: CG-104
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Pred. No. 3e-07;
4; Mismatches
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Query Match
Best Local Similarity

59.1%; 57.6%;

DB 1;

Length 36;

19;

Conservative

6; Mismatches Score 127; DB 1 Pred. No. 4e-08;

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US-08-340-539A-24
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                                                                                                                                      Sequence 26, Application US/08340539A Patent No. 5808025 GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
TITLE OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                    APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC S
TITLE OF INVENTION: BLOCKING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539A
FILING DATE: 16-NOV-1994
CLASSIFICATION: 514
                CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/ACENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                        l Similarity
19; Conserv
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amino acid
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1251 Avenue of the Americas
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                                                                  CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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Pred. No. 5.2e-08;
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RESULT 19
US-08-252-493C-9
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Best Local Similarity
Matches 19; Conserv
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                        APPLICATION NUMBER: US/08/2
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-596-900
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                               COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WoddPerfect 6.0
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                             STREET: 25 Scien
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ZIP: 06511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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57.6%;
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                                                                                                                                                                                   750 Kb storage
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Pred. No. 6.7e-08;
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Gaps

NAME: Fidel, Seth A. REGISTRATION NUMBER:

38,449

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RESULT 20
US-09-276-197-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09276197 Patent No. 6040428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                  TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (203) 772-36: INFORMATION FOR SEQ ID NO:
                               MOLECULE TYPE:
                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          COMPUTER: PC compatible OPERATING SYSTEM: DOS 6.2 SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rother, Russell P. APPLICANT: Evans, Mark J. APPLICANT: Matis, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 CTPTSCSGHGECIETINSSTCQCYPGFRGLQCE 176
                                                                                                                                                                       NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
               DESCRIPTION:
                                           TOPOLOGY:
                                                         STRANDEDNESS:
                                                                                                                                             TELEPHONE:
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CITY: New Haven
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                     LENGTH:
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TOPOLOGY: Lin
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Pred. No. 8.7e-07
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US-08-110-158-4
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                                                Sequence 2, Application PC/TUS9105059 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                            Matches
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Best Local
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 APPLICANT: Regents of the Board of the, University of APPLICANT: Oklahoma
TITLE OF INVENTION: Functionally Active Selectin-Deri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                             163 CQDMSCSKQGECLETIGNYTCSCYPGFYGPECE 195
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1100 Peachtree Street, Suite
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Pred. No. 1.5e-06;
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Pred. No. 8.7e-07;
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PATENT NO. 5378464
PATENT NO. 53
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5378464-2
5378464-2
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19; Conservative
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glycosylation site"
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glycosylation site"
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glycosylation site"
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Pred. No. 1.5e-06;
6; Mismatches 8
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                                          Sequence 27, Application US/08340539A Patent No. 5808025
GENERAL INFORMATION:
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Best Local Similarity 57.0
Matches 19; Conservative
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Patent No. 5808025
GENERAL INFORMATION:
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Best Local Similarity
Matches 19; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
 APPLICANT:
APPLICANT:
TITLE OF INV
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APPLICANT: Kansas, Ge
TITLE OF INVENTION: C
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1993
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OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gunnison, Jane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/340,539A FILING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
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                                                                                                                                               3 CNPTPCGSHGECVEIINNYTCQCHPGFKGLKCE
                                                                                                                                                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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                                                                                                                                                                                                                                                                                                                                     amino acid
   INVENTION:
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                               Tedder,
                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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                               Thomas F.
Geoffrey S.
CHIMERIC SELECTINS AS
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57.6%;
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BLOCKING
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Pred. No. 1.1e-07;
4; Mismatches 10
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Pred. No. 1.5e-06;
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                                                                                                                                               35
SIMULTANEOUS
                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                Length 36;
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                 SEQ ID NO 3
LENGTH: 520
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/068,740A CURRENT FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: JP 7-299611 PRIOR EILING DATE: 1995-11-17 PRIOR APPLICATION NUMBER: JP 7-311811 PRIOR EILING DATE: 1995-11-30
                                                                                           PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 1996-11-15 NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                  APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: GUNDISON, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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TO TO NO:
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 16-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                           PatentIn Ver.
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.4e-07;
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MOLECULE TYPE:
US-08-872-855-10
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                                                                                                                   Sequence 4, Application US/09068740A Patent No. 6337387
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             Matches
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION. BIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-847
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AIROLD, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MATELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                       428 CASSPCANGGTCVDAVNSYTCSCTLGYGGKDCTL 461
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                                                                                                                                                                                                                                                                                                          Local Similarity 41.2 hes '14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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38.2%;
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                                                                                                                                                                                                                                                                                                    Score 93; DB 3;
Pred. No. 0.0044;
7; Mismatches 1
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JP 7-311811

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US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFE
TITLE REFERENCE: KP-8447
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: JP 7-
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JI
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEO ID NOS: 48
                                                                                                                                                                                Patent No. 5750652
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
LENGTH: 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING-DATE: 1995-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1995-11-30
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PRIOR FILING DATE: 1996-
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver.
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TYPE: PRT
ORGANISM: Homo sapiens
               APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                     APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: xu, Tian
APPLICANT: Matsuno, Kenji
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ADDRESSEE:
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PENNIE & EDMONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1
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Pred. No. 0.0048;
7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 4; Length 723; Pred. No. 0.0049; Indels 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                       0;
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US-08-872-855-7
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                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 61210%.

Patent No. 61210%.

GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
THERAPEUTIC USES THEREFOR
THERAPEUTIC USES THEREFOR
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Best Local Similarity
Matches 15; Conserv
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0)
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 CQPNPCHNGGSCSDGINMFFCNCPAGFRGPKCE 942
                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-872-855-7
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                                                                         Query Match
Best Local Similarity
                                                             Matches
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                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lewis, Julia APPLICANT: Artavanis-Ts APPLICANT: Gray, Grace
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
334 CDANPCKNGGSCSDLENSYTCSCPPGFYGKNCEL 367
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                                                                                                                                                                                                                                                               TELEPHONE: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: NY
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                    NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                           COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                  amino acid
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                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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                                                                                                                                                   peptide
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38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE AND PROTEIN SEQUENCES
OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
                                                                        41.9%;
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                                                      Score 90; DB 4;
Pred. No. 0.011;
7; Mismatches 1
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                                                                                                                                                                                                                                                                                                                            7326-038
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                                                           14;
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                                                                                      Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 721;
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                                                        Gaps
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RESULT 34
US-08-083-590A-19
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US-08-185-432-16
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STATE:
COUNTRY: U.S...
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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APPLICANT: Artavanis
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08083590A Patent No. 5786158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Appli
Patent No. 5750652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 2471 amino aci TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  CORRESPONDENCE ADDRESS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 41.28; les 14; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 73:
                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
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                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 COPWSCSGHGECVEIINNHTCNCDVGYYGPOCOL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                 New York
New York
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                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2471 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                             Artavanis-Tsakonas, S. et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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VENTION: DELTEX PROTEINS, NUCLEIC ACIDS,
VENTION: ANTIBODIES, AND RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Busseau,
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                                                                                                                                                                                                                                                           Therapeutic And Diagnostic Methods
And Compositions Based On No. 5786158ch Proteins And
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 35
US-08-532-384-19
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Best Local Similarity 41.3
Matches 14; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
Applicant Applicant
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEW JACKSTON: 435
ATTORNEW JACKSTON: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Misrock, S. Leslie
                                REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9090
                                                                                                                                                                                         FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 CQSNPCVNNGQCVDKVNRFQCLCPPGFTGPVCQI 531
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STATE: New York
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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41.2%;
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RESULT

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US-08-872-855-5
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                                                                                                                                   ; MOLECULE TYPE: protein US-08-872-855-5
В
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                                                                                                                                                                                                                                            TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HC
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LENGTH: 2471 amino aci
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330 CAPSPCKNGGSCTDLEDSYSCTCPPGFYGKVCEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Match 41.48;
Local Similarity 41.28;
nes 14; Conservative
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TOPOLOGY: unl
                                                                       Local
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                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                LENGTH:
                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                            l Similarity
12; Conserv
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                                                                                                                                                                                                : 713 amino acids amino acid
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                                                              Conservative
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35.3%;
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David
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                                                                            Score 88; DB 3; Pred. No. 0.018;
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Pred. No. 0.046;
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                                                            Mismatches
                                                                                            DB 3;
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                                                                                          Length 713;
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US-08-872-855-8
; Sequence 8, Application US/08872855
; Patent No. 121045
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TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-981-392-2
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,3:
APPLICATION UMBER: US/08/981,3:
APPLICATION: 114
ATTORNEY_AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 32,605
                                                                                                                                                                                                                                        GENERAL INFORMATION:
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LENGTH: 728 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                    NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                            APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gray, Grace
TITLE OF INVENTION: NUC
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 94
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                  339 CDANPCKNGGSCTDLENSYSCTCPPGFYGKNCEL 372
         COUNTRY: USA
ZIP: 02109-2170
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                                                                   CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                     1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
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Lewis, Julian Hart
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds LLP
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OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
: 94
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                                                                                                           HOAG & ELIOT LLP
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US-08-185-432-19
; Sequence 19, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
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5514582-22
;PATENT NO. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                            RESULT
                                                                                                                                                                                                                                      5514582-22
                                                                                                                                                                                                                                                               SEQ ID NO:22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNOGLOBULINS
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Best Local
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MA TELECOMMUNICATION INFORMATION: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 CDANPCKNGGSCTDLENSYSCTCPPGFYGKNCEL 372
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                      1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ 33
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                                                                                                       CTESSCLNGGSCIDGINGYNCSCLAGYSGANCQ 33
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                                                                                                                                                                           Score 86; DB 6; Pred. No. 0.0015;
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APPLICANT:

Artavanis-Tsakonas, Spyridon

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APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Diederich, Robert J.
APPLICANT: William Konji
TITIE ON INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITIE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITIE OF INVENTION: DELTEX PROTEINS
ANDRESSE: PENNIE & EDMONIS
STREET: New York
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score greater than or equal to the score of the result being point
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd
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(without alignments)
52.061 Million cell updates/sec
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	Human lymphocyte c Human lymphocyte c Human lymphocyte c

ALIGNMENTS

RESULT AAR98125

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AAR98125;

AAR98125 standard; Protein;

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01-NOV-1996 (first entry)

Human lymphocyte cell surface glycoprotein (HuLHR) variant.

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Key
Region
                                                                                                                                                                                      Immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation;
US5514582-A
                                                                             Binding-site
                                                                                                Domain
                          Domain
                                           Domain
                                                            Binding-site
                                                                                                                 Domain
                                                                                                                                                             Homo sapiens
                                                                                                                                                                               metastasis.
                                                                              /label= EGF domain.
194..255
                                                                                              /label= Signal region.
38.152
/label= Lectin domain.
157.190
                                          330..352
                                                                                                                                          Location/Qualifiers
                /label- Cytoplasmic domain
                                 /label= Transmembrane domain.
                                                            256..314
                                                                    'label - Complement binding repeat 1.
                                                  label- Complement binding repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates progress.
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                       Immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                          Homo sapiens
                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                         01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                      AAR98126;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Gly96-Ile97 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capon
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                                                                                                                            .mmunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cqpwscsghgecveiinnhtcncdvgyygpqcql 190
                                                                                                                                                                                                                                            lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                      (first entry)
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91US-0808122.
92US-0986931.
94US-0185670.
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                                                                                                                            cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 3e-14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Вb

158 1

Qy

CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL

Query Match
Best Local Similarity
Matches 34; Conser

100.0%; ilarity 100.0%; Conservative 0

0; Score Pred.

Mismatches 215; No. 3

3e-14; DΒ 17; 0;

Length Indels

370; 0;

Gaps

0;

34

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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                    the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A hybrid immunoglobulin chain cc
a single transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
Sequence
                                                facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymph cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is an Asn136 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by discrete genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 19; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
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370
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89US-0315015.
91US-0808122.
92US-0986931.
AA;
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331..353
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257..315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
195..256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF domain
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                                                                                                   lymphocyte
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RESULT
AAR98128
     A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in CV vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and callitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                               Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; therap
immunomodulator;
                                                                                                                                                                                                                                     Disclosure; Page 19; 41pp; English
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                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte cell surface
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                                                                                                                                                                                                                                                                                                                                                  Lasky LA;
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89US-0315015.

91US-0808122.

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94US-0185670.
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257..315
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331..353
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159..192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label≖ EGF domain
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RESULT
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Best Local S
Matches 34
                                                                                                          22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
               Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   facilitates recovery improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Ser220 deletion mutant.
                                                      WPI; 1996-238773/24.
                                                                       Capon
                                                                                                                                                                                    07-MAY-1996
                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                  23-FEB-1989;
                                                                                                                                                                                                       US5514582-A
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                                                                                                                                                                                                                                                                                                                                                                                              metastasis
                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocyte
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Similarity 100.0%;
34; Conservative
                                                                      Lasky LA;
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                                                                                                          89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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354..37(
                                                                                                                                                                                                                                                                       /label=
258..315
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38..154
                                                                                                                                                                                                                                                                                                           /label=
159..192
                                                                                                                                                                                                                                                                                           196.
                                                                                                                                                                                                                         /label=
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                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                           cell
                                                                                                                                                                                                                                                                                                             . 192
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                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                                                                                                                                                                                          surface
                                                                                                                                                                                                                        Cytoplasmic domain
                                                                                                                                                                                                                                            Transmembrane
                                                                                                                                                                                                                                                             Complement binding
                                                                                                                                                                                                                                                                               Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                   EGF domain
                                                                                                                                                                                                                                                                                                                    Lectin domain
                                                                                                                                                                                                                                                                                                                                      Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 215; I
Pred. No. 3e-
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                              repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (HuLHR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                      inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                           variant.
                           the ligand - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Disclosure; Page 19; 41pp; English.

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RESULT
AAR98109
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
               23-FEB-1989;
                                             07-MAY-1996
                                                                        US5514582-A
                                                                                                                       Domain
                                                                                                                                                                               Binding-site
                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                              metastasis.
                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; transmembrane receptor; adhesion; targetting;
diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR98109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR98109 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymph cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is an Ile296 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A hybrid immunoglobulin chain comprising the ligand binding site
                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cqpwscsghgecveiinnhtcncdvgyygpqcql 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
               89US-0315015
                                                                                                                                                                                                             196.
                                                                                                                                                                                                                                         /label= Lectin domain 159..192
                                                                                                                                                                                                                                                                     /label= Signal region.
38..154
                                                                                                                       355
                                                                                                     /label= Cytoplasmic domain
                                                                                                                                                                                 258..316
                                                                                                                                                                                             /label= Complement
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                   /label= Transmembrane domain
                                                                                                                                                                 /label= Complement binding repeat
                                                                                                                                                                                                                            /label= EGF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                              ..257
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                                                                                                                                                    .354
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Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                               binding
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                                                                                                                                                                                             repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoylobulin super family, nor a multiple subunit polypeptide
cencoded by discrete genes. The hybrid immunoylobulin chain combines
the adhesion/targetting of a ligand binding partner (LBP) with the
ceffector functions of immunoglobulin and can bind to and/or activate
more than one ligand. It can be used diagnostically for the in
vitro assay of LBP and their targets; or therapeutically to deliver
CLBP such as toxins, enzymes, growth factors to particular cells.
Typical applications are as antiviral, neuromodulating and
immunomodulating agents, or as modulators of cell adhesion (e.g. in
treating graft rejection; inflammation; metastasis of lymphoma etc.)
The immunoglobulin component increases plasma half life and
cfacilitates purification while deletion of the transmembrane region
facilitates recovery, improves aqueous solubility and removes
potentially immunogenic epitopes. Variants of the human lymphocyte
cell surface glycoprotein described in AAR98106 are given in
ARP8109-R98135. This variant contains a Arg58-Asp59; Lys-Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                  Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane receptor without an extive transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to {\rm Ig} constant region - useful for diagnosis and treatment e.g. of inflammation
                                  Region
                                                                                    Homo sapiens
                                                                                                                    metastasis
                                                                                                                                                                                                          Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                            01-NOV-1996
                                                                                                                                                                                                                                                                                                            AAR98110 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 159 cqpwscsghgecveiinnhtcncdvgyygpqcql
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                 1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 215; DB 1
Similarity 100.0%; Pred. No. 3e-14;
34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lasky LA;
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                                                                                                                                                                                                                                          (first entry)
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
/label= Signal region 38..154
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                        inflammation
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Domain

AAR98111;

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AAR98111
ID AARS
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                                                                                                                                                                                                           RESULT
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                                                                                                                                                     Query Match
Best Local
                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                             A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
              AAR98111 standard;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 19; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capon
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                                                                                                                                                  Local
                                                                              1996-238773/24
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                                                                                                                                                   Similarity
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                                                                                                                                                                                                          371
                                                                                                                                     100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment e.g. of inflammation
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89US-0315015.
91US-0808122.
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332..354
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258..316
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196..257
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159..192
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              Protein;
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              371
                                                                                                                                      0;
                                                                                                                                  Score 215; DB 17
Pred. No. 3e-14;
0; Mismatches 0
              AA
                                                                                                                                                                17;
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                                                                                                                                                                Length
                                                                                                                                                                371;
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                                                                                                                                     Gaps
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immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98106. This variant contains an Lys786ln substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                       A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide considered the subunit polypeptide than th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidingnosis and treatment e.g. of inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; therap
immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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92US-0986931.
94US-0185670.
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89US-0315015
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332..354
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258..316
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196..257
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159..192
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Best Local
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                          Disclosure; Page 19;
                                                                                                                                     diagnosis and treatment e.g. of inflammation
                                                                                                                                                       Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region
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                                                                                                                                                                                                                                                                                                               ) GENENTECH INC.
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Similarity 100.0%;
34; Conservative (
                                                                                                                                                                                                                                                                    Lasky LA;
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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258..316
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332..35
/label= Transmembrane domain
355..371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell surface
                                                                                          41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic
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Pred. No. 3e-14;
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 22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                            07-MAY-1996
                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Aspli6Glu substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                  23-FEB-1989;
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89US-0315015.
91US-0808122.
92US-0986931.
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159..1
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38..154
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196..257
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                      Domain
                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                             metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98117 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a single
                                 Binding-site
                                                                                           Domain
                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 19; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1996-238773/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cqpwscsghgecveiinnhtcncdvgyygpqcql 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fused at its C-terminus with the N-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin chain comprising the ligand binding site transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0185670.
                                 /label=
196..257
                                                                                                                                                   /label= Signal region 38..154
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     py; drug delivery; antiviral; neuromodulator;
cell adhesion; graft rejection; inflammation;
/label= Complement binding repeat 1.
                                                                                                                       /label= Lectin domain
                                                                                           ..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                             EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 215; DB 1
Pred. No. 3e-14;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the ligand - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 11
AAR98118
ID AAR981
XX
AC AAR981
XX
DT 01-NOV
XX
DE Human

AAR98118;

AAR98118 standard;

Protein;

371

A

0

01-NOV-1996 (first entry)

Human lymphocyte cell surface glycoprotein (HuLHR) variant.

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                                                                             Query Match
Best Local
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                          Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Thr211ser substitution.
                                                                                                                                                                                                                                                                                                                                    encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a single transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 19; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                         a single transmembrane receptor without an active transmembrar region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5514582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
159 cqpwscsghgecveiinnhtcncdvgyygpqcql 192
                                                                                                                                                                                                                                                                                                                           LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                1 COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DJ,
                                                                Similarity 100 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin chain comprising the ligand binding site
                                                                                                                                                 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-0440625.
89US-0315015.
91US-0808122.
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94US-0185670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Complement binding repeat 332..354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Transmembrane domain 355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Cytoplasmic domain
                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                 0
                                                              Score 215; DB 1
Pred. No. 3e-14;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an active transmembrane
                                                                                              DB 17;
                                                                   0
                                                                                                Length
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the ligand - useful for
                                                                                                 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o
f
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Pred. No.

3e-14;

0;

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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                         immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                 Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
 Sequence
                                          potentially immunogenic epitopes. Vacell surface glycoprotein described
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                         facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                                                           A hybrid immunoglobulin chain comprising the ligand binding site
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidingnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5514582-A
                                                                                                                                                                                                                                                             a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis.
                           surface glycoprotein
109-R98135. This vai
                                                                                                                                                                                                                                                                                                                                                                                                                               1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasky LA;
   371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Transmembrane domain
355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .316
                             variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                             contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region
                             Phe214Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat 1.
                           are given in 4Leu substitution
                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                            of.
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Query Match

100.0%;

Score

215;

DΒ

17;

Length 371;

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RESULT 12
AAR98119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100 Matches 34; Conservative
                                                                                                                                                                                                                22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                         nucleic acid encoding hybrid immunoglobulin binding site of a receptor fused to Ig const diagnosis and treatment e a cf :-?
        A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the
                                                                                         Disclosure;
                                                                                                                                                      WPI;
                                                                                                                                                                         Capon
                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                              23-FEB-1989;
                                                                                                                                                                                                                                                                                                 07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                           Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                    US5514582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [mmunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                           and treatment e.g. of inflammation
                                                                                                                                                                        Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy;
                                                                                       Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                91US-0808122.
92US-0986931.
94US-0185670.
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89US-0315015.
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                                                                                                                                                                                                                                                                                                                                                                       /label=
332..354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane receptor; adhesion; targetting; apy; drug delivery; antiviral; neuromodulator; cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                         /label
258..3
                                                                                                                                                                                                                                                                                                                                                                                                             196.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Lectin domain
159..192
                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            'label= Transmembrane domain
o<sub>f</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                   371
                                                                                                                                                                                                                                                                                                                                                                       354
                                                                                                                                                                                                                                                                                                                                                                                         316
immunoglobulin
                                                                                                                                                                                                                                                                                                                                      Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                             Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                  Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                       EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein (HuLHR) variant.
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and
                                                                                                                     bulin comprising constant region
can bind
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and/or activate
                                                                                                                      the ligand - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 1
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Ser226Thr substitution.
Capon
                                                                                                                                                                                                                                                                                                       Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation;
                (GETH ) GENENTECH INC
                                                                                      23-FEB-1989;
                                                                                                      07-MAY-1996
                                                                                                                       US5514582-A
                                                                                                                                                  Domain
                                                                                                                                                                  Domain
                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                  metastasis.
                                                                                                                                                                                                                                                                                                                                           Human lymphocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more than one ligand. It can be used diagnostically for the in
                                                                                                                                                                                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 COPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                        cqpwscsghgecveiinnhtcncdvgyygpqcql 192
Ďď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 215; DB 1 larity 100.0%; Pred. No. 3e-14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                      89US-0315015
                                                                                                                                                                                                                      /label= Lectin domain
159..192
                                                                                                                                                                                   /label= Complement binding repeat 258..316
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                              /label-
                                                                                                                                                         'label
                                                                                                                                                                         'label - Complement binding repeat
                                                                                                                                                                                                            'label- EGF domain
                                                                                                                                                                                                                                                                                                                                           cell surface glycoprotein (HuLHR) variant.
                                                                                                                                        Cytoplasmic domain.
                                                                                                                                                          Transmembrane domain
                                                                                                                                                                                                                                              Signal region
                                                                                                                                                                                                                                                                                                                                                                                               371
                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
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                                                                                                                                                                                                                                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                    Sequence
Domain
                 Domain
                                                                     Domain
                                                                                                     Region
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                                                                                                                                                                                                                                                                                        159
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Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Phe244Met substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment {\rm e.g.} of inflammation
                                                                                Binding-site
                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; therapy; drug delivery; antiviral; neuromodulator;
immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98121;
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cqpwscsghgecvelinnhtcncdvgyygpqcql 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                        196.
                                                                                                                                                                                                                                                       /label= Signal
38..154
                          332..354
                                                                                258..316
                                                                                                                                                                                                 /label= Lectin domain
159..192
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..37
                                                                                                                                                                   /label=
/label=
                                                        'label-
                                                                                                                 /label=
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Transmembrane domain
                                                     Complement binding
                                                                                                           Complement binding repeat 1.
                                                                                                                                                                      EGF domain
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Pred. No. 3e-14;
Mismatches
                                                                                                                                                                                                                                                                                    region
                                                     repeat 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
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RESULT 1
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Best Local S
Matches 34
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
               diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Thr282Ser substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the subunit polypeptide encoded by discrete genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                              Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                             AAR98122 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
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                                                [mmunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                      h 100.0%;
Similarity 100.0%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
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91US-0808122.
92US-0986931.
94US-0185670.
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                                                                                                                                                                           Protein; 371
                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41pp; English.
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                      Score 215; DB 1
Pred. No. 3e-14;
; Mismatches
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                  inflammation
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CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL

Query Match Best Local S Matches 34

Similarity

100.0%;

Score 215; Pred. No. Mismatches

Вď 17; 0;

Length Indels

0;

Gaps

0,

34;

Conservative

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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                     Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc. The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                              immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                             facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymph cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Ile288Val substitu
                                                                                                                                                                                                                                                                                                  A hybrid immunoglobulir a single transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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Sequence
                                                                                                                                                                                                                                                                                    region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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89US-0315015.

91US-0808122.

92US-0986931.

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                                                            lymphocyte
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RESULT
AAR98123
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binding
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
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                                                                                                                                                                                                                                                        immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                         region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; dimmunomodulator; cell adhesion; graft rejection; inflammation;
                                        Typical applications are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98123 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                        hybrid immunoglobulin chain comprising the ligand binding site of single transmembrane receptor without an active transmembrane egion; fused at its C-terminus with the N-terminus of an member of the munoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding hybrid immunoglobulin comprising the ligand site of a receptor fused to Ig constant region - useful for % \left( 1\right) =\left( 1\right) +\left( 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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92US-0986931.
94US-0185670.
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89US-0315015
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258..316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= EGF domain
196..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159..192
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    agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane
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    or
    as
                                            antiviral, neuromodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein
    modulators
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    of
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Best Local
                                                                                         23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases in the immunoglobulin component increases facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR99106 are given in AAR9109-R88135. This variant contains a Lys298-Lys299; Arg-Arg
                   WPI; 1996-238773/24.
                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; therapy; drug
immunomodulator; cell adf
                                       Capon
                                                                               21-JAN-1994;
                                                                                                                                                                  07-MAY-1996
                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR98124 standard;
                                                          (GETH )
                                                                                                                         22-NOV-1989;
                                                                                                                                             23-FEB-1989;
                                                                                                                                                                                      US5514582-A
                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cqpwscsghgecveiinnhtcncdvgyygpqcql 192
                                       ď,
                                                          GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                      Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 AA;
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                               94US-0185670
                                                                                          91US-0808122
92US-0986931
                                                                                                               89US-0315015
                                                                                                                         89US-0440625
                                                                                                                                             89US-0315015
                                                                                                                                                                                                                                                                                                       /label=
159..192
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
l..37
                                      LA;
                                                                                                                                                                                                                                                                                                                            38..154
                                                                                                                                                                                                                              'label-
                                                                                                                                                                                                                                                    label-
                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                            'label=
                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                        oy; drug delivery; antiviral; neuromodulator; cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                          354
                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                          Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                 Lectin domain
                                                                                                                                                                                                                              Transmembrane domain
                                                                                                                                                                                                                                                  Complement binding repeat 2.
                                                                                                                                                                                                                                                                      Complement binding repeat 1.
                                                                                                                                                                                                                                                                                            EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 215; DB 1
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein (HuLHR) variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Nucleic acid encoding hybrid immunoglobulin comprising the ligand

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RESULT 1
AAR98129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
             US5514582-A
                                                         Domain
                                                                                                               Binding-site
                                                                                                                                             Binding-site
                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                  diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A hybrid
a single
                                                                                     Domain
                                                                                                                                                                         Domain
                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                         metastasis.
                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98129 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                                                                                             Immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell surface glycoprotein
AAR98109-R98135. This var
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the adhesion/targetting of a ligand binding partner (LBP) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment \mathbf{e}.\mathbf{g}. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acilitates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cqpwscsghgecveiinnhtcncdvgyygpqcql 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d immunoglobulin chain comprising the ligand binding site of
e transmembrane receptor without an active transmembrane
fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
A
                                                                                     /label=
331..35
                                                                                                               258.
                                                      /label= Transmembrane domain 354..370
                                                                                                                                                                       /label= Lectin domain 159..192
                                                                                                                                             196..
                                       /label= Cytoplasmic domain
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                             /label= Complement binding repeat 1.
                                                                                                                                                           /label=
                                                                                                                                                                                                                  /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This variant contains an
                                                                                  353
                                                                                                                .315
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                                                                                                                                             257
                                                                                                                                                           EGF domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 215; DB 1
Pred. No. 3e-14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ile302Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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Best Local
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                      Peptide
                                                                                                                                                 Human lyphocyte cell surface glycoprotein (LHR).
                                                                                                                                                                                     09-SEP-1991
                                                                                                                                                                                                                   AAR12469;
                                                                                                                                                                                                                                                  AAR12469 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Asn271 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                     Homo sapiens
                                                                                                Ligand binding partner; lbp; stable plasma protein; spp; antiviral; immunomodulatory; neuromodulatory; receptor mediated abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1996
                                                                                                                                                                                                                                                                                                                              160 cqpwscsghgecveiinnhtcncdvgyygpqcql 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-гев-1989;
                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                              1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-238773/24.
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 AA;
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
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Location/Qualifiers
20..32
/label= signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 215; DB 17;
Pred. No. 3e-14;
                                                                                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             371;
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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ARESULT 2
AARAZ2802
ID AARA
XX AARA
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CXX HOMC

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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The gene product may be used as a ligand binding partner in combination with a stable plasma protein eg. IgG1-IgG4, IgA, IgE, IgD or IgM. The fusion product is joined by N- or C-terminal groups, preferably the N-terminal of the Fc region of the spp is linked to the C-terminal of lbp. They may be used to provide antiviral, immunomodulatory and neuromodulatory treatment as well as in treatment of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
   Modified-site
                                 Modified-site
                                                              Modified-site
                                                                                             Modified-site
                                                                                                                            Modified-site
                                                                                                                                                       Modified-site
                                                                                                                                                                                      Region
                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                HuLHR; LHR; binding; endothelium; immunogens; graft; or
rejection; inflammation; rheumatoid arthritis; lymphoma
                                                                                                                                                                                                                                                                                                             Human lymphocyte homing receptor.
                                                                                                                                                                                                                                                                                                                                            01-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                            AAR22802;
                                                                                                                                                                                                                                                                                                                                                                                                           AAR22802 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 67pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid immunoglobulin(s) ligand binding molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQPWSCSGHGECVEIINNHTCNCDVGYYGPOCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1991-193202/26
                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 100.0%;
Similarity 100.0%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ12118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lasky LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 AA;
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0444625
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                             /note- "N
232..234
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/label=
                                                              /note= "|
216..218
                                                                                             /note- "I
                                                                                                                          /note= "!
104..106
                                                                                                                                                         /note=
60..62
   /note=
271..2
                                                                                                                                                                                    Location/Qualifiers 20..32
                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                      "N-glycosylation
                                                                                                                                                                    "potential signal sequence"
                "N-glycosylation site
                                             "N-glycosylation site"
                                                                           "N-glycosylation
                                                                                                          "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0

    for use as diagnostic reagents for
to treat organ and graft rejection

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 215; DB 1
Pred. No. 3e-14;
; Mismatches
                                                                                                                                       site"
                                                                                                          site"
                                                                             site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                organ;
                                                                                                                                                                                                                                                                    metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                    RESULT 2
AAR24026
ID AAR2
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 34; Conserv
                                                             Sequence of (HuLHR).
                                                                                                                                                                      AAR24026 standard;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
 Homo sapiens
                                                                                                            22-NOV-1992
                                                                                                                                         AAR24026;
                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR22803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lasky LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV OF CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        reduced side effects and better aq.
                                                                                                                                                                                                                                                160 cqpwscsghgecveiinnhtcncdvgyygpqcql 193
                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                  1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1992-123385/15
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                                                                                                                                                                                                                                                                                                                                                                                           372 AA;
                                                                           human
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0315015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "1335..357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-glycosylation site"
311..313
                                                                           lymphocyte
                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stachel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-glycosylation site!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                       372
                                                                                                                                                                                                                                                                                                             0;
                                                                           cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transfer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SE,
                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Singer MS,
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an EGF-like domain, a complement binding domain and a transmembrane domain. The protein contains 26 cystein residues. Cells transformed by the hLHR DNA are used to produce LHR (which mediates binding of lymphocytes to the endothelium of lymphoid tissue). LHR or its variants are useful as reagents for assaying LHR or anti-HR anti-bodies, to purify the antibodies, as immunogens, and therapeutically to compete with normal binding of lymphocytes (to prevent graft/organ rejection; to treat inflammation (such as rheumatoid arthritis or other autoimmune diseases); for control of lymphocyte metastasis, and to treat conditions associated with accumulation of lymphocytes). Derivs. and variants of LHR may be produced having modified properties, e.g. increased activity, longer plasma half-life,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein sequence was deduced from the DNA sequence obtd. by screening an oligo dT primed lambda gtl0 cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells, with a 2.2 kb EcoRI insert of the murine Mel 14 antigen cDNA clone. The protein contains regions encoding a carbohydrate binding domain,
Lyphocyte cell surface glycoprotein; ligand binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding at least one domain of lymphocyte homing receptor - useful for treating graft rejection, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 215; DB 1
Pred. No. 3e-14;
); Mismatches
                                                                                                                   surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solubility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane anchoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 2
AAR37960
ID AAR3
XX
AC AAR3
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                                                                                          Qy
                                                                                                                Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                         LHR mediates the binding of lymphocytes to the endothelium of lymphoid tissue. Full length cDNA clones and DNA encoding the human and the murine LHR (HuLHR and MLHR, respectively) have been identified and isolated (see AAQ24987 and AAQ24989). LHR is glycoprotein which contains the following protein domains: a signal sequence, a carbohydrate binding domain, and epidermal growth factor-like (egf) domain, at least one and preferably two complement binding domain repeat, a transmembrane binding domain (TMD), and a charged intracellular or cytoplasmic domain. LHR is used as the ligand-binding partner in fusion polypeptides with an immunoglobulin,
 AAR37960;
                                                                                                                                                                                                                                                                                                                                            Nucleic
binding
                  AAR37960 standard;
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1-1 - 1-3; 43pp;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                        Capon DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1989;
22-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                       160
                                         22
                                                                                 1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                     cqpwscsghgecveiinnhtcncdvgyygpqcql 193
                                                                                                                                                                                                                                                                                                                                                                                    1992-199589/24.
                                                                                                                34;
                                                                                                                                                                                                                                                                                                                                 acid encoding polypeptide fusions - comprising ligand partner protein and immunoglobulin chain, for use in is and therapy
                                                                                                              Similarity 100.
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                           AAQ24987
                                                                                                                                                                                      in
                                                                                                                                                                                                                                                                                                                                                                                                        Lasky LA;
                                                                                                                                                                  372
                                                                                                                                                                                      diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-0315015
89US-0440625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-0440625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
177..17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= see above
333..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= stop transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104..106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label=
                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..313
                                                                                                                       100
                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273
                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potential N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal
                                                                                                                                                                                     therapy
                                                                                                            ; Score 215; D); Pred. No. 3e-
0; Mismatches
                    372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    above
                    AA
                                                                                                                                                                                                                                                                                                             English.
                                                                                                                       215; DB 1
No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosylation
                                                                                                             0;
                                                                                                                                 Length
                                                                                                              Indels
                                                                                                                                 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site
                                                                                                             0;
                                                                                                             Gaps
                                                                                                             0;
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Claim 1;
                                                                                        Human and
                                                                                                       N-PSDB; AAQ43154
                                                                                                                                                              23-FEB-1989;
31-OCT-1991;
                                                                               rejection
                                                                                                                               Lasky
                                                                                                                                                                                       23-FEB-1989;
                                                                                                                                                                                                       01-JUN-1993
                                                                                                                                                                                                                       US5216131-A.
                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HULHR; lymphocyte binding inhibition; lymphoma metastasis; transplant rejection; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1993
                                                                                                               1993-188588/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                               ĮĄ,
                                                       Fig 1
                                                                             murine lymphocyte homing receptors to treat graft and inflammation - comprise carbohydrate binding,
                                                                       growth factor and complement binding
                                                                                                                               Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                        and
                                                                                                                                                              89US-0315015
91US-0786149
                                                                                                                                                                                      89US-0315015
                                                                                                                                                                                                                                                                                                                                                                      /Label= (
216..218
                                                                                                                                                                                                                                                                                                                                                       /note= "
232..234
                                                                                                                               SD,
                                                                                                                                                                                                                                              /note= "stop transfer sequence" 356..372
                                                                                                                                                                                                                                                                                                                       /note=
259..3
                                                                                                                                                                                                                                                                                                                                      /note=
246..2
                                                                                                                                                                                                                                                                                                                                                                                       /note=
197..2
                                                                                                                                                                                                                                                                                                                                                                                                      /label=
177..179
                                                                                                                                                                                                                                     /label= Cytoplasmic_Domain
                                                                                                                                                                                                                                                                       333..355
                                                                                                                                                                                                                                                                                       311..313
                                                                                                                                                                                                                                                                                                        /label= Complement_Binding_Repeat_2
271..273
                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
160..19
                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                       104..106
                                                                                                                                                                                                                                                                                                                                                                                                                                                             39..155
/label= Lectin_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Trp39 is probable N-terminus of mature LHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homing Receptor
                                                       Fig
                                                                                                                                                                                                                                                                                                                                     ce= "potential ..248
                                                                                                                                                                                                                                                                                                                                                                                                      .179
                                                                                                                                                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                      = "potential N-glycosylation site'
193
                                                                                                                               Singer
                                                       ω
••
                                                                                                                                                                                                                                                                                            "potential N-glycosylation site"
                                                                                                                                                                                                                                                                              "potential
                                                                                                                                                                                                                                                                                                                                                                                            "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                             "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                              "potential
                                                                                                                                                                                                                                                                                                                                                                            Complement_Binding_Repeat_1
                                                                                                                                                                                                                                                                                                                                                                                                              EGF_domain
                                                      32pp;
                                                                                                                               , SM
                                                      English.
                                                                                                                               Stachel SE,
                                                                                                                                                                                                                                                                            N-glycosylation
                                                                                                                                                                                                                                                                                                                            N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                            N-glycosylation site"
                                                                        domains
                                                                                                                               Yednock TA;
                                                                                                                                                                                                                                                                              site"
                                                                                                                                                                                                                                                                                                                                                                                             site'
                                                                                                                                                                                                                                                                                                                                                                                                                                             site"
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A human peripheral blood lymphocyte cDNA library in lambda gt10 was screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was isolated and sequenced. The ORF codes for 372 amino acids with a mol. wt. of approximately 42,200. Comparison of the HuLHR amino acid sequence with the murine LHR sequence (AAR37961) showed a high degree

lymphocyte mediate

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RESULT 2
ARR38908
AD ARR3
XX ARR3
XX ARR3
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                          23-FEB-1989;
22-NOV-1989;
16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; murine; lymphocyte; cell surface glycoprotein; homing receptor; LHR; endothelium; lymphoid tissue; signal; domain; complement binding; carbohydrate binding; epidermal growth factor-like; egf; intracellular;
New lymphocyte homing receptor immunoglobulin polypeptide(s) - used to inhibit binding of ly therapeutic and diagnostic uses
                                                                                                                       Capon
                                                                                                                                                                                                                                                              23-FEB-1989;
                                                                                                                                                                                                                                                                                              06-JUL-1993
                                                                                                                                                                                                                                                                                                                                US5225538-A
                                                                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HuLHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38908 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of amino acid conservation in each of the LHR domains, e.g. 96% in the transmembrane domain and 83% in the carbohydrate binding domain. The LHRs could be used to compete with the normal binding of lymphocytes to lymphoid tissue to treat inflammation or graft rejection. They could also be used to control lymphoma metastasis and to treat conditions involving lymphocyte accumulation.
                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
                                                                                     1993-226664/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LBPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cqpwscsghgecveiinnhtcncdvgyygpqcql 193
                                                                                                                       밍,
                                                                     AAQ44243.
                                                                                                                       Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding;
                                                                                                                                                                                        89US-0315015.
89US-0440625.
91US-0808122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                                                                                                                                                                                              89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
39..15
                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "1
160..193
                                                                                                                                                                                                                                                                                                                                                                                  333..355
/note- "Transmembrane binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 20..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                    197..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytoplasmic; ligand binding partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Lectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature protein"
                                                                                                                                                                                                                                                                                                                                                              "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complement factor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "egf domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 1
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                 lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                   Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96% in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
   RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAR38908-09 represent human and murine lymphocyte cell surface glycoprotein (LHR) respectively. These proteins mediate the binding of lymphocytes to the endothelium of lymphold tissue. LHR is a glycoprotein which contains a signal domain, a carbohydrate binding domain, an epidermal growth factor-like (egf) domain, at least one complement binding domain repeat, a transmembrane binding domain (TMD) and a charged intracellular or cytoplasmic domain. The murine and human amino acid sequences show a high degree of overall homology (83%), however degrees of homology between the various domains is variable. These proteins may be fused to a ligand binding partner protein (LBPP) which causes an increase in the half life of the LHR. The fusions may be caused therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue. They may be used in organ or graft rejection and for the treatment of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human LHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76506 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
   Domain
                                   Modified-site
                                                                   Modified-site
                                                                                                       Modified-site
                                                                                                                                                                        Modified-site
                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphocyte homing receptor; lymphocyte cell surface glycoprotein; LHR; ligand binding partner; immunoglobulin; constant region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig
                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Æ
                                   /label=
311..31
                                                                                                                                                                                                                                                                            /note=
60..62
                                                                                                                                                                                                                                                                                                            label= 1
39..334
                                                                     /label-
271..27:
                                                                                                                                                                                                           /label= N-glycosylation_site
177..179
                                                                                                                                                                                                                                            104.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 20..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; 44pp;
   /label = 1
                                                                                                                                                                         216..218
                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
/note= "hydrophobic domain,
                                                                                                                                                                                      /label = N-glycosylation_site
                                                                                                                       /label-
                                                                                                                                                        /label
                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulator.
                                                                                                                                                                                                                                                                                          "putative extracellular
                                                                                                                                                                                                                                                                                                                            Mat_protein
                                                  N-glycosylation_site
                                                                                    N-glycosylation_site
                                                                                                                                                      N-glycosylation_site
                                                                                                                                                                                                                                                          N-glycosylation-site
                                                                                                                      N-glycosylation_site
                 N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                            for insertion into reticulum lumen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 215; DB 1
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                              may act as signal the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                              domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372;
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0

Gaps

0,

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RESULT 2
AARB3050
ID AARB
XX AARB
AC AARB
AC Hunna
XX Lymp
KW Lymp
KW Immu
KW vect
XX Homc
XX Homc
FT Pept
FT Doma
FT Doma
FT Doma
FT Doma
FT Doma
                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                               뮹
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 34; Conser
   Domain
                                                                                                                Lymphocyte cell surface glycoprotein; immunoglobulin; IgG; constant region; vector; plasma-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                  Domain
                                               Domain
                                                             Domain
                                                                            Peptide
                                                                                                  Homo sapiens.
                                                                                                                                               Human LHR
                                                                                                                                                             31-JAN-1996
                                                                                                                                                                                                                                                                                                            cDNA library derived from obtd. from primary cells.
                                Domain
                                                                                                                                                                            AAR83050;
                                                                                                                                                                                          AAR83050 standard;
                                                                                                                                                                                                                                                                                                                      A murine Mel
cDNA library
                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig.la-1c; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                            half-life
                                                                                                                                                                                                                                                                                                                                                                 New hybrid ligand binding constant region sequences
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                              Capon
                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5428130-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                         25
                                                                                                                                                                                                                                     1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                                                                                                             cqpwscsghgecveiinnhtcncdvgyygpqcql 193
                                                                                                                                                                                                                                                                                                                                                                                              1995-240086/31.
                                                                                                                                                                                                                                                                                                                                                                                                              Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                         AAQ92802
                                                                                                                                                                                                                                                                                                372
                                                                                                                                                                                                                                                                                                                                                                                                              Lasky LA;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                             14 antigen cDNA clone was used to screen derived from human peripheral blood lymph rimary cells. A cDNA clone encoding LHR v
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
                              /label=
197..317
   /label= Complement_factor_binding_domain 333..55
/label= Transmembrane_binding_domain 356..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0315015
                                              /label= Carbohydrate_binding_domain 160..193
                                                             20..32
/label= Sig_peptide
39..155
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "putative domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                          Protein;
                              .317
                                                                                                                                                                                                                                                                  100.0%;
                                      Epidermal_growth_factor_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "putative intracellular region"
                                                                                                                                                                                                                                                                                                                                                                partner molecules - fused to increase stability and
                                                                                                                                                                                          372
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                          Score 215; DB 1
Pred. No. 3e-14;
Mismatches
                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stop
                                                                                                                        receptor-mediated disease;
                                                                                                                               LHR; transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transfer or membrane anchor
                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                              lymphocyte mRNA
LHR was isolated.
                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                 to
                                                                                                                                                                                                                                                                                                                            a lambda
                                                                                                                                                                                                                                                                                                                                                                immunoglobulin
vivo plasma
                                                                                                                                                                                                                                                                         372;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                            gt10
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          0;
RESULT 2
AAR98106
ID AAR9
XX
AC AARS
AC AARS
COMMON 31-C
XX
DE Huma
                                                                                                                                                           В
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Query Match 100.
Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
Human lymphocyte cell surface glycoprotein
                                                                                                                                                                                                                                                                                                                                  A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used to screen an oligo-dT primed lambda gtl0 cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells. A 2.2 kb clone (sequence given in AAT05869) was isolated that encoded the human LHR protein (AAR83050). LHR-IgG hybrids were constructed for use in the targeting of therapeutic moieties to lymphoid tissue.
                               31-OCT-1996
                                                             AAR98106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector encoding fusion protein t comprises receptor ligand binding site and treatment of receptor mediated disease
                                                                                          AAR98106
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT05869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-350776/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH
                                                                                                                                                                      160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5455165-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENENTECH INC
                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lasky LA;
                              (first entry)
                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0808122
92US-0986931
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89US-0315015
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271..273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= N-glycosylation_site 104..106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential stop transfer sequence" 60..62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-glycosylation_site
311..313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= N-glycosylation_site 248..248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216..218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label = N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Cytoplasmic_domain
                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-glycosylation_site
                                                                                                                                                                                                                                              .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycosylation_site
                                                                                          372
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                            Score 215; D
Pred. No. 3e-
); Mismatches
                                                                                          A
                                                                                                                                                                                                                                         3e-14;
                                                                                                                                                                     193
                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to increase plasma
d Ig constant region
(HuLHR).
                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region,
                                                                                                                                                                                                                                                          372;
                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       life
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                              0;
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immunoglobulin super family, nor a multiple subunit polypeptide
cencoded by discrete genes. The hybrid immunoglobulin chain combines
the adhesion/targetting of a ligand binding partner (LBP) with the
effector functions of immunoglobulin and can bind to and/or activate
concretant one ligand. It can be used diagnostically for the in
cylitro assay of LBP and their targets; or therapeutically to deliver
LBP such as toxins, enzymes, growth factors to particular cells.
Typical applications are as antiviral, neuromodulating and
immunomodulating agents, or as modulators of cell adhesion (e.g. in
treating graft rejection; inflammation; metastasis of lymphoma etc.)
The immunoglobulin component increases plasma half life and
facilitates purification while deletion of the transmembrane region
facilitates recovery, improves aqueous solubility and removes
contentially immunogenic epitopes.
Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A hybrid
a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5514582-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1996-238773/24.
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98106.
                                                                                                                    372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Figure 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lasky LA;
100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
197..258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Lectin domain.
160..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abel Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abel- Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
    0;
  Score 215; DB 1
Pred. No. 3e-14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat 1.
                                             17;
                                                                                                                                                                                                                                                                                                                                                                                             to and/or activate
                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the ligand
- useful fo
                                                                                                                                                                                                                                                                                                                                                                                                                                          combines
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RESULT 3
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region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver
                                                                                                                                                                                                                                                                            22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                 Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                           A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane
                                                                                                                             Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding-site
                                                                                                                                                                                                                                                                                                                                     23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                           07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                 US5514582-A
                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98133
                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                     Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                               89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                                                                                                                                                                                                     89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
333..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Signal region 38..154 /label= Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                            41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane domain
                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein (HuLHR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variant.
                                                                                                                                                              the ligand - useful for
                                                                                                                                                               for
                                                                                                      of.
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AAW37781
IID AAW
XX
AC AAW
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AC AAW
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DT 17-
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DE HOM
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DT 17-
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LTG
KW LTG
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ET PEF
FT REG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 34
22-NOV-1989;
23-FEB-1989;
19-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 209-Asn insertion.
                                                                                                                     23-FEB-1989;
                                                                                                                                                                                                  US5714147-A
                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphocyte treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1998
                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW37781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW37781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homing receptor; LHR; HuLHR; organ; graft; rejection; inflammatory disorders; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocyte homing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 20.33 /note= "potential si 60.62 /note= "potential N-104.106 /note= "potential N-177.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                       89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "F
                                                                                                                                                                                                                                                          /note=
335..3
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                                                                                                                                                                                                                                                                                           /note=
311..31
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271..27
                                                                                                                                                                                                                                                                                                                                                                                                              /note=
232..23
                                                                                                                                                                                                                                      /note=
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                                                                                                                                                                                                                                                          . 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                 .313
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                                                                                                                                                                                                                                                                                                                                                                                                                                "potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "potential signal sequence"
                                                                                                                                                                                                                                      "membrane
                                                                                                                                                                                                                                                                                                               "potential
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                                                                                                                                                                                                                                                                             "potential
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                                                                                                                                                                                                                                                                                                                                                                                            "potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis; control; lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 215; DB 1
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                      domain/stop transfer'
                                                                                                                                                                                                                                                                                                               glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g. in etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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AAW 77.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                 23-FEB-1989;
31-OCT-1991;
06-MAY-1993;
10-AUG-1995;
WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a human lymphocyte homing receptor (LHR) which may be used in the construction of a chimeric molecule comprising an LHR fused at its C terminus to the N terminus of an immunoglobulin constant region. This can be used for the prevention of lymphocyte attachment to endothelial cells. Such a method may be used for preventing organ or graft rejection, for treating inflammatory disorders, e.g. rheumatoid arthritis or other
                                                                                                                                                                                                                            lymphocyte arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases, for for treating conditions
                              Lasky
                                                  (REGC
                                                                                                                                   10-AUG-1995;
                                                                                                                                                       24-NOV-1998
                                                                                                                                                                           US5840844-A
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                       Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein; lymphocyte binding; endothelium; graft rejection; inflammation; therap
                                                                                                                                                                                                                                                                      Human lymphocyte homing receptor
                                                                                                                                                                                                                                                                                           02-FEB-1999
                                                                                                                                                                                                                                                                                                               AAW73264;
                                                                                                                                                                                                                                                                                                                                   AAW73264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prevention of lymphocyte attachment to endothelial cells - using chimeric molecule comprising lymphocyte homing receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-129805/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capon DJ,
                                                                                                                                                                                                                   lymphocyte accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin constant region
                                                             GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH
                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                    29
1999-034122/03
DB; AAV08321.
                              LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                 GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV19012.
                                                                                                                                                                                                                                                                                                                                  standard;
                              Rosen SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lasky LA;
                                                                                                                                                                                                                            autoimmune disease; lymphoma metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig
                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                  CALIFORNIA.
                                                                                                                                                                                                                                                                                          (first
                                                                                 89US-0315015.
91US-0786149.
93US-0059029.
95US-0513278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0451848
                                                                                                                                   95US-0513278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; 43pp;
                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for controlling lymphoma metastasis and ons in which there is an accumulation of
                              Singer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                    372
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                              NS,
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Pred.
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                               Stachel
                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                      193
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                               SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                       therapy;
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention. LHR is a lymphocyte cell-surface glycoprotein that mediates the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble LHR polypeptides, lacking signal peptide (amino acids 1-38), transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino acids 356-372), can be used therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue and are especially useful for organ or graft rejection treatment protocols, for treating inflammations such as arthritis and other autoimmune diseases, for control of lymphoma metastasis and for treating conditions involving lymphocyte accumulation. LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies or competitive inhibitors of LHR activity, and for purifying anti-LHR antibodies.
                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
22-NOV-1989;
23-FEB-1989;
                                        23-FEB-1989;
                                                                  07-MAY-1996
                                                                                           US5514582-A
                                                                                                                                   Domain
                                                                                                                                                             Domain
                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9661-AON-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98131 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the human lymphocyte homing receptor (LHR) of the invention. LHR is a lymphocyte cell-surface glycoprotein that medi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphocyte homing receptor polypeptides - useful for inhibiting lymphocyte binding to lymphoid endothelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Fig 1; 33pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%;
Similarity 100.0%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 89US-0440625
89US-0315015
                                      89US-0315015
                                                                                                                                                                                                                                                                  /label=
38..157
                                                                                                                                 /label= Transmembrane domain
358..374
                                                                                                                                                                                                                                       /label- Lectin domain 162..195
                                                                                                                                                                                       261..319
                                                                                                                                                                                               /label= Complement binding repeat
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                   /label= Cytoplasmic domain
                                                                                                                                                                      label Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                            cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                            'label- EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                              Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 2
Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AARPSULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           communication super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in the control of the same of their targets; or therapeutically to deliver the control assay of LBP and their targets; or therapeutically to deliver the control applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and capilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in the control of the control of the immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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08-DEC-1992;
21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                     diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                              metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98132 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capon DJ, Lasky LA;
                                                                                        Domain
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 100.0%;
Local Similarity 100.0%;
hes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cqpwscsghgecvelinnhtcncdvgyygpqcql 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 AA;
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92US-0986931.
94US-0185670.
                          38..157
/label= Lectin domain
162..195
                                                                                                                                                          Location/Qualifiers
1..37
                                                                                                                   /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 374 AA
                                                                                                                      Signal
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                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                               inflammation
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- useful for
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Domair

EGF domain

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RESULT 3
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AC AAR9
XX
AC OAR9
XX
DT 01-1
                                                                                                                                                                                                                                                                                 Вp
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                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                  encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation, metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery immoves account account of the transmembrane region
   01-NOV-1996
                                  AAR98134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                AAR98134 standard;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                             facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 83-Gly-Thr-Thr insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a single
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                                                                                               32
                                                                                                                                                                      1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL 34
                                                                                                                                    cqpwscsghgecveiinnhtcncdvgyygpqcql 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-238773/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DJ,
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d immunoglobulin chain comprising the ligand binding site of e transmembrane receptor without an active transmembrane fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lasky LA;
                                                                                                                                                                                                                                                                                   374
                                                                                                                                                                                                       Conservative
 (first entry)
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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335..357
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/label= C
261..319
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                                                               Protein;
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                                                                                                                                                                                                                    100.0%;
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                                                                374
                                                                                                                                                                                                     0;
                                                                                                                                                                                                                  Score 215; DB 17;
Pred. No. 3.1e-14;
                                                                AA
                                                                                                                                                                                                     Mismatches
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immunoglobulin super family, nor a multiple subunit polypeptide
cencoded by discrete genes. The hybrid immunoglobulin chain combines
the adhesion/targetting of a ligand binding partner (LBP) with the
effector functions of immunoglobulin and can bind to and/or activate
more than one ligand. It can be used diagnostically for the in
vitro assay of LBP and their targets; or therapeutically to deliver
LBP such as toxins, enzymes, growth factors to particular cells.
Typical applications are as antiviral, neuromodulating and
immunomodulating agents, or as modulators of cell adhesion (e.g. in
treating graft rejection; inflammation; metastasis of lymphoma etc.)
The immunoglobulin component increases plasma half life and
facilitates purification while deletion of the transmembrane region
facilitates recovery, improves aqueous solubility and removes
potentially immunogenic epitopes. Variants of the human lymphocyte
cell surface glycoprotein described in AAR98106 are given in
AAR98109-R98135. This variant contains a 241-Val-Glu-Asn insertion.
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                         A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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89US-0315015.
91US-0808122.
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159..192
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Sequence

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ARESULT 3
AAR98135
ID AAR9
ID AAR9
XX AAR9
AC AA hy
CCC A sit
CCC immu
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Best Local S
Matches 34
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                               A hybrid immunoglobulin chain comprising the ligand binding sit a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                  WPI;
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Region
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immunoglobulin constant region. The receptor is not a immunoglobulin super family, nor a multiple subunit poencoded by discrete genes. The hybrid immunoglobulin
                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                   Capon
                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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llarity 100.0%;
Conservative (
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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258..319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
38..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Lectin domain.
159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= EGF domain
196..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 AA
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                  on. The receptor is not a member o nor a multiple subunit polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 17;
Pred. No. 3.1e-14;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                   member of
                                                                                                                                                                 the ligand - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374;
                                                                                   site
   combines
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AAR98115
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Best Local :
                              22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; therapy;
immunomodulator; cel
                                                                                                                                                                 07-MAY-1996
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                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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 (GETH ) GENENTECH INC
                                                                                                                                 23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 AA;
                                                                                                                                                                                                                                                                                                                                                                                /label=
159..192
                                                                                                                                                                                                                                                                                                                                                                                                             /label=
38..154
                                                                                                                                                                                                                                               /label=
355..371
                                                                                                                                                                                                                                                                                   /label=
332..354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQL
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89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                 89US-0315015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      py; drug delivery; antiviral; new
cell adhesion; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                       Transmembrane domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lectin domain
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Pred. No. 3.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
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RESULT 35
AAR98116
ID AAR981
XX AAR981
XX INMUNO
DT 01-NOV
DT U1-NOV
XX IMMUNO
KW IMMU
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                                                                                             Binding-site
                                                                                                                                                                                 Binding-site
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immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98116 standard; Protein;
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a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin; transmembrane receptor; adhesion; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d immunoglobulin chain comprising the ligand binding site e transmembrane receptor without an active transmembrane fused at its C-terminus with the N-terminus of an entering the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lasky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                        /label= Complement binding repeat 1. 258. 316
                                                                                                                                                                                                                                                                     /label= Lectin domain 159..192
                                                                                                                                                                                                                                                                                                                                                     /label= Signal region 38..154
                                                                                                                                                                                          196
                                                /label= Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                         /label= EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yy; drug delivery; antiviral; neuromodulator;
cell adhesion; graft rejection; inflammation
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97.1%;
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Pred. No. 4.8e-14;
1; Mismatches 0;
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                                                                                                                                                                 AAR98114
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Best Local S
Matches 33
Immunoglobulin; transmembrane receptor; adhesion;
diagnosis; therapy; drug delivery; antiviral; neu
                                                                                                                                                                                                                                                                                                                                                                                                      effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogencie epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R08135. This variant contains an Asn181Gh substitution.
                                             Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                 01-NOV-1996
                                                                                                                  AAR98114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region, fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                           AAR98114 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5514582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin chain comprising the ligand binding site transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                            371 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Transmembrane domain. 355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Cytoplasmic domain
                                                                                                                                                                                                                                                                                                          97.2%;
97.1%;
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                         Score 209; DB 17;
Pred. No. 1.2e-13;
0; Mismatches 1
                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                                                                         Length 371;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                         Gaps
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Query Match
Best Local Similarity
Matches 33; Conserv
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08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                 Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an His168Cln substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-1989;
23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                          LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ک</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d immunoglobulin chain comprising the ligand binding site transmembrane receptor without an active transmembrane fused at its C-terminus with the N-terminus of an active transmembrane fused at its C-terminus of an active transmembrane with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lasky LA;
                                                                                                                                        371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 19; 41pp; English.
             Conservative
                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0808122
92US-0986931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0440625
89US-0315015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label - Complement binding repeat 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= EGF domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell adhesion; graft rejection; inflammation;
                                96.3%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane domain
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        Score 207; 1
Pred. No. 1.9
0; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The receptor is not a member of the
                                DB 17;
.9e-13;
                                                        Length 371;
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site
          0
        Gaps
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                                                         CC regulation of cellular proliferation. The compound comprises, a control of call and a nucleotide cyclic-3'-5' monophosphate attached to the linker group through a heterocyclic base. The bifunctional compounds can be used for regulating cell proliferation, cell adhesion and cell compounds can be used for treating e.g. tumours, neoplasty, cancer or inflammation. They can also be used to serve as immunosuppressants in corratin applications such as organ or tissue transplantation, as control of compounds can be used for provide immunosuppressants in corration and growth for new tissue. This can be useful in the repair can control and growth for new tissue. This can be useful in the repair control and growth for new tissue. This can be useful in the repair control and control of artificial tissue into the body. This can have beneficial effects in the treatment of burns or other replacement control are growth. The present sequence represents a human L-selectin control and con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-selectin; L-selectin; P-selectin; bifunctional molecule; regulation; binding; detection; cellular proliferation; cytostatic; cell adhesion; antiinflammatory; immunosuppressant; immunostimulator; cell migration; tumour; neoplasty; cancer; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a bifunctional compound for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel bifunctional compounds, used for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-072543/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freidman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human L-selectin amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY57762;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998;
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                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
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  196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60pp; English.
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Query Match

95.3%;

Score 205;

DB 21;

Length 196;

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AAR20815 for the major

form

of.

363; 0;

Gaps

0;

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Best Local
Matches
                     Two cDNA clones encoding Leu8 determinants were isolated from a human T cell library using the rapid immunoselection cloning method (see e.g. AAQ21164 for description of method). This protein sequence was deduced from the shorter insert. The weakly hydrophobic C-terminal domain is characteristic of surface proteins that are
attached to the cell membrane by phosphatidylinositol-substituted
                                                                                          Example
                                                                                                                 New CD53 cell surface antigen and DNA encoding it - for immuno-therapy and diagnosis of haematopoietic neoplasms,
                                                                                                                                                                                                                                  13-JUL-1990;
                                                                                                                                                                                                                                                         15-JUL-1990;
                                                                                                                                                                                                                                                                                23-JAN-1992
                                                                                                                                                                                                                                                                                                    WO9201049-A.
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                                                                                                                                                                                                           (GEHO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocyte-specific
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                                                                                                                                                                                     В,
                                                                                                                                                                1992-056864/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoselection cloning technique;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 97.0%; 32; Conservative
                                                                                          14; Page 106; 160pp; English.
                                                                                                                                                     AAQ22500
                                                                                                                                                                                                            GEN HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                  /note- "F
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285..28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-linked_glycosylation
/note= "putative"
230..232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-linked_glycosylation
/note= "putative"
157..159
                                                                                                                                                                                                                                                                                                                                                                                    /note=
299..3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 113..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                        269..27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= N-linked_glycosylation
/note= "putative"
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/note= "putative"
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/note= "putative"
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                                                                                                                                                                                                                                                                                                                                                                                    . 301
                                                                                                                                                                                                            CORP
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                                                                                                                                                                                                                                                                                                                           N-linked_glycosylation putative"
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1; Mismatches 0;
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covalent linkage to glycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surface antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                  etc.
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  RESULT 39
AAR91443
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Best L
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                                                                                                                                                                        01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
18-OCT-1993;
                                                        Cloning of cDNA encoding cell surface antigen of diagnostic and therapeutic proteins  \begin{tabular}{ll} \hline \end{tabular} .
                                                                                           WPI; 1996-200279/20
N-PSDB; AAT14723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; diagnosi antiinflammatory.
 2 cDNA clones isolated from
                                  Example 14; Column
                                                                                                                              Aruffo
                                                                                                                                                                                                                                              25-FEB-1988;
                                                                                                                                                                                                                                                                     09-APR-1996
                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell surface antigen;
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                                                                                                                                                  (GEHO ) GEN HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ21184 for the larger insert and Leu8 antigen that it encodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
 encoding
a human T
                                                                                                                                                                        92US-0983647.
88US-0160416.
89US-0379076.
99US-0553759.
93US-0139273.
                                                                                                                              в;
                                                                                                                                                                                                                                              88US-0160416
                                                                                                                                                                                                                                                                                                                            /label= 324..326
                                                                                                                                                                                                                                                                                                                                                  /label= Glycosylation_site
299..301
                                                                                                                                                                                                                                                                                                                                                                                                /label= Glycosylation_site
269..271
                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
156..158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Glycosylation_site
                                 71-74; 79pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; cloning; immunoselection; immunotherapy;
vector; Leu8 antigen; T-lymphocyte;
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                                                                                                                                                                                                                                                                                                                              .326
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97.0%;
   T-cell
          Leu8
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            determinants
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Pred.
library using
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                                 English.
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(AAR91442
ng a novel
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning method. The longer insert (AAT14723) contained 2,350 residues, while the shorter lacked 436 internal residues. A major transcript of 2.4 kb was present in peripheral blood mononuclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukaemic T-cell lines. Leu8 antigens can be obtd. For diagnostic and therapeutic use. The presence or absence of Leu8 on CD4+ T-cells identifies suppressor-inducer and helper-inducer CD4+ T-cell subsets. Soluble forms of Leu8 can act as antiinflammatory agents by reducing
The present sequence is that of a T-cell specific Leu8 antigen, as predicted from 1 of 2 clones (see AAA50632) isolated from a human T-cell library by the method of the invention. A longer Leu8 antigen is given in AAY96138. The method, designed to isolate cell surface antigen (CSA) cDNAs, is based upon transient expression of a CSA in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to (panning on) an antibody-coated substrate
                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stamenkovic I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunodiagnosis; diagnosis; immunotherapy; gene therapy;
immune disorder; infection; asthma; immune-complex disease;
amyloidosis; multiple sclerosis; inflammation; antiinflammatory.
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                                                                                                                                                                                                                            Column 69-72; 75pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosts and treatment of immune-mediated infections, diseases, and disorders in animals, including humans. These disorders include
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                    migration
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                                       CQPWSCSGHGECVEIINNHTCNCDVGYYGPQCQ
cqpwscsghgecveiinnytcncdvgyygpqcq
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                                                                                                Similarity
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                                                                              Conservative
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Q9UQV2	Q28769	Q28770	062837	Q9DC83	Q22328	060687	Q9H4R2	Q9U6I1	Q9J2M6	002839	Q923L3	Q29528	019122	Q99JA1	008569	Q921P0	Q96RM4	Q96QU9	Q16744	Q16745	Q29530	Q96JU7	Q91YB6	Q9H284	Q9VIU9	Q9NU87	Q9V560	Q917E4
qv2 homo s	769 papio	770 E	062837 saguinus oe	dc83	Q22328 caenorhabdi	687 h	4r2	611	Q9j2m6 macaca mula	002839 sus scrofa	23	5	片	9ja1 cavia	85	21p0 mus	rm4 homo	homo	744	745 homo	530 pan t	Q96ju7 homo sapien	lyb6 ratt	9h284 homo sap	9viu9 drosc	9nu87	560 dro	917e4

ALIGNMENTS

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RESULT

109UJ43

109UJ47

109UJ43

100UJ43

100U
pfam; pF00008; EGF; 1.
pfam; pF00059; lectin_c; 1.
pfam; pF00084; sushi; 2.
prints; pR00343; SELECTIN.
SMART; SM00032; CCP; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; pS00615; C_TYPE_LECTIN_1; 1.
pROSITE; pS50041; C_TYPE_LECTIN_2; 1.
pROSITE; pS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UJ43 PRELIMINARY;
Q9UJ43;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-DEC-2001 (TrEMBLrel. 19, L
L-SELECTIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000561; E
InterPro; IPR001304; I
InterPro; IPR002396; S
InterPro; IPR000436; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fieger C.B.;
Thesis (1998), Freie Universtiaet Berlin, Fachbereich Chemie.
EMBL; AJ246000; CAB55488.1; -.
HSSP; P14151; IKJB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-HEMATOPOIETIC Fieger C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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lectin_c.
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Sushi_SCR_CCP.
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Last annotation update)
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Best Local Similarity 80.3
Conservative
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Best I
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                                                                                                                 PRINTS; PRO0343; SELECTIN.
SMARR; SM00032; CCP; 2.
SMARR; SM00032; CCP; 1.
SMART; SM00031; CEGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; UNKNOW_1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                    Q28629 PRELIMINARY;
Q28629;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-DEC-2001 (TrEMBLrel. 19, L
L-SELECTIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
CHAIN
SEQUENCE
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EGF-like
                                                                                         CHAIN
                                                                                                          PROSITE;
EGF-like
                                                                                                                                                                                                                                                          Submitted (MAY-1995) to the | EMBL; U26535; AAA67896.1; -. HSSP; P14151; 1KJB.
                                                                                                                                                                                                                            InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
                                                                                                                                                                                                                                                                                    Qian J., Marks R.M.; "cDNA for rabbit L-selectin.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=KIDNEY CORTEX;
                                                                               SEQUENCE
                                                                                                  SIGNAL
                                                                                                                                                                                                                      InterPro; IPR000436;
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197
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        CEPLEAPELGTMDCTHPFGNESFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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PF00059; lectin_c; 1.
                                                                                                                                                                                           PF00084; sushi;
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31; Conservative
                                                                                                            domain;
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376 t
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                                                                                                                                                                                  sushi; 2.
SELECTIN.
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51 POTENTIAL.
5385 L-SELECTIN.
A; 43617 MW; 1205F691BA638EF1 C
                                                                                                   Glycoprotein; Lectin; 38 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
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                                                                                376
42346 MW;
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; lectin_c.
                                          81.7%;
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Last
                                 Score 599; DF Pred. No. 3.868; Mismatches
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L-SELECTIN.
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annotation
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les 18;
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Best Local
Matches 9
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Interpro; IPRO0336; Selectin_C.
Interpro; IPRO0236; Sushi_SCR_CCP.
IPRO0008; Sef; 1.
IPfam; PF00008; Sef; 1.
IPfam; PF00089; lectin_C; 1.
IPfam; PF00084; Sushi; 2.
IPRINTS; PR00343; SELECTIN.
IPFAMRT; SM00034; CCP; 2.
IPRINTS; SM00034; CCP; 2.
IPRINTS; SM00181; EGF; 1.
IPROSITE; PS00181; EGF; 1.
IPROSITE; PS00181; EGF; 1.
IPROSITE; PS00022; EGF; 1.
IPROSITE; PS00022; EGF; 1.
IPROSITE; PS00023; EGF; 1.
IPROSITE; PS00023; EGF; 1.
IPROSITE; PS00023; EGF; 1.
IPROSITE; PS00023; EGF; 1.
IPROSITE; PS000023; EGF; 1.
IPROSITE; PS000023
Q29097
Q29097;
01-NOV-1996
01-NOV-1996
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"Evidence of post-transcriptional r
expression in rat lymphoid cells.";
Immunology 85:198-204(1995).
EMBL; S79523; AAC60710.2; -.
HSSP; P14151; 1KJB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SPRAGUE-DAWLEY;
MEDLINE=95369821; PubMed=7543874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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Similarity 71.2%;
94; Conservative (
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                                                                                                 PRELIMINARY;
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1, Last annotation
N A.11.
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Pred. No. 1.6e-55;
5; Mismatches 23;
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Sciurognathi; Muridae;
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                O95508 PRELIMINATION OF THE PROPERTY OF THE PR
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EMBL; L39075, AAA79007.1; -.
EMBL; AF163766; AAF43272.1; -.
EMBL; AF163766; AF43272.1; -.
HSSP; P16109; IFSB.
InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP
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Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN.
SMART; SM00034; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
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PROSITE;
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SIGNAL 1 41 POTENTIAL.
CHAIN 42 646 P-SELECTIN.
SEQUENCE 646 AA; 71127 MW; 3863F4AFE09F0BB6 CRC64;
Homo sapiens (Human)
Eukaryota; Metazoa;
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Stocker C.J., Sugars K.L., Harari
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Mammalia; Eutheria;
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PS50041; C_TYPE_LECTIN_2;
PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
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    Chordata;
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EMBL/GenBank/DDBJ databases
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22; Mismatches
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    Vertebrata;
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    Euteleostomi;
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Sus.
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                                                                                                                                                                     ANTIGEN
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Best Local S
Matches 54
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95LG1 PRELIMINAKY;
Q95LG1;
O1-DEC-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 8.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCLP; 8.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1
PROSITE; PS00615; C_TYPE_LECTIN_2; 1
PROSITE; PS00041; C_TYPE_LECTIN_2; 1
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                       "Characterization of equine E-selectin.";
Immunology 103:498-504(2001).
EMBL; AF307972; AR488712.1; -.
Lectin; Selectin.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-21421234; PubMed-11529941;
Hedges J.F. Demaula C.D., Moore B.D.,
MacLachlan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Verto
Mammalia; Eutheria; Perissodactyla; Equidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like domain; Glycoprotein.
NON_TER 740 740
SEQUENCE 740 AA; 81390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL022146; CAA
HSSP; P16109; 1KJD.
                                                                                                                                                               SEQUENCE
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[1]
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                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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IPR002396;
IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOV-1998)
                                                                                                                                                               610
      Conservative
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CAA18143.1; -.
                                                                                                                                                               66191 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%;
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Selectin.
42.3%; Score 310; DB 6; 44.6%; Pred. No. 1.9e-28; 44.6%; Mismatches 51;
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19,
19,
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Last sequence update)
Last annotation updat
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Pred. No. 6e-2
21; Mismatches
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                                                                                                                                                                   F9D3DED12C445382
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No. 6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610
                                                                                                                                                                                                                                                                                                                                                       McLaughlin
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idae; Equus.
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                                                           Length 610;
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Best [
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                                                                                                                                                                                                                                                                               InterPro; IPR000561; EGF-like.
InterPro; IPR001304; lectin_c.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 1.
Pfam; PF00009; lectin_c; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
                                                                                                                                                                                                               PROSITE; PS00615;
PROSITE; PS00041;
PROSITE; PS00125;
PROSITE; PS01186;
EGF-11ke domain;
NON_TER 616
SEQUENCE 616 AA;
95507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O95509 PRELIMINARY; PRT; 616 AA.
O95509;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ780M13.1.3 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140
CD62, GMP140)) (ISOFORM 3) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1998) to the EMBL; AL022146; CAA18144.1; HSSP; P16109; IXJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia; 1
                                                320
                                                                   121
                                                                                       260
                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                        61
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                                                                                  CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                KAL
                                                                    QKL 123
                                                                                                                       CGELELPQHVLMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTNKPPQCLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                          PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 1.
                                                322
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                               42.2%;
nilarity 41.5%;
Conservative 2
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                 ΑĄ,
                                                                                                                                                                                                                         Glycoprotein.
616
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                               67736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                               Score 309; DB 4;
Pred. No. 2.5e-28;
3; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vo
Catarrhini;
                                                                                                                                                                                                               35CD4BFADE61D724 CRC64;
 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata;
i; Hominidae;
  ΑA
                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                  Length 616
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                                                                                                             Gaps
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RESULT Q28290
ID Q2
AC Q2
DT Q2
DT 01
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DT 01
DT 01
Ca CE
GN GM
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00561; EGF-like.
InterPro; IPRO0304; lectin_c.
InterPro; IPRO03396; Selectin_
InterPro; IPRO03436; Sushi_SCR_CCP.
InterPro; IPRO00436; Sushi_SCR_CCP.
InterPro; IPRO00436; Sushi_SCR_CCP.
InterPro; IPRO00436; Sushi_8.
InterPro; IPRO0084; Sushi_8.
InterPro; IPRO0084; Sushi_8.
InterPro; Interpro
                                                                                                                                                                                                                                                                                                               Q28290
Q28290;
Manning A.M., Sanders W.E.Jr. Rosenbloom C.L., Hawkins H.L., Beaudet A.L., Anderson D.C.;
                                                              SEQUENCE FROM N.A. TISSUE=SPLEEN;
                                                                                                                                                                                                                           01-NOV-1996 (TremBLrel.
01-NOV-1996 (TremBLrel.
01-DEC-2001 (TremBLrel.
CELL ADHESION MOLECULE I
                                                                                                                        Mammalia; Eutheria;
NCBI_TaxID=9615;
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                               Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                            GMP140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095507;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
DJ780M13.1.1 (SELECTIN P (GRANULE MEMBRANE E
CD62, GMP140)) (ISOFORM 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1998) to t
EMBL; AL022146; CAA18142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        KAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGELELPQHVLMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTNKPPQCLA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 40. 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 AA;
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.9%;
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. 01, Last sequence update)
. 19, Last annotation update)
PRECURSOR (FRAGMENT).
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2.1;
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Pred. No. 5.4e
24; Mismatches
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                                                                                                                                            Craniata; Ve; ; Fissipedia;
                                                                                                                                                                                                                                                                                                                                   PRT;
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Catarrhini; Hominidae.
                   Michael L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3B5F70A45B1A3CD4
                                        Kukielka G.L.,
                                                                                                                                                                                                                                                                                                                                   754
                                                                                                                                            Vertebrata;
ia; Canidae;
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                   M.L.,
                                                                                                                                            Euteleostomi; Canis.
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                     Smith
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Best Local Similarity
Matches 49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; 1.

Pfam; PF00084; sushi; 8.

PRINYS; PR00343; SELECTIN.

SMART; SM00032; CCP; 8.

SMART; SM00034; CLECT; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00181; ECF; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00041; GEF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 1.
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Q9GLF0;
O1-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                 Interpro; IPR000561; EGF-like.
Interpro; IPR001304; lectin_c.
Interpro; IPR002396; Selectin.
Interpro; IPR000236; Sushi_SCR_C
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
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SEQUENCE
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                                      PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                     Zheng L., Shi Y., Wu H., Zhang G.;
"Cloning and sequencing of beagle E-selectin genomic DNA comparison with other species.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF287257; AAG10039.1; -.
HSSP; P16581; IESL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases. EMBL; M88170; AAA63789.1; -. HSSP; P16109; 1FSB. InterPro; IPR000561; EGF-like. InterPro; IPR001304; lectin_c. InterPro; IPR002396; Selectin. InterPro; IPR000336; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-ENDOTHELIAL CELLS; Zheng L., Shi Y., Wu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of canine GMP140 and studies of expression model of myocardial ischemia/reperfusion.";
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; PR00343; SELECTIN.
SM00032; CCP; 6.
SM00034; CLECT; 1.
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754
82303 <sub>1</sub>
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16,
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                                                                                                                                                                           _SCR_CCP
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Last sequence update)
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CELL ADHESION MOLECULE.
; F0438EEAA521E773 CRC64;
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Canis.
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Best Local Similarity 40...
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Best Local S
Matches 52
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Q28657;
Q28657;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-DEC-2001 (TrEMBLrel. 19, L
                                                                                                                                                                                                            Submitted (OCT-1995) to the EMBL/GenB EMBL; U39446; AAABI385.1; -. HSSP; P16109; IFSB. InterPro; IPR000561; EGF-like. InterPro; IPR001304; lectin. InterPro; IPR002396; Selectin. InterPro; IPR000436; Sushi_SCR_CCP. InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Vora D.K., Fang Z., Liva S
Territo M.C., Berliner J.A.
"Induction of p-selectin b
"theroselerosis.";
                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS50042; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 1.
EGF-11ke domain; Glycoprotein; Lect:
SEQUENCE 649 AA; 71755 MW; ECCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00181; EGF; 4.
SMART; SM00001; EGF like; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS00022; EGF_1; UNKNOWN_1.
Lectin; Selectin.
SEQUENCE 609 AA; 66073 MW; 41E6
                                                                                                                                   PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                              Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
                                                                                                                                                                                                                                                                                                                                    atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                        Warden C.H.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-SELECTIN.
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52; Conservative
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Pred. No. 2.9e
18; Mismatches
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Last annotation updat
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                           Score 291;
Pred. No. :
                                                                     Lectin; Selectin ECCD8C847B84BC31
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.9e-27
                            .7e-26;
                                      DB 6;
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Best Local :
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01-DEC-2001
01-DEC-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
Lectin;
                                    "Characterization of equine E-selectin.";
Immunology 103:498-504(2001).
EMBL; AF307971; AAK48711.1; -.
                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=21421234; PubMed=11529941;
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Q95LG3;
01-DEC-2001
                                                                                                                                Hedges J.F., Demaula MacLachlan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-SELECTIN.
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"Characterization of equine E Immunology 103:498-504(2001).
EMBL; AF307970; AAK48710.1; --
Lectin; Selectin.
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Cervidae; Odocoileinae; Odocoileus.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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53; Conservative
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(TrEMBLrel. 19,
(TrEMBLrel. 19,
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Last sequence update)
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Pred. No. 3.1e-26;
9; Mismatches 48
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                                                                                                                                                                                                                                                                                                                                                          Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                 S.I.,
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                                                                                                              Query Match
Best Local
                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Best I
                                                                                                                                                                    Pfam; PF00008; EGF; 1.

Pfam; PF00059; lectin_c; 1.

Pfam; PF00084; sushi; 4.

PRINTS; PR00343; SELECTIN.

SMART; SM00032; CCP; 4.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS000186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                  PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                     "The intron-exon sta
Gene 176:67-72(1996)
                                                                                                                                                                                                                                                                                          InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                  EMBL; U37521; AAC48680.1; HSSP; P16581; 1ESL.
                                                                                                                                                                                                                                                                                                                                                                           Bach F.H.;
                                                                                                                                                                                                                                                                                                                                                                                   Winkler H.,
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=97075911; PubMed=8918234;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                  InterPro; IPR002396;
                                                                                                                                                                                                                                                                                                              InterPro; IPR000561;
InterPro; IPR001304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-SELECTIN
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119
                    300
                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028982;
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                                         60
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                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
ICQ
                                                                      CEPLEAPELGTMDCTH-PFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59
                              CDTVGHPQNGDVSCNHSSIGEFAYKSTCHFTCAEGFGLQGPAQIECTAQGQWTQQAPVCK
                   AVKCPAVSQPKNGLVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKCDALSNPDNGVVNCSQNHGSLPWNTTCMFECQEGYKLTGPQHLQCTSSGIWDNKQPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQAQKHPEHGHLVC-NPLGKFTYNSSCSISCAEGYLPSSTEAARCMSSGEWSTPLPKCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
49; Conserv
                                                                                                                                                                 domain;
                                                                                                                                                        482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Brostjan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                      Glycoprotein; Lectin; Selectin
A; 52341 MW; 97DC5D70BF115944
                                                                                                                                                                                                                                                                                                                                                                 structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniai
Cetartiodactyla;
                                                                                                              33.4%;
                                                                                                                                                                                                                                                                                                              EGF-like.
lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52951 MW;
                                                                                                                                                                                                                                                                                                                                                                                   c.,
                                                                                                                                                                                                                                                                                         Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                    Selectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.6%;
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01,
19,
                                                                                                                                                                                                                                                                                                                                                                                    Csizmadia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 275.5;
Pred. No. 1.9e
21; Mismatches
                                                                                                              Score 245; DB 6;
Pred. No. 8.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Veri
actyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617930C1C2F47B44 CRC64;
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                 porcine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
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ches 50;
                                                                                                                                                                                                                                                                                                                                                                                   Natarajan
                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                              E-selectin-encoding gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Suidae;
                                                                                                                                                       CRC64;
                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                   G.,
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi; Sus.
                                                                                                                                                                                                                                                                                                                                                                                   Anrather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484;
                                                                                                   2
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                            299
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Best Local Similarity
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00032; CCP; 34.
SMART; SM00181; EGF; 15.
SMART; SM00179; EGF_CA; 9.
SMART; SM00001, EGF_11ke; 3.
SMART; SM00159; PTX; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ES77 PRELIMINARY;
Q9ES77;
O1-MAR-2001 (TrEMBLrel. 16, C
O1-MAR-2001 (TrEMBLrel. 16, L
O1-DEC-2001 (TrEMBLrel. 19, L
POLYDOM PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0010; 1
PRINTS; PR00895; 1
PRINTS; PR00453; 1
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                              2140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilges D., Vinit M.-A., Callebaut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                              2200 PVSCNEPPKVENGFLEHTTGRTFESEARFQCNPGYKAAGSPVFVCQANRHWHSDAPLSCT 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001759; Pentaxin.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF206329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Polydom :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20517255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                               60
  70 DLGIMNCSHPL------ASFSFTSACTFICSEGTELIGKKKTICESSGIWS-NPSPI 119
                                                                                                                                                                                       1 CEPLEAPELGIMDCTHPFG-NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1928849;
                                                                                                                                              CIPVRCGEPPSIANGYPSGTNYSFGAVVAYSCHKGFYIKGEKKSTCEATGQWSKPTPTCH 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00008; EGF; PF02494; HYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -H., Vigon I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. 352:49-59(2000).
206329; AAG32160.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermal growth factor and von willebrand factor A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000742; EGF_2.
IPR001881; EGF_Ca.
IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000152; Asx_hydroxyl.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                         1
3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a secreted protein with pentraxin, complement control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; sushi; 33.
92; vwa; 1.
0010; EGFBLOOD.
0895; PENTAXIN.
0453; VWFADOMAIN.
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEDM
                                                                                                                                                                                                                                                                                                                                                            AA:
                                                                                                                                                                                                                                                                                                                                                                                                                              ASX_HYDROXYL; UNKNOWN_1.VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pentaxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polydom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11062057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.
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Rodentia;
                                                                                                                                                                                                                                                          26.2%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYR.
                                                                                                                                                                                                                                                                                                                                                            387391
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
MW; 8FBA8276E12293E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                    Score 192; DB 11;
Pred. No. 1.7e-13;
7; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3567
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                                                                                                                                                                                                                                      51;
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                                                                                                                                                                                                                                                                                  Length 3567;
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                      64;
                                                                                             PLSAP
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Burler G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Buryarktaroglu Lu., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Berraz C., Ferriera S., Fleischmann W.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glabart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lain X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mcherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherefi A.,
RA Reinert K., Reinighton K., Nursh K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Reinighton M., Skupski M.P., Smith T.,
RA Mann S.M., Wolfer E., Spradling A.C., Stapleto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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Q917E3;
Q917E3;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                 InterPro;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                             HSSP; P10998; IVVD.
FlyBase; FBgn0010114; hig.
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                                                              IPR003599; Ig.
IPR003006; Ig_MHC.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlaw R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barlaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Mattei B., Marphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
RA Shue B.C., Shen S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R., Wenter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wei
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Q917E4;
01-MAR-2001
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Fndnoterygota; Diptera; Brachycera; Musc
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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NCBI_TaxID=7227;
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HIG OR CG2040.
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SMART; SM00032; CCP; 4.
SMART; SM00409; IG; 1.
SEQUENCE 866 AA; 96747
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No. 3.9e-13;
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Ballew R.M., Basu A., Baxendale J., Bayakataroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Borkova D., Botchan M.R., Bouck J., Boven F., Davies P.,
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RA Borkova D., Botchan M.R., Bouck J., Boven F., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Boven F., Botchan M., Caller P.,
RA Borkova D., Botchan M.R., Bouck J., Boven F., Botchan M., Gloser K.,
RA Botchan M., Gabart M.M.,
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NCBI_TaxID=7227;
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR002396; Selectin.
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SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002396;
InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 TFICSEGTELIGKKKTICESSGIWSNPSPICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LEAPELGTMDCTHPFG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR CG2040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFKCQWGFKLTGPAQLDCEPSGVWSGPVPRCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNLTGIEETTCGPFGNWSSPEPTCQVIQCE--PLSAPDLGIMNCSHPLASFSFTSA---C 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IENNDSGTFTCTSPRGLTNSIAVVVATSTCPQLTEPLAPLKLRLEGNKLGQRAHYECPEG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  933 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104178
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ح
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hropoda; Tracheata; Hexapoda; Insecta;
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13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 183; DB 5;
Pred. No. 4.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
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Smith
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H.O.,
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RESULT
ID Q9
AC Q9
AC Q9
AC Q9
DT 00
DT 00
DT 00
DT 00
C DT 00
C DT D
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Limel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLedd M.P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., McLedd M.P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., McLedd M.P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., Mortis J., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McIkulov G., Milshina N.V., Mobarry C., Mortis J., McPherson D.L.,
RA McIkulov G., Milshina N.V., Wobarry C., Mortis J., McPherson D.L.,
RA McIkulov G., Milshina N.V., Mobarry C., Mortis J., McPherson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shlee B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Shen B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhug G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
DR EMBL; AB50860.1; -.

Brown H. Strong J.A., Landou J., Jane J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 46; Conser
                                                                                                                                                                                                                                                                                                                                             Q9NU87;
Q9NU87;
Q9NU87;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
DJ177p10.1.1 (H FACTOR 1 (COMPLEMENT) ISOFORM 1).
                                   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL049744; CAB70597.1; -. HSSP; P08603; 1HFH.
                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NU87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 1.
Pfam; PF00084; sushi; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP
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HSSP; P10998; 1VVD
                                                                                                                                           Bird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0010114; hig.
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                         NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFKCQWGFKLTGPAQLDCEPSGVWSGPVPRCK 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFICSEGTELIGKKKTICESSGIWSNPSPICQ 121
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   IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                             Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            958 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107027 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 183; DB 5;
Pred. No. 4.4e-13;
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT
Q9VIU9
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 RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mchulov G., Milshina N.V., Mobarry C., Morits J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morits J., Moshrefi A.,
RA Mentalov G., Milshina N.V., Mobarry C., Morits J., Moshrefi A.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stapleton M., Skupski M., Sauth T.,
RA Shue B.C., Stapleton M., Stong R., Sun E.,
RA Williams S.M., Woodaeq G., Worlds K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VIU9; PRELIMINARY;
Q9VIU9;
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG10186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG10186 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 KCVEI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTH----PFGNFS------FSSQCAFSCSEGTNLTG-IEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQCEPLSAPDLG--IMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00084; sushi; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00032;
CE 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.8%;
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16,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 173;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8F5B954C4B4FA454 CRC64
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.7e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Yao Q.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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RESULT
Q9H284
ID Q9
DT Q1
DT 011
DT 0
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9H284;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                            EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00084; sushi; 14.
Pfam; PF00095; wap; 1.
SMART; SM00032; CCP; 17.
SMART; SM00217; WAP; 1.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SEQUENCE 1653 AA; 180864 MW; 174E77756
                                                                                                                   Pfam; PF00084; sushi; SMART; SM00032; CCP;
                                                                                                                                                                                               Quantitative Analysis of mRNA Expression."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ EMBL; AF308289; AAG48257.1; -.
                                                                                                                                                                                                                                                                              Scanlan M.J., Gout Old L.J.;
                                                                                                                                                                                                                                                                                                                TISSUE=BREAST;
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TERMBLrel. 16, Created)
01-MAR-2001 (TERMBLrel. 16, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation updat
SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1490
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                                                                                                 SEQUENCE
                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1610
                                                                                                                                                                                                                                                          "Humoral Immunity to Human Breast Cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1550
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InterPro; IPR000566; Lipocln_cytFABP.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0032797; CG10186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEPLEAPELGIMDCTHPFGNFSFSS------QCAFSCSEGTNLTGIEETTCGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWSSAIPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARWSGGLPKCVQACSYPGTVISGRMSSVKFYYAIGESITFTCDAGLDLRGSKVLKCLKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IMNCSHP-----LASFSFTSA----CTFICSEGTELIGKKKTICESSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGEWSAPLPTCVEVQCDNPGAPQNGYAQGSAPYRAGDVVQFNCNPEYMMQGQPIIACQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGNWSSPEPTCQVIQCEPLSAPDLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CESVECGDI----PLGMGSNASSPRVSVLSREVGGRAAFSCASGYGLRGPAEAICNP
                                                                                                                                                                              P10998; 1VVD
  Similarity 31. 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                      IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1618
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                                                                                                                                                                                                                                                                                            Ι.,
                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
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                    23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.6%;
                                                                                                                                                                                                                                                                                              Stockert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i J.S., Zhan M., Zhang G. Zhong W., Zhou X., Zhu S Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.S.,
                                                                                                 MW;
    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
Score 172.5;
Pred. No. 3.6e
L8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 173; DB 5;
Pred. No. 1.3e-11
6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
MW; 174E7775C51FD60F
                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                               FD99724DE7C69B0B
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                                                                                                                                                                                                                                                                                                Gure
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Zhu S., '
                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
es 59;
                                                                                                                                                                                                                                                                                            A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                          Antigen
                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                      4;
                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                            Jaeger
                                                                                                 CRC64
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                                                                                                                                                                                                                                                        Definition
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, zhu
                                    Length
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                                                                                                                                                                                                                                                                                            D.,
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                                        481;
                                                                                                                                                                                                                                                                                                Chen
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Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76;
  9
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  Gaps
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RESULT
Q96JU7
        Qy
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Q91YB6
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Best Local
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Q91YB6;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ14964 FIS, CLONE PLACE4000581, MODERATELY S
FIBROPELLIN PRECURSOR.
     TISSUE=PLACENTA;
Isogai T., Ota T
Nishikawa T., Na
                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                     SEQUENCE FROM N.A.
                                                      NCBI_TaxID=9606;
                                                                                                                                                   Q96JU7;
                                                                                                                                                              Q96JU7
                                                                                                                                                                                                                                                                                                                                                                                   in tissues and isolated cells.";
in tissues and isolated cells.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AJ320522; CAC67513.1;
SEQUENCE 1236 AA; 140343 MW; 1AC89FFA28232
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER; Demborg T., Goetze O., Schlaf G.; Rat complement factor H: molecular cloning, in tissues and isolated cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, COMPLEMENT INHIBITORY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                               204 QCVEI
                                                                                                                                                                                                                                   119
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T.,
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                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
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                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
     a T., I
Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIID---
    Hayashi
i K., Sug
                                                                                                                                                                                                                                                                                                                                                23.1%;
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     shi K.,
Sugano
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Last sequ
Last anno
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Pred. No. 2
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Sciurognathi; Muridae
                                                                  Craniata; Va
Catarrhini;
     Sugiyama T.
S., Aotsuka
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                Т.,
                                                                             Vertebrata;
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                Otsuki
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                T.,
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                                                                             Euteleostomi;
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; Murinae; Rat
                Suzuki
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Best Local S
Matches 46
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Best Local S
Matches 42
                                              1432
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Q29530;
 1489
                                                                                                                                                      SEQUENCE
                                                                                                                                                                NON_TER
                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                        Pfam; PF00084; sush1; 30
SMART; SM00032; CCP; 30
                                                                                                                                                                                                                                                                                 J. Immunol. 153:691-700(1994).
EMBL; L24920; AAA51438.1; -.
HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                               MEDLINE-94292799; PubMed-8021505;
Birmingham D.J., Shen X.P., Hourcade D., Nicke
"Primary sequence of an alternatively spliced
for the 75,000 M(r) complement receptor expres
                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT RECEPTOR 1 (FRACMENT).
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"NEDO hamar cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027870; BAB55420.1; -.
SEQUENCE 1316 AA; 144524 MW; 80615BBA3A4F00A5 CRC64;
                                                                                                                                                                                                                                                                                                                      erythrocytes.
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                                                                                                                                                                                                                                                                       interPro;
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                                                                                                                                                                                                                                                 nterPro;
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                                                           CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT
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CEIISCEPPPTISNGDF----YSNNRASFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT
                    CQVIQCEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
                                             CGPPPEPFNGMV----HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI
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                                                                                            46;
                                                                                                        Similarity
                                                                                                                                                                                                  PS00133;
PS00087;
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IPRO00436; Sushi_SCR_CCP.
IPR000834; Zn_carbOpept.
0084; sushi; 30.
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2014
                                                                                           Conservative
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AA; 221281 MW;
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SOD_CU_ZN_1; UNKNOWN_1.
                                                                                                      22.9%;
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                                                                                                                                                                                                                                                                                                                                          X.P., Hourcade D., Nickells M.W., Atkinson an alternatively spliced form of CR1. Candio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                           16;
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                                                                                        Score 167.5; I
Pred. No. 7.4e
16; Mismatches
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Pred.
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Catarrhini;
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                                                                                                                                                     6D6C3A74D81F1DB9 CRC64;
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No. 3.
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nes 56;
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                                                                                           23;
                                                                                                                                                                                                                                                                                                                                             Candidate
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Q16745
Q16745;
Q1-NOV-1996
Q1-NOV-1996
Receptor.
SEQUENCE
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                           Pfam; PF00084; sushi; 30
SMART; SM00032; CCP; 30.
PROSITE; PS00133; CARBOY
PROSITE; PS00087; SOD_CU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the gene for the F allele of complement receptor type and sequence of the coding region unique to the S allele."; Immunol. 151:6214-6224(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=94065175; PubMed=8245463;
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Mammalia; Eutheria;
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                                                                                                       InterPro;
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                                                                                                                       InterPro;
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L117399
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                                                                                      IPR001424; SOD_CU_ZN.
IPR000436; Sushi_SCR_CCP
IPR000834; Zn_carbOpept.
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 AA;
                            CARBOXYPEPT_ZN_2;
SOD_CU_ZN_1; UNKNO
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Primates;
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в82FCB11C6B16635
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Best Local Similarity
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01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
COMPLEMENT RECEPTOR 1.
Homo Saniens 'n-----'
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Q16744;
Q1-NOV-1996 (TrEMBLrel.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=94065175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d sequence of the coding region unique to the S allele."; Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT
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L17420 AAB60695.
L17421 AAB60695.
L17423 AAB60695.
L17424 AAB60695.
L17425 AAB60695.
L17426 AAB60695.
L17427 AAB60695.
L17428 AAB60695.
L17429 AAB60695.
L17429 AAB60695.
L17429 AAB60695.
L17391 AAB60695.
L17391 AAB60695.
L17392 AAB60695.
L17392 AAB60695.
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L17393 AAB60695.
L17394 AAB60695.
L17395 AAB60695.
L17396 AAB60695.
L17397 AAB60695.
L17400 AAB60695.
L17400 AAB60695.
L17401 AAB60695.
L17402 AAB60695.
L17403 AAB60695.
L17403 AAB60695.
L17404 AAB60695.
L17406 AAB60695.
L17406 AAB60695.
L17407 AAB60695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQVIQCEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKDDQVGVWSSPPPRCISTNK 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS----GIWSNPSPICQKLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEIISCEPPPTISNGDF----YSNNRTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L17418; AAB60695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wong W.W.;
(JUN-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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AAB60695.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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   JOINED
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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No. 2.3
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nes 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                          Sun P.C., Uppaluri R., Schmidt A.P., Sunwoo J.B., Gollin S.M., Scholnick ("Transcript map of the 8p23 putative Genomics 75:17-25(2001).

EMBL; AY017307; AAG52948.1; -. SEQUENCE 3389 AA; 370293 MW; 53C:
                                                 2673
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21365705; PubMed=11472063;
Sun P.C., Uppaluri R., Schmidt A.P
                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CUB AND SUSHI MULTIPLE DOMAINS PROTEIN 1 SHORT FORM.
  2732 LPTCRVV-----
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                 Q96QU9
                                                                                                                                                                                                                                                                                                                                                                                                                                             2020
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00084; sushi; 37.
SMART; SM00032; CCC; 37.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L17410; AAB60695.1;

L17411; AAB60955.1;

L17411; AAB60695.1;

L17412; AAB60695.1;

L17413; AAB60695.1;

L17414; AAB60895.1;

L17415; AAB60895.1;

L17416; AAB60895.1;

L17417; AAB60895.1;

L17417; AAB60895.1;

L17417; AAB60895.1;

L17417; AAB60895.1;

L17417; AAB60895.1;
                      EPTCQVIQCEPLSAPDLGIMNCSHP-----
                                             EAPELGTMDCTHPFGN-----FSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDDQVGVWSSPPPRCISTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS----GIWSNPSPICQKLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQVIQCEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
                                                                                              Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2489 AA;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                                                                                                            21.8%; 26.4%;
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; Sushi_SCR_CCP.
; Zn_carbOpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%;
31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272846 MW;
NCSDPGFVENAIRHGQQNFPESFEYGMSILYHCKKGFHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125
                                                                                              Score 160; DB 4;
Pred. No. 1.1e-09;
7; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163.5;
                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEE11B53F2B4FAF6
                                                                                                                                                          53C3009FCD3ED76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 2
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                                                                                                                                                                                                         Pashia M.E.,
                                                                                                                                                                                               tumor
                     ----LASFSFTSACTFICSEGTELI 100
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                                                                                                                                                                                             suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                     Length 3389;
                                                                                              Indels
                                                                                                                                                                                                                      Quant E.C.,
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2778
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2779

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GSSALTCMANGLWDRSLPKC

120 2798

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Best Local S
Matches 37
                                                                                                                                         Query Match
Best Local S
Matches 42
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SEQUENCE FROM N.A.

MEDLINE=21365705; PubMed=11472063;

Sun P.C., Uppaluri R., Schmidt A.P., Pasl
Sunwoo J.B., Gollin S.M., Scholnick S.B.

"Transcript map of the 8p23 putative tum
Genomics 75:17-25(2001).

EMBL; AF333704; AAK73475.1; -.

EMBL; AF333704; AAK73475.1; -.

SEQUENCE 3508 AA; 382824 MW; 9268C3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q921PO PRELIMINARY; PRT; 390 AA.
Q921PO;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence up
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
SIMILAR TO DECAY ACCELERATING FACTOR 1.
                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC011314; AAH11314.1; -.
SEQUENCE 390 AA; 42637 MW; 3FB68595F07A67FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2779
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
CUB AND SUSHI MULTIPLE DOMAINS 1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96RM4;
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
   158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
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   CKKKSCPNPKDLDNGHINIPTG-ILFGSEINFSCNPGYRLVGVSSTFCSVTGNTVDWDDE
                                                                    CEPLEAPELGIMDCTH---PFGNFSFSSQCAFSCSEGINLIGIEETICGPFGN---WSSP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPTCQVIQCEPLSAPDLGIMNCSHP------LASFSFTSACTFICSEGTELI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 26.4
                                                                                                                                                42;
                                                                                                                                                Similarity 30.9
12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NCSDPGFVENAIRHGQQNFPESFEYGMSILYHCKKGFHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rođentia;
                                                                                                                                                                               21.4%;
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Pred. No. 1.1e
17; Mismatches
                                                                                                                                            Score 156.5;
Pred. No. 2.3e
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor suppressor region.";
                                                                                                                                                2.3e-10;
hes 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
.1e-09;
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                                                                                                                                                                                                                        DB 11;
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                                                                                                                                                Indels
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                        390;
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                                                                                                                                                15;
                                                                                                                                                Gaps
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Best Local :
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01-JUL-1997 (
01-JUL-1997 (
01-JUN-2001 (
                                                                                                                            Q99JA1 PRELIMINARY;
Q99JA1;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 272:12714-12722(1997).
J. Biol. Chem. 272:12714-12722(1997).
EMBL; U75654; AAC13888.1; -.
HSSP; P10998; 1VVD.
InterPro; IPRO00436; Sushi_SCR_CCP.
SEQUENCE FROM N.A.
TISSUE-EPIDIDYMIS, AND LIVER;
MEDLINE-21154058; PubMed-11254714;
Nonaka M.I., Wang G., Mori T., Oka
                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                        C4BPA.
                                                                                                                  C4BP ALPHA-CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000436;
Pfam; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "AM67, a secretory component of
is related to mouse sperm protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clson G.E., Kim K.S., Gerton G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-HARTLEY; TISSUE-TESTIS; MEDLINE-97284752; PubMed-9139729; Foster J.A., Friday B.B., Maulit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
aCROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008569
                                                          NCBI_TaxID-10141;
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                                                                                                                                                                                                                                                                                               FSSQCAFSCSEGTNLTGIEETTC---GPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIWSNPSPICQKLDKS 126
                                                                                                                                                                                                                                   GTDEDLYTYGSLVTYVCDPNYSLLGNASISCLVANKTVGVWSSNPPTCEKV
                                                                                                                                                                                                                                                                               FGSTIEFSCSKGYSLIGSTTSQCESQGKTVDWSDPLPECVIVKCD--SPPD--ISNGKHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPVCTEIHCPEPPKINNGIMRGESD--SYTYSQVVTYSCDKGFVLVGNASIYCTVSKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPTCQVIQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESS----
                                                                                                                                                                                                                                                         LAS---FSFTSACTFICSEGTELIGKKKTIC----ESSGIWSNPSPICQKL 123
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533 /
                                                                                                                                                                                                                                                                                                                             Conservative
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Last annotation update)
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Pred.
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ACROSOMAL MATRIX COMPONENT
EDBDDED487A45389 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                      Hystricognathi; Caviidae;
                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                           PRT;
   Okada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                             Mismatches
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.9e-10;
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   Nonaka
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the
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complement component 4-
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                                                                       Cavia.
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Matches 37
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Best Local
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000436; Sushi_SCR_CCP pfam; pF00084; sushi; 3. SMARR; SM00032; CCP; 3. NON_TER 222 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Virol. 71:6144-6154(1997).
EMBL; U87916; AAB66816.1; -.
HSSP; P10998; IVVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97366679; Pub. Hsu E.C., Dorig R.E., Richardson C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
MEMBRANE COFACTOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Virol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Artificial mutations
from human and monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  019122;
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J. Immunol. 166:4570-4577(2001).

EMBL; AB049465; BAB39737.1; -.

EMBL; AB049465; BAB39738.1; -.

EMBL; AB049467; BAB39738.1; -.

EMBL; AB049467; BAB39738.1; -.

EMBL; AB049467; BAB39738.1; -.

EMBL; AB049467; BAB39738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Callimico goeldii (Goeldi's marmoset)
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Pfam; PF00084; sushi; 8.
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                                                                                                                                                                                       GNFSFSSQCAFSCSEGTNLTGIEETTC---GPFGNWSSPEPTCQVIQCEPLSAPDLGIMN
                                                       GKHTLSDADVFEYLDAVTYTCDPAPGPDPFSLIGESTIYCRDNSVWSGDAPECKVVKCRF
                                                                                                                                                          GSYSFGNQLHFICNDGYYLIGKEILYCELKGSDAVWSGRPPICQKILCKP--PPE--INN
                                                                                                       CSHPLAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEDLYTYGSSVTYSCDPSYSLLGNPSISCTVVNKTVGVWSPSPPVCKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQCAFSCSEGTNLTGIEETTCGPFG----NWSSPEPTCQVIQCEPLSAPDLGIMNCSHPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SFSFTSACTFICSEGTELIGKKKTIC----ESSGTWSNPSPICQKL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKIEFSCSEGFNLVGPTTSVCEIHDKGVDWSVPFPICEIIKCR--SPPD--ISNGKHSGA
                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00032; CCP; 8.
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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14
555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                       222 AA;
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                  FSFTSACTFICS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9223509;
.E., Sarangi F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
555
61628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                         24523
                                                                                                                                                                                                                                                                                       21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and natural variations in the CD46 cells define regions important for
                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                          Score 154.5; DB Pred. No. 2e-10; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 155; DB 11;
Pred. No. 5.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
; 7AFA5462AFC7B6AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                       7CD336D0620CC0E9
                                                                                     -EGTELIGKKKTICESSGIWSNPSPICQKLDKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marcil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rtebrata; Euteleostomi;
Callitrichidae; Callimico.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update;
                                                                                                                                                                                                                                                            51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iorio
                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                                                                                         Length
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measles virus
                                                                                                                                                                                                                                                            15;
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                                                                                                                                                       107
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     δÃ
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
Sun P.C., Uppaluri R., Schmi
Sunwoo J.B., Gollin S.M., Sc
"Transcript map of the 8p23
Genomics 75:17-25(2001).
EMBL; AY017475; AAG54083.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q29528;
Q29528;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1363
                                                                            STRAIN=C57BL/6;
MEDLINE=21365705; PubMed=11472063;
                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                  01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                              Q923L3;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                         1419
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                       CSMD1.
                                                                                                                                                                                                                    CSMD1.
                                                                                                                                                                                                                                                                                              Q923L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1995) to t. EMBL; L39791; AAA62170.1; HSSP; P08603; LHFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation updat
COMPLEMENT COMPONENT RECEPTOR TYPE 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00032; CCP; 29.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_4

PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001424;
InterPro; IPR000436;
InterPro; IPR000834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemenza L., Subramanian Atkinson J.P.; "Primary sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                23 FSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPTCQVIQCEP---LSAPDLGIMNC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 39; Conserv
                                                                                                                                                                                                                                                                                                                            34
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                                                                                                                                                                                                                                                                                                                                                                     SNNRTSFHSGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGAWSSPPPRCISTNK
                                                                                                                                                                                                                                                                                                                                                                                                    SHPLASFSFTSACTFICSEGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  FGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKEAPICEIISCKPPPTISNGDF----Y
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                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                (TrEMBLrel.
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                                                                                                                                                                                                                                                                                              PRELIMINARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1911
A; 210174 MW;
                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOD_CU_ZN.
Sushi_SCR_CCP.
Zn_carbOpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.9%;
                                               Schmidt A.P., P
M., Scholnick S.
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19,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                 putative
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 153;
Pred. No. 3
                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                    ELIGKKKTICESS----GIWSNPSPICQKLDK
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                                  tumor
                                                             Pashia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                              A
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                                 suppressor region.";
                                                               м. Е.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1911;
                                                               Quant E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                        Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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RESULT
Q9J2M6
ID Q9
AC Q9
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Best Local S
Matches 38
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Best L
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Q9J2M6 PRELIMINARY;
Q9J2M6;
Q9J2M6;
Q1-OCT-2000 (TremBLrel. 15, 0)
O1-OCT-2000 (TremBLrel. 15, 1)
O1-DEC-2001 (TremBLrel. 19, 1)
COMPLEMENT BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                   EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JBC-2001 (TrEMBLrel. 19, Last annotation updat
PORCINE MEMBRANE COFACTOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            002839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2733
                                                                                                                                                                                                                                                                                                                                                                         Toyomura K., Fujimura T., Murakami
Inoue N., Takeda J., Kinoshita T.;
"Molecular cloning of a pig homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                             InterPro; IPR000436; Pfam; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97343414; PubMed=9199970;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  (CD46).";
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                   166
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Local (
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                                                                                                          WSSDPPECK
                                                                                                                                                                                                                                                                                                                                           Immunol. 9:869-876(1997).; D70897; BAA20476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEPLEAPELGIMDCTHPFGN------FSFSSQCAFSCSEGINLTGIEETTCGPFGN
                                                                                                                                                                                           CSNLPDPLNGQV--SYPNGDMLFGSKAQFTCNTGFYIIGAETVYCQVSGNVMAWSEPSPL 165
                                                                                                                                                                                                                CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVPI-----TCGHP-GNPAHGLTNGTEFNLNDLVNFTCHTGYRLQGASRAQCRSNGQ
                                                                                                                             WSNPSPICO
                                                                                                                                                  CEKILCKPPGEIPNGKYTNSHK-DVFEYNEVVTYSCLSSTGPDEFSLVGESSLFCIGKDE
                                                                                                                                                                       CQVIQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGT----ELIGKKKTICESSGI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSSPLPICRVVNCSDPGSVENAVRHGQQNFPESFEYGTSVMYHCKTGFYLLGSSALTCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSSPEPTCOVIOCEPLSAPDLGIMNCSHPL-ASFSFTSACTFICSEGTELIGKKKTICES
                                                                                                                                                                                                                                                                                                                                   P10998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGLWDRSLPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
35; Conser
                                                                                                                                                                                                                                                                                                    SM00032;
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3564
                                                                                                                                                                                                                                                                                          363 AA;
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                   BAA20476.1;
1VVD.
                                                                                                            233
                                                                                                                                                                                                                                                                                                     CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Ver
Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                          39692 MW;
                                                                                                                                                                                                                                               20.8%;
                                                                                                                                                                                                                                                                                                                       Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 78;
                                                                                                                                                                                                                                                                                                                                                                          pig homologue
                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
              Last
Last
                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                               Score 152.5; DB 6
Pred. No. 6.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                         8A5FF329B8E03153 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                      Mismatches
            sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70824C55B0674609
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No. 7
                                                                                                                                                                                                                                                                                                                                                                                               Η.,
                                                      395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                             of membrane
                                                                                                                                                                                                                                                                                                                                                                                                Natsume
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
ina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
'.7e-09;
es 59;
                                                      Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3564;
                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                           cofactor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                Shigehisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2783
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RESULT OF THE PROPERTY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Ma
Best Loc
Matches
Query Match
Best Local :
                                                                                                                               PRINTS; PROC.
PRINTS; SM00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U6I1
Q9U6I1;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                        NON_TER
                                                                                                                                                                                                            Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF185289; AAF03885.1; -. FlyBase; FBB9n0014574; Dana\fw. InterPro; IPR002396; Selectin. InterPro; IPR002396; Selectin. Company Selectin. InterPro; IPR00436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                Marsh B.J., Chen Y., Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΞW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00084; sushi; 4.
SMART; SM00032; CCP; 4.
PROSTTE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 395 AA; 43922 MW; B4C9C6F2E226AE06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF210726; AAF59982.1; -. HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The primary sequence of rhesus monkey rhadinovirus i sequence similarities to Kaposi's sarcoma-associated rhesus monkey rhadinovirus isolate 17577.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MACACA MULATTA RHADINOVIRUS MEDLINE=20173730; PubMed=10708456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta rhadinovirus 26-95. Viruses; dsDNA viruses, no RNA stage; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                  ananassae."
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila ananassae (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FURROWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rhesus monkey rhadinovirus iso
J. Virol. 74:3388-3398(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001230; Prenyltn.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desrosiers R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alexander L., Denekamp L., Knapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKYYPVQEFYNYLETITFTCNKDFSLIGNTTTTCMTNGTWSSPVPKCQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CS-HPLASF-SFTSACTFICSEGTELIGKKKTICESSGIWSNPSPICQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKFGSNITYKCNTGYLLLGATVRTCLLKYDSNLVDWQPAAPTCEIEKCK--KQPD--IEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSFSSQCAFSCSEGTNLTGIEETTC-----GPFGNWSSPEPTCQVIQCEPLSAPDLGIMN
                                                                                                                                                                     PF00084; sush1; 6.
S; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 31.8
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRAGMENT).
                                                                               354
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13,
) (TrEMBLrel. 13,
L (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                      Ā
                                                                                                                                                     CCP;
                                                                                    354
38526
20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%;
                                                                                                                                                     <u>ه</u>
                                                                                                                                                                                                                                                                                                                                                  Stephan W.; ral Selection
                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Score 151.5; DB Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 152.5; DB 1
Pred. No. 6.9e-10;
8; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                      AD02699F25DF9CAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                    and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Auerbach M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                À
                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexapoda; Ins
a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                       Flow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                    ĺ'n
                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
                      354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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Matches

Similarity

Conservative

19;

Mismatches

Indels

15;

Gaps

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Вb
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Q9H4R2
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                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
SEQUENCE FROM N.A.
Kurosawa H., Inukai T., I
Rakestraw K.M., Naeve C.W
Submitted (APR-1998) to ti
                                                                                                                            060687;
060687;
01-AUG-1998
01-AUG-1998
01-JUN-2001
                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                        SRPUL.
                                                                                                                    SUSHI-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001128; Cyt_P450.
InterPro; IPR003410; HYR.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCP; 3.
                                                            NCBI_TaxID=9606;
                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TremBLrel. 16, Created)
01-MAR-2001 (TremBLrel. 16, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
BA524D16A.1 (SUSHI-REPEAT-CONTAINING PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL391688; CAC16060.1; -.
InterPro: TDBOALLACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9H4R2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9H4R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
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                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38
                                                                                                                                                                                                                               PFITSGTYTCTNGVL---LDSRCDYSCSSGYHLEGDRSRICMEDGRWSGGEPVCVDID 125
                                                                                                                                                                                                                                                   SAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPICQKLD
                                                                                                                                                                                                                                                                         GEATCYSPKGGNYHSSLGTRCELSCDRGFRLIGRRSVQCLPSRRWSG-TAYCRQMRCHAL
                                                                                                                                                                                                                                                                                              GTMDCTHPFG---NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQVIQCEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDASPKCEEI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNPSPICQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PICEYIDCGPI----LPIPYGGHKYVTNSTYVGSEVVFSCTQSHNLSGVVKRQCLESGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTCQVIQCEPLSAPDLGIMNCSHPLASFS--FTSACTFICSEGTELIGKKKTICESSGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAPVCELVTCEMPPVPPGSYVVGYDYNVHSKIKYSCDPGHIMHGISDLECLDSGEWSTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAPELGTMDCTHP---
                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                            B (TrEMBLrel. 07,
B (TrEMBLrel. 07,
l (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                            410
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human).
letazoa; Chordata;
ltheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                    PROTEIN
                                                                                                                                                                                                                                                                                                                                                                            ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                            46781 MW;
                                                                                                                                                                                                                                                                                                                   20.7%; Score 151.5; DB 4; 29.7%; Pred. No. 9.4e-10; tive 13; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FG-NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPE
     Inaba T., Goi K., Chang .W., Look T.A.; the EMBL/GenBank/DDBJ da
                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                     Craniata; Vo
Catarrhini;
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                           D32228E1AA1AF370 CRC64;
                                                                                                                                                                         465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410
                                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                          DB 4;
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InterPro; IPR003410; HYR.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF002494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCP; 3.
SMART; SM00032; CCP; 3.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                  "Direct Submission.";
Submitted (JUL-2001) to tl
EMBL; U53344; AAA96225.1;
HSSP; P10998; IVVD.
                                                                                                        Hypothetical protein SEQUENCE 560 AA;
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SMART; SM00032; CCP; 7.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 61.6 KDA PROTEIN.
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Science 282:2012-2018(1998).
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	human leukocyte a es and neutrophil	baldi A., Spertir human leukocyte a .es and neutrophil	; plogue of the murine	of the Mel-14 lymph	T.J., Demetri G.D., Adler D. Tization of cDNAs encoding a blecule, LAM-1. Homology with	e homing receptor: tion domains."; 62-5566(1989).	Vertebrata; ; Hominidae;	ed) sequence update) annotation update) node homing receptor) (Leukocy yte surface antigen Leu-8) (TO) adhesion molecule 1) (LECAM1)	372 AA.	ALIGNMENTS	PPO WIN WAN MAN CCV CCV CRO MAN MAN MAN MAN MAN MAN
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3D-STRUCTURE MODELING

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EMBL; M25280; AAC63053.1; EMBL; X16150; CAA34275.1; -
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EMBL; M32414; AAB60700.1; J
EMBL; M32405; AAB60700.1; J
EMBL; M32406; AAB60700.1; J
EMBL; M32409; AAB60700.1; J
EMBL; M32409; AAB60700.1; J
EMBL; M32410; AAB60700.1; J
EMBL; M32412; AAB60700.1; J
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SMART; SM00101; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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Biochem. Blophys. Res. Commun. 216:1018-1023(1995).
-!- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHER
                                                                                                                                                                                         Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin; Selectin; Signal; Sushi; Repeat; 3D-structure.
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InterPro; IPR000436; S
InterPro; IPR001304; 1
Pfam; PF000008; EGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane prote SIMILARITY: TO OTHER SELECTINS/LECANS. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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PF00084; sushi; 2.
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                Query Match
Best Local
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                                                                          SEQUENCE FROM Budman J.I., F Tsurushita N.;
                                                                                                                                                                        LEM1_PANTR
Q95237;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                 Eukaryota;
                                                                                                                             SELL.
                                                                                                    NCBI_TaxID=9598;
                                                                                                                Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
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                                                                                                           Mammalia; Eutheria;
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Institute
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D -> Y (I
F -> D (I
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Pred. No. 7
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Bioinformatics
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> S (IN REF. 3).
> F (IN REF. 4).
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MEDIATE THE
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Pfam; PF00084; sushi; 2.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CLECT; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                            CARBOHYD
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                     CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                      QKLDKSFSMIKE 132
                                                                                             IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                          CEPLEAPELGTMDCTHPLGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                   IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
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IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
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SUSHI 1.
SUSHI 2.
SUSHI 2.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                               Score 727; DB Pred. No. 7.5e 0; Mismatches
                                                                                                                                                                  0;
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BY SIMILARITY.
L-SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                          727;
No. 7
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.5e-64;
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3 CRC64;
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    PRINTS; PRO0343; SELECTIN.

SMART; SM00032; CCP; 2.

SMART; SM00034; CLECT; 1.

SMART; SM00018; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS01186; EGF=2; 1.

PROSITE; PS01186; EGF=2; 1.

PROSITE; PS01186; EGF=2; 1.

PROSITE; PS0041; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
                                                                                                                                                                                                                                                                                                   Pfam; PF00008; Pfam; PF00059; Pfam; PF00084;
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Q95235;
Q1-NOV-1997
                                                                                           DOMAIN
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InterPro;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAN-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                                             TRANSMEM
                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Budman J.I., Fu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                              Selectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsurushita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a seen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                IPR000561; I
IPR002396; S
IPR000436; S
IPR001304; I
                                                                                                                                                                                              Signal;
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                                                                                                                                                                                               Sushi;
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Primates;
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Sushi_SCR_CCP.
lectin_c.
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BY SIMILARITY.

BY SIMILARITY.

L-SELECTIN.

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

C'TOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM).

EGF-LIKE.

SUSHI 1.

SUSHI 2.

BY SIMILARITY.

BY SIMILARITY.
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Catarrhini;
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i; Hominidae;
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01-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1) (LECAM1) (CD62L).
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SEQUENCE
                     InterPro;
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                                                                                                                                                                                                                                                                               SEQUENCE FROM Budman J.I., F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACMU
           InterPro;
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                                                                                                                                                                                                                                                                                                                           Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
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Local
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                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                    FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADJOF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
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                                                    U73730; AAB18246.1;
P14151; 1KJB.
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                                                                                     an
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and this statement
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IPR002396;
IPR000436;
IPR001304;
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                                                                                                                                                                                                                                                                                                                            Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328
          ; EGF-like.
; Selectin.
; Sushi_SCR_CCP.
; lectin_c.
                                                                                                                                                                                                                                                                                Johnson C.E.,
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SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
                                                                                                                                                                                                _PAPHA
                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAW-1) (Leukocyte-endothelial cell adhesion molecule 1)
(LECAM1) (CD62L).
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SEQUENCE
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CARBOHYD
Cercopithecinae;
               Mammalia; Eutheria;
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92.48;
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SUSHI 2.
SUSHI 2.
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Pred. No. 3e-60;
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CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
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BY SIMILARITY.
               Catarrhini;
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EXTRACELLULAR
                               Craniata;
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                               Vertebrata; Euteleostomi;
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              Cercopithecidae,
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pfam; pr00059; lectin_c; 1.
pfam; pr00084; sushi; 2.
prnyrs; pr00343; SELECTIN.
SMART; SM00034; CCEC; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
PR0SITE; ps00022; EGF_1; 1.
pr0SITE; ps001186; EGF_2; 1.
pr0SITE; ps0014; C_TYPE_LECTIN_1; 1.
pr0SITE; ps00041; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycopi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97128794; PubMed=8973334;
Tsurushita N., Fu H., Berg E.L.;
"PCR cloning of the cDNA encoding baboon L-selectin.";
Gene 181:219-220(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENULES IN PERIPHERAL LYMPH NODES.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
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IPR001304;
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IPR002396;
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CYTYPE LECTIN (SHORT FORE
EGF-LIKE.
SUSHI 1.
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY GICLARC. . . ) (!
N-LINKED (GLCNAC. . . ) (!)
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BY SIMILARITY.
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Matches
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InterPro;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (Leukocyte-endothelial cell adhesion molecule 1)
                                                                                                                                                                                       EMBL; X62882; CAA44676.1; HSSP; P14151; 1KJB.
                                                                                                                                                                                                                                                                                                                                                                              This
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"Bovine L-selectin: a peripheral lymphocyte homing receptor.";
Vet. Immunol. Immunopathol. 37:201-215(1993).
-i- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94055053; PubMed=7694420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SELL.
Bos taurus
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                 PRINTS;
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Bovidae; Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest
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QKLDRSFSMIKE 328
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sushi; 2.
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                                                                                                   lectin_c.
                                                                                                                       Selectin.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                  institutions as long as its content
                                                                                                                                                                   EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%;
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370
                                                                                                                                                                                                                                                                      (See http://www.isb-sib
                                                                                                                                                                                                                                                                                          Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chords
Mammalia; Eutheria; Rodent
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                         RAT
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DOMAIN
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TRANSMEM
DOMAIN
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SMART; SM
PROSITE;
PROSITE;
                                                                                                     ILEM1_RAT STANDARD; PRT; 372 AA.

p30836;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (LY-22) (Lymphocyte surface MEL-14 antigen)
(Leukocyte-endothelial cell adhesion molecule 1) (LECAM1) (CD62L).

SELL OR LNHR OR LY-22.

SELL OR LNHR OR LY-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
CHAIN
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PROSITE; PS00015; EGF_2; 1.

PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selectin;
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                                                                                                                                                                                                                                                                                                                                                    317
   EQUENCE
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                                                                                                                                                                                                                                                                                                                                                    QKINRTISINEE
                                                                                                                                                                                                                                                                                                                                                                     QKLDKSFSMIKE
                                                                                                                                                                                                                                                                                                                                                                                                                      SM00034; CLECT;
SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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                                                                                                                                                                                                                                                                                                                                                    328
                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.

CYTOPLASNIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM EGF-LIKE.

SUSHI 1.

SUSHI 2.

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 537; DB Pred. No. 2.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-SELECTIN.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SY SIMILARITY.

3Y SIMILARITY.

4N SIMILARITY.

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
2.5e-45;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                          Euteleostomi;
                                                         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pfam; PF00084; Sushi; 2.

Pfam; PF00084; Sushi; 2.

PFAM; PF00084; SELECTIN.

SMART; SM00032; CCP; 2.

SMART; SM00032; CCP; 1.

SMART; SM00031; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS01022; EGF_1; 1.

PROSITE; PS01055; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Dive
PIR; S23936; S2
GSSP; P14151; TPRO
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DARBOHYD
CARBOHYD
CARBOH
CAR
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
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Watanabe T., Song Y., Hirayama Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000561;
      S23936.
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          A
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; Selectin.
; Sushi_SCR_CCP.
; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat.
          WW.
   POTENTIAL.
CYTOPLASMIC (POTENTIAL
CYTOPLASMIC (SHORT
EGF-LIKE.
SUSHI 1.
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
L-SELECTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like
                CRC64;
                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Query Match Best Local S Matches 94

Similarity 71.:
94; Conservative

15;

Score 535; DB 1 Pred. No. 4e-45; 5; Mismatches

٠.

Length 372;

23;

Indels

0;

Gaps

0;

73.0%; 71.2%;

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RESULT
LEM1_M
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[2]
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01-NOV-1990
01-NOV-1990
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       This
                                                                                                                                                                                                                                                                   MEDLINE=91169529; PubMed=2004776; Dowbenko D.J., Diep A., Taylor B.A., Lu "Characterization of the murine homing correspondence between protein domains Genomics 9:270-277(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=90253086; PubMed=1693096;

MIDDINE=90253086; PubMed=1693096;

Siegelman M.H., Cheng I.C., Weissman I.L., Wakeland E.K.;

The mouse lymph node homing receptor is identical with the lymphocyte cell surface marker Ly-22; role of the EGF domain endothelial binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89162048; PubMed-2646713;
Siegelman M.H., van de Rijn M., Weissman I.L.;
Siegelman M.H., van de Rijn M., Weissman I.L.;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-360 FROM
                                                                                                                                                                                                                                                                                                                                                                                      Lasky L.A., Singer M.S., Yednock T.A., Rodriguez H., Nguyen T., Stachel S., R "Cloning of a lymphocyte homing recept cell 56:1045-1055(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-89168433; PubMed-2647302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mouse lymph node homing receptor cDNA revealing tandem interaction domains."; Science 243:1165-1172(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-selectin precursor (Lymph node homing receptor) (Leukocyte adhesion molecule-1) (LAM-1) (LY-22) (Lymphocyte surface MEL-14 antigen) (Leukocyte-endothelial cell adhesion molecule 1) (LECAMI) (CD62L). SELL OR LNHR OR LY-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEM1_MOUSE
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                                                                                                                             VENULES IN PERIPHERAL LYMPH NODES.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DC
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                    FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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Sciurognathi;
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receptor reveals
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osen S.D.;
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M36005;
M36058;
M25324;
M64549;
M64545;
M64545;
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E; PS00022; EGF_1; 1.
E; PS01186; EGF_2; 1.
TE; PS00615; C_TYPE_LECTIN_1; 1.
TE; PS50041; C_TYPE_LECTIN_2; 1.
*Ahesion; Transmembrane; Glycoprotein; EG
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PF00084;
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              Similarity
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; IPR000561; EGF-like.
; IPR002396; Selectin.
; IPR001212; Somatomedin_B.
; IPR000436; Sushi_SCR_CCP.
; IPR001304; lectin_c.
                                                              372
 Conservative
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AAA75651.1;
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SUSHI 1.
SUSHI 2.
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01-AUG-1990
16-OCT-2001
                                                                                                                                                                                                         VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756.

WARDLINE-9834547; PubMed-9668170;

Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,

Ruidavets J.B., Arveiler D., Luc G., Cambien F.;

"The P-selectin gene is highly polymorphic: reduced frequency of the pro-715 allele carriers in patients with myocardial infarrction.

Hum. Mol. Genet. 7:1277-1284(1998).

-i- FUNCTION: CA(2+)-DEDENDENT RECEPTOR FOR MYELOID CELLS THAT TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES TH INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WILLEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
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J. Biol.
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MEDILINE-89168432; PubMed-2466574;

MEDILINE-89168432; PubMed-2466574;

Johnston G.I., Cook R.G., McEver R.D.;

TCloning of GMP-140, a granule membrane protein of platelets and 
"Cloning of GMP-140, a granule membrane protein of platelets and 
endothelium: sequence similarity to proteins involved in cell 
adhesion and inflammation.";

Cell 56:1033-1044(1989).
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01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140) (PAD (CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bajorath J., Stenkamp R., Aruffo A.; "Knowledge-based model building of proteins: concepts Protein Sci. 2:1798-1810(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94093388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE
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Fujimoto T., Stroud E., Whatley R.E.,
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TISSUE SPECIFICITY: STORED IN THE ALPHA-GRAN AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSP THE CELL SURFACE.

SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY STMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 9 SUSHI (SCR) DOMAINS.
                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
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3388; PubMed=7505680;
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PROSITE; PS01186; EGF_2; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1;

PROSITE; PS50041; C_TYPE_LECTIN_2;
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InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR
InterPro; IPR001304; lectin_c.
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MIM; 173610;
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M60225;
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M60217;
M60218;
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; SM00034; CLECT; 1
; SM00181; EGF; 1.
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M60227;
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           EGF-like.
Selectin.
Sushi_SCR_CCP.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                      collaboration
L outstation -
                                                                                                                                                                                                                              outstation
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CYTOPLASMIC (P C-TYPE LECTIN EGF-LIKE. P-SELECTIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL. Glycoprotein; E at; Lipoprotein; SIMILARITY.
SIMILARITY.
SIMILARITY. (POTENTIAL) (SHORT FORM) EGF-like domain; Palmitate; Polymorphism; Lectin;

BINDS

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RESULT
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CARBOHYD
                                                                                        SELP.
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Manmalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
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Pred. No. 2.6e
21; Mismatches
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BY SIM
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T -> P (REDUCED FREQUENCY IN WITH MYCCARDIAL INFARCTION).
/FTIG-VAR_004195.
; FBC407BA2579F6EB CRC64;
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S -> N.
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/FTId=VAR_004193
L -> V.
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                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
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                                                                                           protein 140) (GMP-140) (PADGEM) hesion molecule 3) (LECAM3).
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.6e-23;
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                                    Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830;
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       pfam; pF00059; lectin_c; 1.

pfam; pF00084; sushi; 8.

pRINTS; pR00343; SELECTIN.

sMART; SM00032; CCP; 8.

SMART; SM00031; CCP; 1.

SMART; SM00181; EGF; 1.

SMORT; SM00181; EGF; 1.

PROSITE; pS00186; EGF_2; 1.

PROSITE; pS00186; EGF_2; 1.

PROSITE; pS00187; CTYPE_LECTIN_1; 1.

PROSITE; pS00161; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
    DOMAIN
TRANSMEM
DOMAIN
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InterPro;
InterPro;
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Gene 145:251-255(1994).
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                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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HSSP; P16109; 1FSB.
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"Cloning, sequence comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000561; EGF-like.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equires a license agreement (S email to license@isb-sib.ch).
      N. A.
                                                                                                                                                                                                                                                                                                                                                                                      Sushi;
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=7520013;
      Repeat;
EXTRACELLULAR (
POTENTIAL.
CYTOPLASMIC (PACTYPE LECTIN E)
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SUSHI 3.
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SUSHI 6.
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BY SIMILARITY BY SIMILARITY
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P-SELECTIN.
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n; Palmitate
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RESULT
LEM2_MC
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-92340571; PubMed=1378846;

MEDLINE-92340571; PubMed=1378846;

Weller A., Isenmann S., Vestweber D.;

"Cloning of the mouse endothelial selectins. Expr

"Cloning of the mouse endothelial selectins. Expr

and p-selectin is inducible by tumor necrosis far

J. Biol. Chem. 267:15176-15183(1992)

"I FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELES

"I FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELES

"I FUNCTION: THE BINDING TO LEUKOCYTES. THE LI
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                                                                                                                                                             "Murine endothelial leukocyte-adhesion structural and functional homologue of Eur. J. Biochem. 206:401-411(1992).
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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SITE
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Delamarter J.F.;
                                                                                                                                                                                                                                                           SEQUENCE
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54; Conservative
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s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; (
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van Huijsduijnen
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BY GLCNAC. . .) (POTONING COLUMN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 313; DB
Pred. No. 3.7e
17; Mismatches
                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 313; DB 1; L
. No. 3.7e-23;
ismatches 52;
                                                                                                                                                                                                                            R.H.,
                                                                                                                                                                            molecule 1 is a close
the human protein.";
                                                                                                                                                                                                                            Losberger
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                                    ENDOTHELIAL
                                                                Expression of sfactor alpha.
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                   LIGAND
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CRC64;
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                   RECOGNIZED
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                   ELAM-1 IS SIALYL-LEWIS X ()
POLYLACTOSAMINE THAT ARE F(
GLYCOLIPIDS).

-!- SUBCELLULAR LOCATION: Type
-!- SIMILARITY: TO OTHER SELECT
-!- SIMILARITY: CONTAINS 1 CC-TY
-!- SIMILARITY: CONTAINS 5 SUSH
                                 CARBOHYD
CARBOHYD
                                                                CARBOHYD
CARBOHYD
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DOMAIN
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DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SMUJULL, PROSITE; PS00022; EGF_1; 1.

PROSITE: PS01186; EGF_2; 1.

PROSITE: PS00615; C_TYPE_LECTIN_1; 1.

PROSITE: PS50041; C_TYPE_LECTIN_2; 1.

PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR001304;
Pfam; PF00008; EGF;
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M87862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S; PR00343; SELECTIN.
; SM00032; CCP; 6.
; SM00034; CLECT; 1.
; SM000181; EGF; 1.
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PF00084; sushi; 6.
S; PR00343; SELECTIN.
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M87862; AAA37577.1;
P16581; 1KJA.
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                  COCATION: Type I membrane protein.
TO OTHER SELECTINS/LECAMS.
CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CONTAINS 1 EGF-LIKE DOMAIN.
CONTAINS 6 SUSHI (SCR) DOMAINS.
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E-SELECTIN.
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Pfam; PF00005; lectin_
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P33730;
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9615; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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P16581; 1ESL.
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zoa; Chordata; C
ria; Carnivora;
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22; Mismatches
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SMART; SM00032; CCP; 6.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 2.
SMOSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0155; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycopr
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Similarity 43.0%;
52; Conservative 1
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18; Mismatches
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EXTRACELLULAR
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(Rel.

25, Created) 25, Last sequence

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THE POSSO SET AND THE POST OF 
                                                                                                                  SMART; SM00032; CCP; 8.

SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprote

Selectin; Signal; Sushi; Repeat; Lipoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000561; EC
InterPro; IPR000742; EC
InterPro; IPR000743; EC
InterPro; IPR000436; Su
InterPro; IPR000436; Su
InterPro; IPR001304; le
Pfam; PF00008; EGF; 1.
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Pfam; PI
PRINTS;
SMART; S
SMART; S
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between
the Euro
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"Cloning of th
and P-selectin
J. Biol. Chem.
[2]
SEQUENCE FROM
                                CHAIN
DOMAIN
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EMBL; M72332; AAA37712.1;
PIR; A42755; A42755.
HSSP; P16109; IFSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
THE CELL SURFACE.

INDUCTION: BY TNF-ALPHA.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
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Blood 80:795-800(1992).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sanders
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Sanders W.E. Jr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        swIISS-PROT entry is copyright. It is produced ween the Swiss institute of Bioinformatics are European Bioinformatics Institute. There are represented by non-profit institutions as long as its control of the control 
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PF00059; lectin_c; 1.
PF00084; sushi; 8.
S; PR00343; SELECTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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, Isenmann S., Vestweber D.;
of the mouse endothelial selectins. Expression of both lectin is inducible by tumor necrosis factor alpha."; chem. 267:15176-15183(1992).
1; Transmembrane;

jnal; Sushi; Repea

1 41 P

42 768 P

42 709 E

710 733 P
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Wilson R.W., Ballantyne of
g and analysis of in vivo
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EGF_2.
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Sushi_SCR_CCP.
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POTENTIAL.
P-SELECTIN.
EXTRACELLULAR
POTENTIAL.
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Sciurognathi; Muridae
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expression of muri
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n; Palmitate
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                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140)
CCD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECA
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CARBOHYD
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Mammalia;
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52; Conserv
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; Metazoa;
Eutheria;
                             (Sheep).
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                                                                                                                                                   STANDARD;
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C.TYPE LECTIN (SHORT FORM).
EGF-LIKE.
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SUSHI 3.
SUSHI 3.
SUSHI 6.
SUSHI 6.
SUSHI 7.
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 Vertebrata; Eute
minantia; Pecora;
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5.9e-22;
nes 54;
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               Euteleostomi;
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EMBL; L34270; AAB532C.

EMBL; L34270; AAB532C.

HSSP; P16109; IFSB.

InterPro; IPR000561; EGF-like.

InterPro; IPR002396; Selectin.

TherPro; IPR000436; Sushi_SCR_CCP.

TherPro; IPR001304; lectin_c.
 DISULFID
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SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00012; EGF_1; 1.

PROSITE; PS001186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selectin;
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NCBI_TaxID=9940;
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mitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
mitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
FUNCTION. CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS.
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F00084; sushi; 8.
PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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C-TYPE LECTIN.
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POTENTIAL.
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C SIMILARITY
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VARIANT
                                                                                                                           ROSENDIOOM C.L., Auchampach J.A., Anderson D.C., Manning A.M.;
Submitted (NOV-1993) to the EMBL/GenBank/DBBJ databases.

-I FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUROCYTES. THE LIGAND RECOGNIZED E ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEM2_RAT P98105;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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NCBI_TaxID=10116;
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Pfam; PF00084; sushi; 5.
SMART; SM00032; CCP; 5.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
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180
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                                      CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETT-CGPFGNWSSPEPTCQ
CQEQEYPDHGSLNCTHPFGLFSYNSSCSFSCERGYVPSSMETTVRCTSSGEWSAPAPACH
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PS50041; C_TYPE_LECTIN_2; 1.
esion; Transmembrane; Glycoprotein;
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PS01186; EGF_2; 1.
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Sushi_SCR_CCP.
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BY SIMILARITY
BY SIMILA
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3; Mismatches
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POTENTIAL.
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                                                        Graves B.J., Crowther R.L., Char
Huang K.-S., Presky D.H., Famill
"Insight into E-selectin/ligand
structure and mutagenesis of the
Nature 367:532-538(1994).
                                                                                                                                                                                                                                                                                                                                                        ligand,
Science
                                                                                                                                                                                                                                              Mills A.;
"Modelling
                                           Nature [7]
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91068005; PubMed=1701274; Phillips M.L., Nudelman E., Gaeta Hakomori S., Paulson J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-91115870; PubMed-1703529;
Collins T., Williams A., Johnston
MEDLINE=95179107;
                     VARIANT ARG-149
                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
MEDLINE=94150646; PubMed=7509040;
                                                                                                                                                                                                                                 FEBS Lett.
                                                                                                                                                                                                                                                                                           MEDLINE=93202275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gimbrone M.A. Jr., Bevilacqua M.P.; "Structure and chromosomal location leukocyte adhesion molecule 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bevillacqua M.P., Stengelin S., Gimbrone M.A.
"Endothelial leukocyte adhesion molecule 1: a
neutrophilis related to complement regulatory
science 243:1160-1165(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=90175359; PubMed=1689848;

Hession C., Osborn L., Goff D., Chi-Rosso

Pasek M., Pittack C., Tizard R., Goelz S.
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SELE OR ELAMI.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM-2)
                                                                                                                                                                                                                                                                                                               [5]
3D-STRUCTURE
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                                                                                                                                                                                                                                                                                                                                                                                               "ELAM-1 mediates cell adhesion
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266:2466-2473(1991).
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DR SMART; SM00034; CLECT; 1.

DR SMART; SM00181; EGF; 1; 1.

DR PROSITE; PS00122; EGF_1; 1.

DR PROSITE; PS001186; EGF_2; 1.

DR PROSITE; PS001615; C_TYPE_LECTIN_2; 1.

PROSITE; PS001615; C_TYPE_LECTIN_2; 1.

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THE THE THE TENT OF THE TRANSPORT OF THE
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XX MEDLINE-93249394; PubMed-7683458;
XA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;
XI Tisolation and characterization of a bovine cDNA encoding a
YI functional homolog of human P-selectin.
XI Biochem, Biophys. Res. Commun. 192:338-344(1993).
XI Diochem, Biophys. Res. Commun. 192:338-344(1993).
XI DIOCHEM, BIOPHYS. ON NEUTROPHILS AND MONOCYTES. MEDLATES THAT BINDS
XI CONTRACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
XI LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
XI SUBCELLULAR LOCATION: Type I membrane protein.
XI CONTRACTION OF ACTIVE STORED IN THE ALPHA-GRANULES OF PLATELETS
XI SUBCELLULAR LOCATION: Type I membrane protein.
XI SUBCELLULAR LOCATION: Type I membrane protein.
XI CONTRACTION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO00561; EGF-like.
InterPro; IPRO02396; Selectin.
InterPro; IPR002396; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
Pfam; PF00008; EGF; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 6.
PRINTS; PR00343; SELECTIN.
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Mammalia; Eutheri
Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                         SIGNAL
CHAIN
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PROSITE;
PROSITE;
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SMART;
SMART;
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the Euro
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-selectin precursor (Granule membrane protein 140) (GMP-140)
P-selectin precursor (Granule membrane protein 140) (GMP-140)
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HSSP; P16109; 1FSB.
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS;
THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
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                                                                                                                                                                                                                                                                             adhesion;
                                                                                                                                                                                                                                                                                              I; SM00032; CCP; 6.
I; SM00034; CLECT; 1.
I; SM00181; EGF; 1.
ITE; PS00022; EGF=1; 1.
ITE; PS00186; EGF=2; 1.
ITE; PS00615; C_TYPE_LECTIN_1; 1.
ITE; PS00611; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collab-
en the Swiss Institute of Bioinformatics and the EMBL outsi
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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Eutheria;
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Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                     Repeat
EXTRACELLULAR (POTENTIAL POTENTIAL).
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FOR EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                                                                                                                         BY SIMILAR:
P-SELECTIN
                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                           EGF-like
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cora; Bovoidea
                                                                                                                                                                                                                                                                           domain;
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(LECAM3).
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Best Loc
Matches
TISSUB=Heart;
MEDLINE=92189729; PubMed=1372169;
Larigan J.D., Tsang T.C., Rumberger J.M.,
"Characterization of cDNA and genomic sequence of the company of t
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E-selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
                                                                                                                                                                                                                                                                                                                                                                                                              RABIT
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SEQUENCE
                                                                                                                                                                                   Oryctolagus cunicul
Eukaryota; Metazoa;
                                                                                                                                                                  Mammalia; Eutheria;
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warazoa; Chordata; Craniata; Ver
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Pred. No. 5.5e
24; Mismatches
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BY SIMILARITY

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    sequences encoding rabbi
functional interactions
                                                                                                                                                                                   Vertebrata; Euteleostomi;
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.5e-21
                                           Burns
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A CRC64;
                                           D.K.;
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Pfam: PF00084; SUSHI, ...

PFINTS; PR00343; SELECTIN.

SMART; SM00032; CCCP; 5.

R SMART; SM00034; CLECT; 1.

R SMART; SM00081; EGF; 1.

PROSITE; PS01082; EGF=1; 1.

PROSITE; PS01186; EGF=2; 1.

DR PROSITE; PS01615; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EGF
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DOMAIN
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InterPro;
InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOLIPIDS).

GLYCOLIPIDS).

SUBCELLULAR LOCATION: Type I membrane protei INDUCTION: BY CYTOKINES.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Biol. 11:149-162(1992).

FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M91004;
M91005;
P16581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00059; lectin_c; 1. PF00084; sushi; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000561; EGF-like.
IPR002396; Selectin.
IPR000436; Sushi_SCR_CCP.
IPR001304; lectin_c.
     AAA31243.1;
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      CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORI
EGF-LIKE.

SUSHI 1.

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SUSHI 3.

SUSHI 4.

SUSHI 5.

SUSHI 5.

SUSHI 6.

SUSHI 7.

SUSHI 17.

BY SIMILARITY.

BY SIMILAR
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LEMZ_BOVIN

STANDARD;

PRT;

40.7

1 01-FEB-1996 (Rel. 33, Created)

T 01-FEB-1996 (Rel. 33, Last sequence updated)

T 01-FEB-1996 (Rel. 33, Last annotation updated)

T 01-FEB-1996 (Rel. 33, Last annotation updated)

T 01-FEB-1996 (Rel. 33, Last annotation updated)
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MEDLINE-9338237; PubMed-7690465;

Nguyen M., Strubel N.A., Bischoff J.;

Nguyen M., Strubel N.A., Bischoff J.;

Nguyen M., Strubel N.A., Bischoff J.;

The role for sialyl Lewis-X/A glycoconjugates in capillary morphogenesis.";

Nature 365:267-269(1993).

-!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECCONIZED ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES POLYLACTOSSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                          This
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Bovidae; Bovinae; Bos.
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                                                                                                   NCBI_TaxID=9913;
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     SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are
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Pred. No. 7.36
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or send a
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SMART; SM00034; CLECT; 1.

SMART; SM00181; EGF; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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HSSP;
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InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
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n; PF00059; lectin_c; 1.
n; PF00084; sushi; 4.
NTS; PR00343; SELECTIN.
                                                                                                                 VKCDALSNLDNGVVNCSPNHGSLPWNTTCTFECQEGYKLTGPQHLQCTSSGIWDNKQPTC
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                                                                                                                                                                                                                                       Similarity
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORE
EGF-LIKE.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

BY SIMILARITY.

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Pfam, PF00084; Sushi, 4.
Pfam, PF00084; Sushi, 4.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 4
SMART; SM0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOCHEM. BIOPHYS. Res. COMMUN. 201:805-805(1994).

-! FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELL FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLONDATES THE LIGAND RECORN MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECORN ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVA POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERM GLYCOLIPIDS).

-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR ALL REJECTION AND PROBABLY ALSO IN XENOGRAFT REJECTION.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.

-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

-!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAINS; PORCINE E-ITHE HUMAN SUSHI-1 AND -4 EQUIVALENTS.
                                                                                                                                                                                                                                                                                                                                                               entities
or send a
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use
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TISSUE-Aortic endothelium;
MEDLINE=94271236; PubMed=7516159;
MEDRINE=94271236; PubMed=750000;
Tsang Y.T.M., Haskard D.O., Robinson
"Cloning and expression kinetics of publications of publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P98110;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-selectin precursor (Endothelial leukocyte ad (ELAM-1) (Leukocyte-endothelial cell adhesion
                                                                                                                                          InterPro; IPR000436;
InterPro; IPR001304;
Pfam; PF00008; EGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is
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TISSUE=Aortic endothelium;
MEDLINE=95071392; PubMed=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR002396;
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by non-profit institutions as long as its content
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U08350; AAA21541.1;
P16581; 1ESL.
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                                                                                                                                                                                                                                                                                                                                                                                            requires a license agreement
                                                                                                                                                                                                                                                                                                                                                               email to license@isb-sib.ch).
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ITTE; PS001186; EGF_2; 1.
ITTE; PS0015; C_TYPE_LECTIN_1; 1.
ITTE; PS50041; C_TYPE_LECTIN_2; 1.
adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                     CEPLEAPELGIMDCTH-PFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ
                                                                                                  SCQ
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E; PS00022;
E; PS01186;
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2; EGF_1
                                       STANDARD;
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  Created)
Last sequence update)
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C -> Y (IN REF. 2).
L -> F (IN REF. 2).
L -> N (IN REF. 2).
Y -> N (IN REF. 2).
KFYPSSSECLOPNGSYQMPSDLI ->
KFYPSSSECLOPNGSYQMPSDLI ->
NLFLPAAPRAFNAFNPMDPTKCLLT (IN RE
                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                            E-SELECTIN.

EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORE
EGF-LIKE.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
BY SIMILARITY.
BY S
                                                                                                                                                                                                                                             Score 245; DB
Pred. No. 9.9e
22; Mismatches
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   InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00300436; Sushi_SCR_CCP.
IPfam; PF00047; ig; 1.
Pfam; PF00084; sushi; 5.
SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
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Sushi; Signal
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EMBL; D13885; 1
EMBL; D13886; 1
EMBL; D13887; 1
HSSP; P10998;
F1yBase; FBgn0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN LOCOMOTOR ACTIVITY.

SUBCELLULAR LOCATION: EXTRACELLULAR.

ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND 4; A PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN PCC NEURONS AND NEUROBLASTS IN THE PROCEPHALIC NEUROGENIC REGION IN THE CENTRAL NERVOUS SYSTEM.

TO EVELOPMENTAL STAGE: MOST ABUNDANT DURING AND/OR AFTER NEURONAL DIFFERENTIATION AND DURING CELL SPECIFICATION OR AXOGENESIS.

TO EVELOPMENTAL STAGE: MOST ABUNDANT DURING AND/OR AFTER NEURONAL DIFFERENTIATION AND DURING CELL SPECIFICATION OR AXOGENESIS.

TO SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN SUPERFRAMILY.

SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93213498; PubMed-8461133;
Hoshino M., Matsuzaki F., Nabeshima Y.-I., Hama C
"Hikaru genki, a CNS-specific gene identified by
in Drosophila, encodes a novel type of protein.";
Neuron 10:395-407(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute
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Locomotion-related protein Hikaru genki precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                Signal
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   BAA02984.1;
BAA02985.1;
BAA02986.1;
BAA02987.1;
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                                                                                                                                                                                                                                                          splicing;
IGCOMOTION-RELATED PROTEIN H
IG-LIKE C2-TYPE DOMAIN.
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VARSPLIC
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SEQUENCE
                                  MEDLINE-91201892; PubMed=1826708; Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss "Cloning of the 1.4-kb mRNA species of human complement fact reveals a novel member of the short consensus repeat family to the carboxy terminal of the classical 150-kba molecule.", Immunol. 146:3190-3196(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
  SEQUENCE
                                                                                                                                                                                                                                                                          "Structural analysis of human complement binding protein, beta 2-glycoprotein I, a J. Immunol. 136:3407-3411(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of the for C3b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 53-445 FROM N.A.
MEDLINE-87054207; PubMed-2946589;
Schulz T.F. Schwaeble W., Stanle
"Human complement factor H: isola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88134059;
Ripoche J., Day A.
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01-AUG-1988 (Rel.
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                                                                                                                                                                                                                                                                                                                                        Kristensen
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16-OCT-2001 (Rel. 40, Last annotation update)
Complement factor H precursor (H factor 1).
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Metazoa; Chordata; C

Metharia; Primates; (
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                                                                                                                                                       1047-1231 FROM
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A.J., Harris T.J.R., S
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Pred. No. 6.
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J. MOI. 33:266-284(1993).

J. MOI. BIOI. 23:266-284(1993).

J. MOI. BIOI. 33:266-284(1993).

J. MOI. BIOI. 33:266-284(1993).

FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

LATERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

LICALIZED BY ALTERNATIVE S
                                 Pfam; I
SMART;
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                                                                                                                                                                                                                     EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                         EMBL;
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Submitted
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Biochem.
               Complement
                               InterPro; IPR000436; Pfam; PF00084; sushi; SMART; SM00032; CCP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barlow P.N., Norman D.G., Steinkasserer A., Driscoll P.C., Sim B., Campbell I.D.; "Solution structure of the fifth repeat of of the complement control protein module."; Biochemistry 31:3626-3634(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in solution.";
J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 264-322 (SUSHI MEDLINE=92232649; PubMed=1533152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 927-985
MEDLINE-91278097; PubMed-18:
Norman D.G., Barlow P.N., Ba
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L; X07523; CAA30403.1; -
L; M12383; AAA52013.1; -
L; AL049744; CAB70598.1; -
L; M65294; AAA359481; -
L; U56979; AAB01987.1; -
L; Z29665; CAA82763.1; -
L; Z29665; CAA82763.1; -
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15-JUL-93.
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                 alternate
 -structure;
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a 1H (Factor H).";
205:285-293(1982).
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                 pathway;
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Polymorphism;
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01-NOV-1990 (Rel. 40, Last annot)
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                                                                                     Wong W.W., Klickstein L.B., Smith J.A., Weis J.H., Fearon D.T.;
"Identification of a partial CDNA clone for the human receptor for complement fragments C3b/C4b.";
Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).
-i- FUNCTION: CRI. PRESENT ON ERVEHPOCYTES, LEUKOCYTES, GLOMERULAR PODOCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT HA ACTIVATED COMPLEXES THAT HA
                                                                                                                                                                                                                                                          "Human C3b/C4b receptor (CR1). Demonstration of l repeating domains that are composed of the short characteristics of C3/C4 binding proteins."; J. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                                                              SEQUENCE OF 761-783; 831-845 AND 1179-1195 FROM N.A. MEDLINE-86067975; PubMed-2933745;
                                                                                                                                                                                                                                                                                                                     Klickstein L
Fearon D.T.;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 503-2039 FROM N.A. MEDLINE-87168191; PubMed-2951479; Klickstein L.B., Wong W.W., Smith
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Fearon D.T.;
Fearon D.T.;
Identification of distinct C3b and
human C3b/C4b receptor (CR1, CD35) k
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Mammalia; Eutheria;
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 SUBUNIT: MONOMER.

SUBCELLULAR LOCATION: Type I membrane protein.

POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM MISCELLANEOUS: SEVEN SHORT CONSUSTED REPEATS (SCR) CONSTITUTE A LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
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Bartow T.J., Miletic V., Rabson L.D.,
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MISCELLANEOUS: THIS IS SIMILARITY: CONTAINS 3
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"Analysis of complement factor H mRNA expression:
IFN-gamma increase the level of H in L cells.";
Biochemistry 28:9891-9897(1989).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-8623353; PubMed-2940596;
Kristensen T., Tack B.F.;
"Murine protein H is comprised of
in length.";
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01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Complement factor H precursor (Protein beta-1-H).
HF1 OR CFH.
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                                                                                                                                                                                       "Demonstration of an unusual allelic
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                                                                                                                  He complete cDNA sequence of the H.2 allotype.";

Immunol. 144:358-362(1990).

FUNCTION. FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHMAY.

POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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Fukuoka Y., Yasui A., Okada N., Oka
"Molecular cloning of murine decay
immunoscreening.";
Int. Immunol. 8:379-385(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and chromosomal localization of the maccelerating factor genes. Duplicated genes encode glycosylphosphatidylinositol-anchored and transmembrane J. Immunol. 155:3079-3091(1995).
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MEDLINE-95403982; PubMed-7545711;
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                    SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En
European Bioinformatics Institute. There are no restr
                                                                                                                 DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY I FUNCTION: SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION ACTIVE SITE ON SCR3 (BY SIMILARITY).

SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.

SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVENT.
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SUBCELLULAR LOCATION: Attached to the membrance subcellular LOCATION: Attached to the membrance subscellular location. Secretory epithelil LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE. DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT IDOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT I
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01-OCT-1994
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                           Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merost Limulidae; Tachypleus.
NCBI_TaxID=6853.
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Pfam; PF00084; sushi; 4.
SMART; SM00032; CCP; 4.
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InterPro; IPRO01254; TIYPSIN.

R InterPro; IPRO01304; lectin_c.

R Pfam; pF00059; lectin_c; 1.

R Pfam; pF00089; trypsin; 5.

R Pfam; pF00089; trypsin; 1.

R Pfam; pF00089; trypsin; 1.

R PRINTS; PR00722; CCTP; 5.

R SMART; SM00034; CLECT; 1.

R SMART; SM00034; CLECT; 1.

R SMART; SM00030; Tryp_SPc; 1.

R SMART; SM00020; Tryp_LECTIN_2; 1.

R SMART; SM00020; Tryp_LECTIN_2; 1.

R PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

R PROSITE; PS00042; EGF_1; 1.

R PROSITE; PS00186; EGF_2; FALSE_NEG.

R PROSITE; PS00186; EGF_2; FALSE_NEG.

R PROSITE; PS01186; EGF_2; FALSE_NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.219; ...
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
InterPro; IPR004043; LCCL.
InterPro; IPR004043; LCCL.
InterPro; IPR001436; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR001304; lectin_c.
                                                                                                                              Hydrolase; Serine pro
Hemolymph clotting; (
Sushi; Repeat.
SIGNAL 1
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Ikehara Y., Iwanaga S.;
"Limulus factor C. An endotoxin-sensitive serine
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BNZYME REGULATION: ACTIVATED BY GRAM-NEGATIVE BACTERIAL LIPOPOLYSACCHARIDES AND CHYMOTRYPSIN.

SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN BY A DISULFIDE BOND.

SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 LCCL DOMAIN.

SIMILARITY: CONTAINS 1 LCCL DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN I
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European Bioinformatics Institute. The
by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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MEDLINE-91010789; PubMed-2145366;
Molina H., Kinoshita T., Inoue K., Carel J.C., Holers V.M.;
"A molecular and immunochemical characterization of mouse C!
"Evidence for a single gene model of mouse complement recepts 2.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                             SEQUENCE FROM N.A STRAIN-BALB/C; MEDLINE-90229735;
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                                                                                                                                                   "Comparative structure and evoluthe human C3d/EBV receptor (CD21 J. Immunol. 144:3458-3467(1990).
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precursor (Cr2) (Complement C3d
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Receptor; Sushi.
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Pfam; PF00084; sushi; 14.
SMART; SM00032; CCP; 14.
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J. Immunol. 143:3058-2067(1989).
-: FUNCTION: RECEPTOR FOR COMPLEMENT C3D.
-: LYMPHOCYTES ACTIVATION.
-: SUBCELLULAR LOCATION: Type I membrane p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fingeroth J.D., Benedict M.A., Levy D.N., Strominger J.L., "Identification of murine complement receptor type 2."; Proc. Natl. Acad. Sci. U.S.A. 86:242-246(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89098890;
Fingeroth J.D., B
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BL; M35684; AAA37448.1; -.
BL; M61132; AAA63295.1; -.
BL; M35685; AAA37450.1; ALT
BL; M35685; AAA37447.1; -.
R; AA3526; AA3526.
SP; P10998; 1VVD.
D; MGI:88489; Cr2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dified and this statement is not removed. Usage by and for this statement is not removed. Usage by and for this statement (See http://www.isb-sib.send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway; Glycoprotein;
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       PubMed=2783485;
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mily. II. Identification
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(Rel. 27, Last sequence update)
(Rel. 40, Last annotation update)
protein alpha chain precursor (C4bp) (Proline-rich
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SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS.
SIMILARITY: TO C48P BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.

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"Visualization of human C4b-binding protein and its complexes with "Visualization of human C4b-binding protein and its complexes with "Vitamin K-dependent protein S and complement protein C4b.";

L Proc. Natl. Acad. Sci. U.S.A. 80:34613465(1983).

C -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PARHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COPACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C4B. IT CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C4B. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SERUM AMYLOID P COMPONENT.

-1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA ACHAINS AND 1 BETA CHAIN, A 530 KDa HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KDa COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN, A 530 KDa HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KDa COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING SITE FOR C4B AT THE END.

-1- TISSUE SPECIFICITY: CHYLOMICRONS IN THE PIASMA
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MEDLINE-90073699; PubMed-2590215;
METSURGHT T., Okamura S., Aso T., Sata T., Niho Y.;
Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
"Molecular cloning of the cDNA coding for proline-rich identity of PRP as C4b-binding protein.";
identity of PRP as C4b-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-85296001; PubMed-4033666; Chung L.P., Gagnon J., Reid K.B.M.; Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited proteolysis with chymotrypsin and the peptides produced by cyanogen bromide treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=86025405; PubMed=3840370; Chung L.P., Bentley D.R., Reid K.B.M.; Chung L.P., Bentley D.R., Reid K.B.M.; Molecular cloning and characterization of the cDNA coding for C4b binding protein, a regulatory protein of the classical pathway of human complement system."; Blochem. J. 230:133-141(1985).
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Lintin S.J., Lewin A.R., Reid K.B.M.;
"Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of the C4bp
CDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELECTRON MICROSCOPY, 3D-STRUCTURE, AND LIGAND B MEDLINE-83221615; PubMed-6222381; MEDLINE-83221615. Smith C.A., Mueller-Eberhard H.J.; Marine B. Smith C.A., Mueller-Eberhard H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 204:77-81(1986). [5]
SEQUENCE OF 80-597 FROM N.A.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86301119; PubMed-3017751;
Lintin S.J., Reid K.B.M.;
"Studies on the structure of the human C4b-binding
FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein gene.";
Biochem. Biophys. Res. Commun. 174:222-227(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELECTRON MICROSCOPY,
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EMBL; M62476; AAA35506.1; JJ
EMBL; M62477; AAA35506.1; JJ
EMBL; M62478; AAA35506.1; JJ
EMBL; M62479; AAA35506.1; JJ
EMBL; M62481; AAA35506.1; JJ
EMBL; M62481; AAA35506.1; JJ
EMBL; M62482; AAA35506.1; JJ
EMBL; M62482; AAA35506.1; JJ
EMBL; M62485; AAA35506.1; JJ
EMBL; M62485; AAA35506.1; JJ
EMBL; X07853; CAA30701.1; -
EMBL; X04286; CAB2647.1; -
EMBL; X04286; CAA27839.1; -
EMBL; X04286; CAA27839.1; -
EMBL; X02865; CAA26617.1; -
EMBL; X03568; NBHUC4.
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Pfam; PF00084; sushi; 8.
SMART; SM00032; CCP; 8.
Complement pathway; Plasma; Glycopr
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M62486;
M62475;
M62476;
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Q -> T.
                            /FTId=VAR_001977
Y -> H
/FTId=VAR_001978.
W -> L (IN DBSNP:1801341).
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Soames C.J., Day A.J., Sim R.B.;
"Prediction from sequence comparisons of residues
in the interaction with complement component C3b."
Biochem. J. 315:523-531(1996).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Complement factor H (H factor 1) (Fragments).
                                                                                                                  SMART;
                                                                                                                                                                                                  modified
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01-MAR-2002
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Pfam; PF00084; Sushi; 11.
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Bovidae; Bovinae;
NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                           C3b by factor I and also increases the rate of dissociation of the C3bbb complex (C3 convertase) and the (C3b)NBB complex (C5 convertase) in the alternative complement pathway (By similarity). SIMILARITY: CONTAINS AT LEAST 13 SUSHI (SCR) DOMAINS.
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P10998; IVVD.
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Pred. No. 2.5e
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01-NOV-1997
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16-OCT-2001
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mouse, and rat proteins.";
J. Immunol. 158:1315-1323(1997).
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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Rattus norvegicus (Rat)
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                                                                                                                                                                                                                   Hillarp A., Wiklund H., Thern A., Dahl
"Molecular cloning of rat C4b binding
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COPACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPICANIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN AND WITH SERUM AMYLOID P COMPONENT.
SUBUNIT: DISSULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHANSIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
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Rodentia;
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Pred. No. 4.6e-07;
5; Mismatches 48;
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Sciurognathi; Muridae; Murinae; Rattus.
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RESULT 31
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                                                                                         GKKKTIC----ESSGIWSNPSPICQKL 123
                                                                                                                                            --GPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSH---PLASFSFTSACTFICSEGTELI
                                                                                                                                                                    CKPLGKWQINIACVKKSCRNPGDLQNGKVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCE
                                                                   GNASITCTVVNKTVGVWSPSPPTCERI
                                                                                                                   IQGKGVSWSDPLPECVIAKCG--MPPD--ISNGKHNGREEEFFTYRSSVTYKCDPDFTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
45
77
104
139
168
204
232
    STANDARD;
                                                                                                                                                                                                                                                                                      491
62266
                                                                                                                                                                                                                                  19.9%;
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BY SIMILARITY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Repeat; BY SIMILARITY.
                                                                                                                                                                                                                                  Score 146;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4B-BINDING PROTEIN ALPHA CHAIN
    PRT;
                                                                                                                                                                                                                       Mismatches
    610
                                                                                                                                                                                                                                  DB 1;
.2e-07;
  A
                                                                                                                                                                                                                                                                                                                                                                BETA CHAIN) (POTENTIAL)
BETA CHAIN) (POTENTIAL)
                                                                                                                                                                                                                                             Length 558;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                     Gaps
                                                                                                                                           100
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01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                         DISULFID DISULFID
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                    Complement
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00084; sushi; SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z31693; CAA83498.1;
HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4BPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4b-binding
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                pathway;
 asma;
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formation with protein S.";

J. Immunol. 153:4190-4199(1994).

J. Immunol. 153:4190-4199(1994).

J. Immunol. 153:4190-4199(1994).

IT ENCOTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B IMACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTAGE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

-1- SUBUNIT: DISULFIDE-LINKED COMPPLEX OF C4BP ALPHA AND BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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Hillarp A., Thern A., Dahlbaech B.;
"Bovine C4b binding protein. Molecular cloning of the alpha- and
beta-chains provides structural background for lack of complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000436; Sushi_SCR_CCP
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SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
protein alpha chain precursor (C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4B-BINDING PROTEIN ALPHA CHAIN.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 7.

SUSHI 8.

SUSHI 8.

BY SIMILARI

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(WITH BETA CHAIN) (POTENTIAL).

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Best Local S
Matches 35
                        Complement
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08607;
01-AUG-1988 (Rel. C
01-FEB-1994 (Rel. 2
16-OCT-2001 (Rel. 4
               DOMAIN
                                                                                                                                        EMBL;
                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                               of the serum complement system.";

Biochemistry 26:4668-4674(1987).

-I FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
-I- SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE BETA CHAIN OF C4BP.
BETA CHAIN OF C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
-I- SIMILARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.
-I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                 SMART;
                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                         InterPro;
                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-88024997; PubMed-3663616;
Kristensen T., Ogata R.T., Chung L.P., Reid K.E
"cDNA structure of murine C4b-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4b-binding protein C4BPA OR C4BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4BP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
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                                                                                                                                                                  send
                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                               A27117; NBMSC4.
                                                                                   MGI:88229; C4bp.
cPro; IPR000436; Sushi_SCR_CCP
                                                              PF00084; sushi; sm00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHPLAS---FSFTSACTFICSEGTELIGKKKTIC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVVWSDPLPQCIIAKCEPPPT----ISNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPTCQVIQCEPLSAPDLGIMNC
                                                                                                                                       M17122; AAA37312.1;
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                                                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
35; Conserv
                                                                                                                                                                          non-profit institutions as long as and this statement is not removed. I requires a license agreement (See htt
                                                                                                                                                                                                                                                             CHAIN OF C4BP.

LARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

LARITY: CONTAINS 6 SUSHI (SCR) DOMAINS.

ION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                email to license@isb-sib.ch).
                                                   pathway;
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66
221
525
602
   57
57
119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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66
221
525
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; Plasma;
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469
116
177
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28,
40,
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor
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30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created;
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                                                                                                                                        ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                Glycoprotein;
  C4B-BINDING
SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH BETA CHAIN) (POTENT AL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (C4bp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469
                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.1e-07;
                                                 Repeat;
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                                                                                                                                                                                     Usage
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                                                                                                                                                                                                  its content
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                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory component
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                                                Sushi;
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                                                 Signal.
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ALD DESCRIPTION OF COLOR OF CO
                                                                                HILLARD A., Wiklund H., Thern A., Dahlback B.;

RT "Molecular cloning of rat C4b binding protein alpha- and beta-chaired structural and functional relationships among human, bovine, rabbin mouse, and rat proteins.";

I. J. Immunol. 158:1315-1323(1997).

I. J. Immunol. 158:1315-1323(1997).

C. C. HORTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT CABRITYATION. IT BINDS AS A COPACTOR TO C3B/C4B IMACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SERVICE.

-i- SIRRINATO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4BB_RAT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
01-NOV-1997
15-JUL-1998
                              -!- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP A-!- SIMILARITY: TO C4BP ALPHA CHAIN AND TO PIG-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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DISULFID
DISULFID
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DISULFID
                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver; MEDLINE-97166082; PubMed-9013975;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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32; Conservative
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
protein beta chain precursor.
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SUSHI 6.
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Pred. No. 6.1e-07;
9; Mismatches 49
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AC 060401: Q6
AC 997256: Q9
DT 01-NOV-199
DT 16-OCT-200
DE Complement
GN DAF.
OS Cavia porc
OC Eukaryota;
OC Hammalia;
OC Mammalia;
OC Mammalia;
AN (D1] TaxID
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O60401; O60402; Q60403; Q60404; Q60405; Qbu4ub; P97256; O9WTI9; O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
"Multiple isoforms of guinea pig decay-accelerating generated by alternative splicing.";
J. Immunol. 155:3037-3048(1995).
                          [1]
SEQUENCE FROM N.A., AND ALLESSE STRAIN-HARTLEY; TISSUE-Spleen;
MEDLINE-95403978; PubMed-7545710;
MEDLINE-95403978; PubMed N., Non
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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                NCBI_TaxID=10141;
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Hystricognathi; Caviidae;
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ALTERNATIVE PRODUCTS: THERE ARE AT LEAST SIX FORMS OF DAF TRANSCRIPTS (DISTRIBUTED IN FOUR CLASSES: GPT, TCL, TCS AND SEC; GENERATED BY ALTERNATIVE SPLICING, ONE GPT-ANCHREED FORM (GDAB-GPT), TWO FORMS WITH LONGER CYTOPLASMIC REGION (GDAB-TCL AND GDAB-TCC), TWO FORMS WITH SHORTER CYTOPLASMIC REGION (GDA-TCS & GDAB-TCS) AND ONE SECRETED FORM (GDAB-SEC).

TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPT & TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY PRESENT IN TRACE LEVELS.
SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION AND

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EMBL; D55660; BAA09519.1; J
EMBL; D55661; BAA09519.1; J
EMBL; D55662; BAA09519.1; J
EMBL; D55663; BAA09519.1; J
EMBL; D55664; BAA09519.1; J
EMBL; D55666; BAA09519.1; J
EMBL; D49416; BAA08396.1; -
EMBL; D49417; BAA08397.1; -
EMBL; D49418; BAA08398.1; -
EMBL; D49419; -BAA08399.1; -
EMBL; D49420; BAA08400.1; -
EMBL; D49421; BAA08401.1; -
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VARSPLIC
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                            157
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                                                                                                                                                                                                                                                                                                                                                                                                                Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                          Complement
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           52
                           CEKKQCPNPGEL----VNGNINVTTDLLLGSQIFFSCDPGYRLTGEASAFCMIKGNAVGW
                                            CEPLEAPELGTMDCTHPFGNFS-----FSSQCAFSCSEGTNLTGIEETTCGPFGN---W
SSPEPTCQVIQC-EPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTIC---
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D556565
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                                                                 43;
                                                                Similarity 32.
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000436; Sushi_SCR_CCP
                                                                                                              507
                                                                                                                                                                                                                                                                                                                                                                                                                          pathway;
                                                                                                                                          459
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452
32
159
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221
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BAA09519.
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                                                                                                             AA;
                                                                                                                                          507
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451
507
93
158
220
228
228
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458
451
57
57
174
442
334
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                                                                                                              55263
                                                                         19.4%;
32.1%;
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GPI-ANCHOR (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTEI

                                                              Score 142; DB
Pred. No. 1.2e
L4; Mismatches
                                                                                                                                                                                                                          MISSING (1
MISSING (1
GDAB-TCL,
TCS AND IS
MISSING (1
SEC).
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SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                                   THYKVDSFACGASNHWLADIAKEDLRRDESNAQNISSLLQ
VLGAAQTQ -> DTCV (IN ISOFORM GDAB-SEC).
THYKVDSFACGASNHWLADIAKEDLRRDESNAQNISSLLQ
VLGAAQTQ -> ANMEHMRTKNPMLYVLT (IN ISOFORM
GDA-TCS AND ISOFORM GDAB-TCS).
                                                                                                                                                                                    GDAB-SEC).
THYYKVDSFACGASNHWLADIAKEDLRRDFSNAQNISSLLQ
                                                                                                                                                                   VLGAAQTQ -> GHMCIKLTVLLVVLVIIG ISOFORM GDAB-GPI).
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                                                                                                                                                                                                          ISOFORM
                                                               DB 1;
.2e-06;
hes 57;
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                                                                                                                                                                                                                                                                                                                                                                                             DECAY-ACCELERATING FACTOR
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<del>..</del>
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                                                                                Length
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) (POTENTIAL).
) (POTENTIAL).
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                                                                                                                                                                                                                                    AND GDAB
                                                               20;
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RESULT 35
APOH_BOVIN
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            EMBL; L07303; AAA3(
EMBL; X60065; CAA4;
PIR; S23597; NBBO.
PIR; S09032; S09033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APOH_BOVIN

P17690; Q28052;

O1-AUG-1990 (Rel

O1-NOV-1997 (Rel
                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                   MEDLINE=90226328; PubMed=2327984;
Li Q., Blacher R., Esch F., Congote L.F.;
"Isolation from fetal bovine serum of an apolipoprotein-H-like
protein which inhibits thymidine incorporation in fetal calf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U1-AUG-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-2-glycoprotein I precursor (Apolipoprotein Apoli
                                                                             entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss_Institute_of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                 Kato H., Enjyoji K.-I.;
"Amino acid sequence and location of beta 2 glycoprotein I: the presence c Biochemistry 30:11687-11694(1991).
                                                                                                                                                                                                     -!- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
-!- TISSUE SPECIFICITY: PLASMA.
                                                                                                                                                                                                                                                                            Biochem. J.
                                                                                                                                                                                                                                                                                       erythroid cells.";
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 20-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92089075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete primary structure of bovine localization of the disulfide bridges. Biochemistry 31:3611-3617(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao B., Virmani M., Ro
Appella E., Kunos G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bendixen E., Halkier Kristensen T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92232647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 4-345 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1992) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270
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                                                                                                                                                                                        TISSUE SPECIFICITY: PLASMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
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                                                                                                                                                                                                                                                                           267:261-264(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Bovine).
                                      AAA30382.1;
CAA42669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1751487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1567819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romm E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE-LINKAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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S
                                                                                                                                                                                                                                                                                                                                                                                                 f the disulfide bonds in bovine
of five Sushi domains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta
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                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sottrup-Jensen
                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2-glycoprotein
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InterPro;

IPR000436; Sushi_SCR_CCP

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RESULT
CR2_HUV
ICR2_HUV
ICR2_HUV
ICR2_HUV
AC P;
AC P;
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DT O
DT O
DT O
OC C
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Best Local :
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                                                                           CR2_HUMAN STANDAND,
CR2_HUMAN STANDAND,
CR2_HUMAN STANDAND,
P20023;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement receptor type 2 precursor (Cr2) (Complement C3d receptor)
Complement receptor type 2 precursor (Cr2) (CD21 antigen).
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                                             Epsuca OR C3DR.
CR2 OR C3DR.
Homo sapiens (Human).
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CONFLICT
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CARBOHYD
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DOMAIN
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 SEQUENCE FROM N.A. MEDLINE-89123277; PubMed-2563370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  142
                                                                                                                                                                                                                                                                                258
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                                                                                                                                                                                                                                                                                PSCK
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                                                                                                                                                                                                                                                                                                                                                                                                                            CEPLEAPELGTMDCTHPF-GNFSF-SSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTC
                                                                                                                                                                                                                                                                                                           PICQ 121
                                                                                                                                                                                                                                                                                                                                                                                               CPPPPIPKFASLSVYKPLAGNNSFYGSKAVFKCLPHHAMFGNDTVTCTEHGNWTQ-LPEC
                                                                                                                                                                                                                                                                                                                                       REVRCPFPSRPDNGFVN--HPANPVLYYKDTATFGCHETYSLDGPEEVECSKFGNWS-AQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00084; sushi; sm00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                261
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SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI-LIKE.
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E -> G (I
F -> R (I
H -> N (I
H -> N (I
H -> N (I
K -> N (I
K -> R (I
K -> R (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 141.5; DB 1
Pred. No. 8.7e-07;
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                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> R (IN REF. 1)
-> R (IN REF. 1)
E117DAB609461C33
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J. Biol.
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"Identification of a partial cDNA clone for the C3d/Epstein-Barr virus receptor of human B lymphocytes: homology with the receptor fragments C3b and C4b of the third and fourth components of
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Sinha S.K., Todd S.
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MEDLINE-86287311; Pul
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: MATURE B LYMPHOCYTES, T LYMPHOCYTES AND
FOLLICULAR DENDRITIC CELLS OF THE SPLEEN.
SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF
COMPLEMENT ACTIVATION (RCA) FAMILY.
SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD21 entry;
WMW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd21.htm".
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3.C., Hedrick J.A.,
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PF00084; sushi; 1: ; SM00032; CCP; 14

pathway; Glycoprotein; Transmembrane; Repeat; Signal;

InterPro; IPR000436; Sushi_SCR_CCP

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RESULT 37

CRAB_HUMAN STANDARD; PRT; 764 AA.

ID CFAB_HUMAN STANDARD; PRT; 764 AA.

P00751; O1506, O29944; O39FF5; O39822;
DT 21-07U-1968 (Rel. 01, Created)
DT 21-07U-1968 (Rel. 01, Created)
DT 01-0CT-1994 (Rel. 04), Last snotcation update)
DT 06-0CT-1994 (Rel. 04), Last snotcation update)
DT 07-0CT-1994 (Rel. 04), Last snotcation update)
DT 08-0CT-1994 (Rel. 04), Last snotcation update)
DT 08-0CT-1995 (Rel. 04), Matanabe I., Fujita S., Rel 06-0CT-1995 (Rel. 04), Matanabe I., Fujita S., Rel 06-0CT-1996 (Rel. 04), Matanabe I., Fujita S., Rel 06-0CT-1997 (Rel. 06), Matanabe I., Rel 06-0CT-1997 (Rel. 06), Matanabe I., Rel 06-0CT-1997 (Rel. 06), Matanabe I., Rel 06-0CT-1997 (Rel. 06),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conversion by site-directed mutagenesis and expression. Immunol. 30:1587-1592(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schwaeble W., Luettig B., Sokolowski T., Estaller C., Weiss E.H., Meyer Zum Bueschenfelde K.-H., Whaley K., Dippold W.; "Human complement factor B: functional properties of a recombinant zymogen of the alternative activation pathway convertase."; Immunobiology 188:221-232(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TRYPSIN FAMILY SIMILARITY: BELONGS

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RR GLYCATION IN POSITION 291.

RX MEDLINE-91174756; PubMed-2006911;

RX Niemann M.A., Bhown A.S., Miller E.J.;

RT "The principal site of glycation of human complement factor B.";

RI Biochem. J. 274:473-480(1991).

CC -I-FUNCTION: FACTOR B WHICH IS PART OF THE ALTERNATE PATHWAY OF THE CCC COMPLEMENT SYSTEM IS CLEAVED BY FACTOR D INTO 2 FRAGMENTS: BA AND 2C TO GENERATE THE C3 OR C5 CONVERTASE. IT HAS ALSO BEEN IMPLICATED B. BB, A SERINE PROTEASE, THEN COMBINES WITH COMPLEMENT FACTOR 3B TO GENERATE THE C3 OR C5 CONVERTASE. IT HAS ALSO BEEN IMPLICATED CILL PROLIFERATION AND DIFFERENTIATION OF PREACTIVATED B LYMPHOCYTES, RAPID SPREADING OF PERIPHERAL BLOOD MONOCYTES, STIMULATION OF LYMPHOCYTE BLASTOGENESIS AND LYSIS OF ERVTHROCYTES.

CILL PROLIFERATION OF LYMPHOCYTES AND LYSIS OF ERVTHROCYTES.

CILL CATALLYTIC ACTIVITY: Cleaves C3 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3a and C3b. Both cleaves C5 in the alpha-chain to yield C3a and C3b. Both cleaves C5 in the alpha-chain to yield C3a and C3b. Both cleaves C5 in the alpha-chain to yield C3a and C5b. Both cleaves C5 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3a and C5b. Both cleaves C5 in the alpha-chain to yield C3a and C5b. Both cleaves C5 in the alpha-chain to yield C3a and C5b. Both cleaves C5b.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 component
EMBO J. 3:
[13]
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MEDLINE-83039428; PubMed-$957884;

Woods D.E., Markham A.F., Ricker A.T., Goldberger G., Colten H.R.;

"Isolation of cDNA clones for the human complement protein factor i
a class III major histocompatibility complex gene product.";

Proc. Natl. Acad. Sci. U.S.A. 79:5661-5665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and characterization complement protein factor B."; Proc. Natl. Acad. Sci. U.S.A. 80:4464-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence of the Bb fragme sequence of the major cyanogen bromic completion of the sequence of the Bb Biochem. J. 209:61-70(1983).
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RESULT 38

VCP_VACCV

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STANDARD; PRT; 26

AC P10998;
DT 01-UUL-1989 (Rel. 11, Created)
DT 01-UUL-1989 (Rel. 11, Last sequence upd
DT 16-OCT-2001 (Rel. 40, Last annotation u
DE Complement control protein precursor (V
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STRAIN-COPENHAGEN;
MEDLINE-91021027; PubMed-2219722;
MEDLINE-91021027; Perkus
          Wiles A.P.,
Barlow P.N.;
                                                                    "Vaccinia virus complement-control protein antibody-dependent complement-enhanced neutand contributes to virulence.";
                                                                                                                                                                                                                                                                                          MEDLINE=89073756; PubMed=2849238;
Kotwal G.J., Moss B.;
"Analysis of a large cluster of nonessential
vaccinia virus terminal transposition mutant.
Virology 167:524-537(1988).
                                                                                                MEDLINE=92115714; PubMed=1731333; Isaacs S.N., Kotwal G.J., Moss B.;
                             MEDLINE=97446168;
                                         STRUCTURE BY
                                                             Proc.
                                                                                                                                                                         Goebel
                                                                                                                                                                                 STRAIN=COPENHAGEN;
                                                                                                                                                                                             COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                  Nature 335:176-178(1988).
                                                                                                                        FUNCTION
                                                                                                                                           Virology
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Vaccinia virus (strain Cope
Viruses; dsDNA viruses, no
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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"Vaccinia virus encodes a secretory polypeptide structurally related
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88318974;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                              PubMed=9299352;
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                                                           complement-enhanced
  virulence.";
Sci. U.S.A. 89:628-6;
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                    Perczel A.,
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EMBL; M22812; AAA69605.1; -.
EMBL; M35027; AAA47997.1; -.
PIR; A31005; WMVZSP.
PDB; 1VVC; 03-DEC-97.
PDB; 1VVD; 03-DEC-97.
                                                                        DAF_HUMAN STANDARD; PRT; 3
P08174; P09679; P78361;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1996 (Rel. 33, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Complement decay-accelerating factor p
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J. MOI. Biol. 272:253-265(1997).

I-FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

I-SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

I-SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal;
  SEQUENCE
                                                      DAF OR CR OR CD55.
Homo sapiens (Human)
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                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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InterPro; IPR000436; Sushi_SCR_CCP
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; Repeat; Sushi;
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 (ISOFORMS
                                Chordata;
Primates;
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Pred. No. 1.1e-06;
                                Craniata; V
Catarrhini;
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precursor
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                                           Vertebrata;
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                                             Euteleostomi;
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VARIANT BLOOD GROUP DR(A-).

MEDLINE-9432573; PubMed-7519480;

Lublin D.M., Mallinson G., Poole J., Reid M.E., Thompson E.S.,

Ferdman B.R., Telen M.J., Anstee D.J., Tanner M.J.A.;

"Molecular basis of reduced or absent expression of decay-accelerating factor in Cromer blood group phenotypes.";

Blood 84:1276-1282(1994).

-1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
                                                                                                                                          "Decay-accelerating factor CD55 is echovirus 7 using CELICS, a rapid i EMBO J. 13:5070-5074(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Decay-acceleration factor (DAF; disease patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leykam J.F., Atkinson J.P., Tykocinski M.L., "Cloning and characterization of cDNAs encoding the complete sequence of decay-accelerating factor of human complement."; proc. Natl. Acad. Sci. U.S.A. 84:2007-2011(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medof M.E., Lublin D.M., Holers V.M., Ayers Leykam J.F., Atkinson J.P., Tykocinski M.L.;
                                                                                                                                                                                                 FUNCTION AS A ECHOVIRUS RECEPTOR.
MEDLINE-95045399; PubMed-7525274;
Ward T., Pipkin P.A., Clarkson N.A.,
                                                                                                                                                                                                                                                                           consensus
                                                                                                                                                                                                                                                                                                                    DISULFIDE BONDS IN SUSHI DOMAINS MEDLINE-92305034; PubMed-1377029;
                                                                                                                                                                                                                                                                                                                                                                           Moran P., Raab H., Kohr W.J., Caras I.W.; "Glycophospholipid membrane anchor attachment. Molecular analysis the cleavage/attachment site.";
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91093238; PubMed-1824699;
                                                                                                                                                                                                                                                                                                                                                                                                                                        GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakano Y., Sugita
"Isolation of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Urine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 35-46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-100 FROM N.A
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Kumar V.B., Hyung C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 35-381 FROM N.A. (ISOFORM 2).
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to generate two
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                                                                                                                                                                                       Almond J.W.
                                                                                                                                                                                                                                                           Nakano Y., Sumida K., Kikuta N., Miura N.-H., Tobe T., Tomita M.; "Complete determination of disulfide bonds localized within the short consensus repeat units of decay accelerating factor (CD55 antigen)."; Biochim. Biophys. Acta 1116:235-240(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91291869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                               Biol.
CONDENSE WITH CELL-SURFACE HYDROXYL
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87175602; PubMed=2436222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1712233;
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                                                                                                                                                          s identified a immuno-focal
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                                                                                                                                                                                                   Stone D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in ,
 OR AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the brain of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.J.,
                                                                                                                                                         as the receptor l cloning method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor (DAF) from human
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 GROUPS WHEN NASCENT
                                                                                                                                                                                                     Minor P.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                          method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                                                                                            of
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--THE COMPLEMENT CASCADE.

FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).

SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT HOMODIMER (MINOR FORM). C48 AND C38 ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
INTERACTION OF DAF WITH CELL-ASSOCIATED C48 AND C38 POLYPEPTIDES
INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES ę

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-II- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-II- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/DAF-1 AND 2/DAF-2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-II- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA COMPLEMENT PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS LINING EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX.
-II- DOMALN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE ACTIVE SITE ON SCR3 (BY SIMILARITY).
-II- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CR(A), CR(A), ES(A), MES(B), UMC, AND IFC) AND LOW-INCIDENCE (CR(A), DR(A), ES(A), MES(B), UMC, AND IFC) AND LOW-INCIDENCE (CR(B), TC(C), AND WES(A)) ANTIGENS THAT RESIDE ON DAF. IN THE CROMER PHENOTYPES A SINGLE NUCLECTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS FOR TWO CHANGES: A SIMPLE ANINO ACID SUBSTITUTION THAT IS THE BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS PHENOTYPE.

PHENOTYPE.
SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
SIMILARITY: BELONGS TO THE RECEPTORS OF CON (RCA) FAMILY. COMPLEMENT ACTIVATION

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd55.htm".

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EMBL; M31516; AAA52169.1; -.
EMBL; M30142; AAA52168.1; -.
EMBL; M30142; AAA52167.1; -.
EMBL; M15799; AAA52167.1; -.
EMBL; M15799; AAA52167.1; -.
EMBL; M64653; AAA52170.1; -.
EMBL; M64653; AAA52170.1; -.
EMBL; M64356; AAA52170.1; -.
EMBL; M64356; AAA52170.1; -.
EMBL; M64356; AAA52170.1; -.
EMBL; M64356; AA652170.1; -.
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EMBL; M6453; AA652170.1; -.
EMBL; M64653; AA66633.1; -.
EMBL; M64653; AA66633; AA66633.1; -.
EMBL; M64653; AA66633; AA66633.1; -.
EMBL; M64653; AA66633; PROPEP DOMAIN DOMAIN CHAIN MIM; SIGNAL Complement pathway; Plasma; Glycoprotein; Membrane; Alternative splicing; GPT-anchor; Signal; Sushi; Po SMART; Pfam; InterPro; 125240; -PF00084; sushi; SM00032; CCP; 4 IPR000436; Sushi_SCR_CCP splicing; GPI-anchor; antigen. 34 353 381 159 . JOINED. COMPLEMENT REMOVED IN SUSHI 1. DECAY - ACCELERATING Polymorphism;

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Best Local :
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01-FEB-1996
01-NOV-1997
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                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-94110622; Pubmed-7506731;

MICKElls M.W., Alvarez J.I., Lublin D.M., Atkinson J.P.;

"Characterization of DAF-2, a high molecular weight form of de

"Characterization" factor (DAF; CD55), as a covalently cross-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID DISULFID
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DISULFID
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Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Primat
                                                                                                                                                                                                                                                                                                                                Complement of DAF OR CD55.
                                                                                                                                                                                                                                                                                                                                                                                                                     P49457;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DAF_PONPY
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DAF-1.";
IMMUNOI. 152:676-685(1994).
IMMUNOI. 152:676-685(1994).
FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT C4B AND C3B ARE LOCALLY GENERAYED DURING C4 AND C3 ACTIVATION.
INTERPERES WITH THEIR ABBLITY TO CAPALYZE THE CONVERSION OF C2 AND THE RESE WITH THEIR ABBLITY TO CAPALYZE THE CONVERSION OF C2 AND C3 AND C3 AND C4 AND C4 AND C4 AND C4 AND C5 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNFSFSSQCAFSCSEGTNLTGIEETTC---GPFGNWSSPEPTCQVIQCEPLSAPDLGIMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSHPLASFSFTSACTFICSEGTELIGKKKTIC---ESSGIWSNPSPICQ 121
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                                                                                                                                                                                                                                                                                                                                                decay-accelerating
                                                                                                                                                                                                                                                                                                                       (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 35, Last annotation update)
(Rel. 35, Cast annotation (CD55) (Fragment).
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29.4%;
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T -> I (IN REF. 1
S -> M (IN REF. 3
S -> T (IN REF. 4
Q -> H (IN REF. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> R (IN WES(A) ANTIGEN).
/FTId=VAR_001999.
S -> L (IN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUSHI 3.
SUSHI 4.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_002000.
A -> P (IN CR(A-) ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_R -> P (I)
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GPI-ANCHOR.

HTCFTLTGLLGTLVTMGLLT -> SRPVTQAGMRWCDRSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSRTPGFKRSFHFSLPSSWYYRAHVFHVDRFAWDASNHGLA
                                                                                                                                                                                                                                                                               Catarrhini;
                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29138EEB6B4B565E
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.7e-06;
                                                                                                                                                                                                                                                                               Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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Best Local
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                         Complement pathway; Plasma; Glycoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00084; sushi; SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S67775; AAC60609.1; -.
HSSP; P08603; 1HFI.
InterPro; IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                              Alternative
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the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
201
                                               141
                       80
                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOI ACTIVE SITE ON SCR3 (BY SIMILARITY).

PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Attached to the membrane by a GPI-ancho ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AN DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE FORMATION OF C4BZA AND C3BBB, THE AMPLIFICATION CONVERTASES THE COMPLEMENT CASCADE (BY SIMILARITY).
SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENI HOMODIMER (MINOR FORM).
--HYGYRQSITYACNKGYTMIGEHSIYCTVNDDEGEWSGPPPECR 243
                                               FGATISFSCNTGYKLFGPTSSLCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGKRD 200
                                                            FSSQCAFSCSEGTNLTGIEETTC---GPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSHP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RCA) FAMILY.
                       LASFSFTSACTFICSEGTELIGKKKTIC---ESSGIWSNPSPICQ
                                                                                                31;
                                                                                                          Similarity
                                                                                                                                                          313

<1

56

121

183

246

24

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88

122

149

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149

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212

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1107

312

340
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                                                                                               Conservative
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37180
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340
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242
107
                                                                                                          18.7%;
                                                                                                                                                                                                                                                                                                                                                                                               GPI-anchor; Sushi
                                                                                                                                                           MW.
                                                                                                                                                      SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SER/THR-RICH.

BY SIMILARITY.

OFTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

GPI-ANCHOR (BY SIMILARITY).
                                                                                                16;
                                                                                                         Score 137;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT REMOVED IN
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                           MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no
                                                                                                                                                                                                                                                                                                                                                                       DECAY-ACCELERATING FACTOR
                                                                                                         DB 1;
.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                           FORM
                                                                                                                     Length 340;
                                                                                               Indels
                       121
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 14-49, 'y',51-190, 'H',192-205, 'L',207-226, 'F',228-385
A; Cross-references: GB:X16070; NID:g38092; PIDN:CAA34203.1; PID:g
A; Cross-references: GB:X16070; NID:g38092; PIDN:CAA34203.1; PID:g
R; Siegelman, M.H.; Weissman, I.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 5562-5566, 1989
A; Title: Human homologue of mouse lymph node homing receptor: evolution evolution in the company of the c C;Species: Homo sapiens (man)
C;ate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;ate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: I55333; S66798; JL0104; A34015; A33912
C;Accession: Sequence_revision | A.J.; Rambaldi, A.; Spertini, O.; Griffin, J.; Tedder
J. Biol. Chem. 265, 7760-7767, 1990
A;Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1, A;Reference number: I55333; MUID:90243637
A;Accession: I55333; MUID:90243637 A; Molecule type: mRNA
A; Residues: 1-230, 'N', 234-254, 'E', 256-385 <TED>
A; Residues: 1-230, 'N', 234-254, 'E', 256-385 <TED>
A; Cross-references: GB:X16150; NID:g34428; PIDN:CAA34275.1; PID:g34429
A; Note: the translated sequence in GenBank entry HSIYAM1, release 111.0,
R; Bowen, B.R.; Nguyen, T.; Lasky, L.A.
J. Cell Biol. 109, 421-427, 1989
A; Title: Characterization of a human homologue of the murine peripheral 1
A; Reference number: A34015; MUID:89308881
A; Accession: A34015 A:Molecule type: mRNA
A:Residues: 1-225, 'S',227-385 <CANS
A;Cross-references: EMBL:X17519; NID:g343444; PIDN:CAB43536.1; PID:g4902829
A;Cross-references: EMBL:X17519; NID:g343444; PIDN:CAB43536.1; PID:g4902829
A;Note: this translation is not annotated in GenBank entry HSLEUB, release 111.0
R;Tedder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Disteche, C.M.
J. Exp. Med. 170, 123-133, 1989
A;Title: Isolation and chromosomal localization of cDNAs encoding a novel human lymph A;Cross-references: GB:M32414; NID:g187259; PIDN:AAB60700.1; PID:g386860 R;Camerini, D.; James, S.P.; Stamenkovic, I.; Seed, B. Nature 342, 78-82, 1989
A;Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node hominal R;Reference number: S06798; MUID:90044046
A;Accession: S06798 A; Status: translated from A; Molecule type: DNA A; Residues: 14-385 < ORD> L-selectin precursor, long splice form - human N;Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc RESULT A34015 A; Accession: JL0104 A; Reference number: JL0104; MUID:89310350 oteins. A; Status: preliminary ral lymph node homing receptor Leu-8 GB/EMBL/DDBJ of the Mel-14 lymph node homing peripheral lymph node differs receptor. ਨ੍ਹ

receptor: evolutionary

conservati

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C; Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology; C; Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation F; 42-168/Domain: c-type lectin homology < CHP F; 52-385/Product: L-selectin #status predicted <SIG> F; 52-385/Product: L-selectin #status predicted <MAT> F; 52-343/Domain: extracellular #status predicted <EXT> F; 73-204/Domain: EGF homology <EGF> F; 210-267/Domain: complement factor H repeat homology <FH1> F; 272-329/Domain: complement factor H repeat homology <FH2> F; 344-368/Domain: complement factor H repeat homology <FH2> F; 364-368/Domain: transmembrane #status #status predicted <FH2> F; 364-368/Domain: complement factor H repeat homology <FH2> F; 364-368/Domain: complement factor H repeat homology <FH2> F; 364-368/Domain: complement factor H repeat homology <FH2> F; 364-368/Domain: complement #status predicted <FH2> F; 364-368/Domain: complement factor H repeat homology <FH2> F; 364-368/Domain: complement factor
C;Superfamily: L-selectin; C-type lectin homology; complemer F;1-38/Domain: signal sequence #status predicted <SIG>F;2-9-155/Domain: c-type lectin homology <LCH>F;39-372/Product: L-selectin #status predicted <MAT>F;39-157/Domain: calcium-binding #status predicted <CAB>F;39-157/Domain: calcium-binding #status predicted <CAB>F;160-191/Domain: EGF homology <EGF>F;197-254/Domain: complement factor H repeat homology <FH1>F;259-316/Domain: complement factor H repeat homology <FH2>F;333-355/Domain: transmembrane #status predicted <NMT>F;356-372/Domain: intracellular #status predicted <NTD>F;356-372/Domain: intracellular #status predicted <NTD
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 37-43;142-148 <TSU2>
C;Comment: This receptor is involved in the initial adhesive sites of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Tsurushita, N.; Fu, H.; Berg, E.L. Gene 181, 219-220, 1996
A;Title: PCR cloning of the cDNA encoding A;Reference number: JC5377; MUID:97128794
A;Accession: JC5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-selectin precursor - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 02-Jun-1997 #sequence_revision 12-Sep
C;Accession: JC537; PC4315
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A; Residues: 1-372 <TSUl>
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F;369-385/Domain: intracellular #status predicted <INT>
F;369-385/Domain: intracellular #status predicted <INT>
F;73,117,190,245,259/Binding site: carbohydrate (Asn) (covalent) #status
F;377,380/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Cross-references: GB:M25280; NID:g187182; PIDN:AAC63053.1; PID:g307134 C;Comment: For an alternative splice form, see PIR:S09702. C;GenetLcs:
A;Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1
A;Cross-references: GDB:120157; GDB:118834; OMIM:153240
A;Map position: 1q22-1q23
A;Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2 C;Function:
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31; Conservative
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 baboon L-selectin
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.2e-57
                                                                                                                                                                                                                                                                                                                                                                                                    complement factor H repeat homology;
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L-selectin precursor - bovine
N;Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)
C;Species: Bos primigenius taurus (cattle)
C;Species: Dos primigenius taurus (cattle)
                                                                                                                                                                                          RESULT
S22124
                   A; Reference number: A; Accession: S22124
                                   submitted to the EMBL Data A; Reference number: S22123
                                                                        C; Accession: S22124; A46531 R; Bosworth, B.T.
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                                                                                                                                                                                                                                                                                                                                            Вþ
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A; Status: preliminary
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F;160-191/Domain: EGF homology <EGF>
F;197-254/Domain: complement factor H repeat homology
F;259-316/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-376 < (21A-2)
A; Residues: 1-376 < (21A-2)
A; Cross-references: GB:026535; NID:9847787; PIDN:AAA67896.1; PID:9847788
A; Cromment: This protein involved in leukocyte-endothelial adhesion; it med; Superfamily: L-selectin; C-type lectin homology; complement factor H ref:1-37/Domain: signal sequence #status predicted <SIG>
F;19-155/Domain: C-type lectin homology < CCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-selectin precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998
C;Accession: JC4892
R;Qian, J; Huang, X; Marks, R.M.
Biochem. Biophys. Res. Commun. 225, 406-412, 1996
A;Title: Cloning of the CDNA for rabbit L-selectin
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JC4892
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A;Accession: JC4892
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92.48;
                                                       Library, October
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Pred. No. 3.1e-46;
8; Mismatches 18
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Pred. No. 2.3e-54;
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317

QKTKRSFSKIKE 328

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L-selectin precursor - rat

N;Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000

C;Accession: $23936

R;Watanabe, T; Song, Y; Hirayama, Y; Tamatani, T; Kuida, K; Miyasaka, M.
Biochim. Biophys. Acta 1131, 321-324, 1992

A;Title: Sequence and expression of a rat cDNA for LECAM-1.
A;Reference number: $23936; MUID:92329548

A;Accession: $23936; MUID:92329548

A;Residues: 1-372 <max/s, A;Residues: 1-372 <max/s, A;Residues: 1-372 <max/s, A;Residues: 1-372 <max/s, A;Residues: 1-372 <max/s, C-type lectin homology; complement factor H repeat homology;
F;29-155/Domain: C-type lectin homology <CCH>
F;29-155/Domain: EGF homology <CEGF>
F;160-191/Domain: EGF homology <CEGF>
F:100-254/C-main: C-monlement factor H repeat homology <FHI>
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A;Cross-references: EMBL:X62882; NID:g515; PIDN:CAA44676.1; PID:g516
R;Walcheck, B.; White, M.; Kurk, S.; Kishimoto, T.K.; Jutila, M.A.
Eur. J. Immunol. 22, 469-476, 1992
A;Title: Characterization of the bovine peripheral lymph node homing recepto
A;Reference number: A46531
A;Reference number: A46531; MUID:92164727
A;Rocession: A46531
A;Status: preliminary
A;Molecule type: mrNA
A;Residues: 39-79,'Q',81-151,'K' <WAL>
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:85686, NCBIP:85687)
C;Superfamily: L-selectin; C-type lectin homology; complement factor H repeat
F;29-155/Domain: C-type lectin homology <CH>
F;197-254/Domain: Complement factor H repeat homology <FH1>
F;259-316/Domain: complement factor H repeat homology <FH2>
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F;197-254/Domain: complement
F;259-316/Domain: complement
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  QKLDKSFSMIKE 132
                                                                                                                                  CEPLKAPELGTMNCIHPLGDFSFQSQCAFNCSEGSELLGNAKTECGASGNWTYLEPICQV 256
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                                           IQCMPLAAPDLGTMECSHPLANFSFTSACTFTCSEETDLIGERKTVCRSSGSWSSPSPIC
                                                                                       IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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71.2%;
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Pred. No. 1.
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No. 1
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.6e-40;
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                                           316
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A; Description: binds with low affinity to oligosaccarides like heparan sulfate and siment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr C; Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homolog C; Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammat F;1-51/Domain: signal sequence #status predicted <SIG> F:42-168/Domain: C-type lectin homology <CCH> F:52-323/Product: L-selectin #status predicted <MAT> F;52-323/Product: L-selectin #status predicted <MAT> F;52-300/Domain: extracellular #status predicted <EXT> F;173-204/Domain: complement factor H repeat homology <FH1> F;210-267/Domain: complement factor H repeat homology *FH1> F;272-33/Domain: com
                                                                                                                       N;Alternate names: lymph node homing receptor MEL-14; lymphocyte surface antigen C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A32375; A35102; A40167; A60906
R;Lasky, L.A.; Singer, M.S.; Yednock, T.A.; Dowbenko, D.; Fennie, C.; Rodriguez, Cell 56, 1045-1055, 1989
A;Title: Cloning of a lymphocyte homing receptor reveals a lectin domain.
A;Reference number: A32375; MUID:89168433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;301-318/Domain: transmembrane #status predicted <TRM>
F;319-323/Domain: intracellular #status predicted <INT>
F;73,117,190,245,259/Binding site: carbohydrate (Asn) (covalent)
F;322/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Map position: 1922-1923
A;Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 303/2
C;Function:
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A;Note: this translation is not annotated in GenBank entry HSLEU8, release 111.0
C;Comment: For an alternative splice form, see PIR:A34015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor. A;Reference number: $506798; MUID:$90044046 A;Accession: $509702
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A; Residues: 1-323 < CAM>
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A; Molecule type: mRNA
A; Residues: 1-372 <LA
                                                                                         A; Accession: A32375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-selectin precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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92; Conservative
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Pred. No. 4
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homology #status atypical <FH2>
icted <TRM>
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F;39-372/Product: L-selectin #status experimental <MAT>
F;39-331/Domain: extracellular #status predicted <EXT>
F;160-191/Domain: EGF homology <EGF>
F;197-254/Domain: complement factor H repeat homology <FH1>
F;297-316/Domain: complement factor H repeat homology <FH2>
F;359-316/Domain: transmembrane #status predicted <TMM>
F;332-355/Domain: intracellular #status predicted <INT>
F;36-372/Domain: intracellular #status predicted <INT>
F;60,104,216,246,278,308,320/Binding site: carbohydrate (Asn) (covalent)
F;364/Binding site: phosphate (Ser) (covalent) #status predicted
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A:Residues: 'X',40,'X',42,'XXX',46,'X',48,'XXXXXX',55-56,'X',58,'XXXXXX',65,'V',67,'XL'
C:Comment: This protein is ubiquitinated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-372 <SIE2>
A; Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
A; Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
A; Note: part of this sequence, including the amino end of the mature protein, A; Note: part of this sequence, including the amino end of the mature protein, A; Neighbor and Sequence, including the amino end of the mature protein, R; St.John, T.; Smith, H.T.; Fried, Science 231, 823-829, 1986
A; Title: Cell surface molecule associated with lymphocyte homing is a ubiquiting A; Reference number: A60906; MUID:86122900
A; Accession: A60906
A; Accession: A60906
                                                                   R; Johnston,
Cell 56, 10
                                                                                                                N;Alternate names: CD62 antigen; granule membrane protein C;Species: Homo sapiens (man) C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_c C;Accession: A30359
                                                                                                                                                                                                                                                RESULT
A30359
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                    A; Title: Cloning A; Reference number
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                                                                                                                                                                                                                        P-selectin precursor - human
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Best Local :
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on: ...
on, G.I.; ...
, 1033-1044, 1989
, nning of GMP-140, a
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                                                                         Cook, R.G.; McEver,
4, 1989
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                       MUID:89168432
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                                                                                                   R.P.
                                              membrane
                                              protein
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V.A.;
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                                                    Matches
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A;Cross-references: GB:L23088; NID:g349552; PIDN:AAA60325.1; PID:g349553 (;Superfamily: unassigned EGF-related proteins; C-type lectin homology; (F;32-158/Domain: C-type lectin homology <CCH> F;163-194/Domain: EGF homology <EGF> F;262-319/Domain: complement factor H repeat homology <FHR> F;262-319/Domain: complement factor H repeat homology <FH06> F;580-637/Domain: complement factor H repeat homology <FH07> F;642-639/Domain: complement factor H repeat homology <FH08>
                                                                                                                                                                                                                                                                                                                                                                     C;Accession: I53821
R;Auchampach, J.A.; Oliver, M.G.;
Gene 145, 251-255, 1994
A;Title: Cloning, sequence compari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:120018; OMIM:173610
A;Map position: 1922-1925
C;Superfamily: unassigned EGF-related proteins; complement C;Keywords: cell adhesion; glycoprotein; phosphohistidine; F;1-41/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 29-May-1998 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
I53821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;772-795/Domain: transmembrane #status predicted <TMN>F;796-830/Domain: intracellular #status predicted <CYT>F;54,98,180,212,219,411,460,518,665,716,723,741/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;642-699/Domain:
F;704-761/Domain:
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A30359
A;Molecule type: mRNA
A;Residues: 1-830 <JOH>
A;Cross-references: GB:M25322
                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-768 < RES>
                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: I53821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;510-567/Domain:
F;572-629/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;386-443/Domain: F;448-505/Domain:
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F;324-381/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F; 42-830/Product: F; 163-194/Domain:
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                     Query Match
Best Local
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54; Conservative
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complement factor H repeat homology <FH02>
complement factor H repeat homology <FH02>
complement factor H repeat homology <FH04>
complement factor H repeat homology <FH04>
complement factor H repeat homology <FH05>
complement factor H repeat homology <FH06>
complement factor H repeat homology <FH07>
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EGF homology <EGF>
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complement factor H repeat homology <FH09>
                                                                                                                                                                                                                                                                                                                                                equence comparison and 153821; MUID:94333817
                     42.7%;
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  17;
                     Score 313; DB 2; Pred. No. 2.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 315; DB 2;
Pred. No. 1.6e-20;
1; Mismatches 48
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on 29-May-1998
  Mismatches
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R; Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins.
A;Reference number: A42755; MUID:92340571
A;Accession: B42755
A;Status: nucleic acid sequence not shown
                                                                                                                   В
                                                                                                                                                                Q
                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:143-174/Domain: EGF homology <EGF>
F:180-238/Domain: complement factor H repeat homology
F:243-300/Domain: complement factor H repeat homology
F:305-363/Domain: complement factor H repeat homology
F:305-363/Domain: complement factor H repeat homology
F:368-426/Domain: complement factor H repeat homology
F:431-489/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1-21/Domain: signal sequence #status predicted <SIG>F;12-138/Domain: C-type lectin homology <LCH>F;22-612/Product: P-selectin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109470)
A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PA;Note: It is uncertain whether the initiator is Met-1 or the AUG codon preceding t C;Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1) C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000 C;Accession: S23174; B42755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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A; Residues: 'MKATAGV', 1-389, 391-612 <WEL>
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A; Accession: S23174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-612 <BEC>
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                                                                                                                                                                                                                                                                  1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETT-CGPFGNWSSPEPTCQ 59
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                              CK 301
                                                                        CQ 121
                                                                                                                        VVECEALTHPAHGIRKCSSNPGSYPWNTTCTFDCVEGYRRVGAQNLQCTSSGIWDNETPS
                                                                                                                                                                   VIQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPI 119
                                                                                                                                                                                                                     CKPQEHPDYGSLNCSHPFGPFSYNSSCSFGCKRGYLPSSMETTVRCTSSGEWSAPAPACH
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                                                                                                                                                                                                                                                                                                                  Similarity 42.6
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      site: carbohydrate
                                                                                                                                                                                                                                                                                                                                         41.78; 42.68;
                                                                                                                                                                                                                                                                                                                                         Score 305.5; DB 2
Pred. No. 8.2e-20;
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N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1); LECAN C;Species: Homo sapiens (man) C;Species: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000 C;Accession: A38615; A35046; A32606 C;Accession: A38615; A35046; A35046; A;Collins, T.; Williams, A.; Johnston, G.I.; Kim, J.; Eddy, R.; Shows, T.; UJ. Biol. Chem. 266, 2466-2473, 1991
                                                                                                                                            A35046
E-selectin
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A; Residues: 1-768 <WEL>
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A; Residues: 1-706 (NRL)

A; Experimental source: endothelial cells

A; Experimental source: endothelial cells

A; Note: Sequence extracted from NCBI backbone (NCBIP:109467)

R; Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.

Blood 80, 795-800, 1992

A; Title: Molecular cloning and analysis of in vivo expression of murine P-sel
A; Title: Molecular cloning and analysis of in vivo expression of murine P-sel
A; Title: Molecular cloning and analysis of in vivo expression of murine P-sel
A; Title: Molecular cloning and analysis of in vivo expression of murine P-sel
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A; Title: Molecular analysis of in vivo expression of murine P-sel
A; Title: Molecular analysis of in vivo expression of murine P-sel
A; Title: Molecular analysis of in vivo
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J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial
A;Reference number: A42755; MUID:92340571
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                                                                        IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                            CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
VQCQSLEAPPHGTMACMHPIAAFAYDSSCKFECQPGYRARGSNTLHCTGSGQWSEPLPTC
                                                                                                                                                    CGKVNIPQHVLMNCSHPLGEFSFNSQCTFSCAEGYELDGPGELQCLASGIWTNNPPKCDA
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Shows, T.; Gimbrone

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F;12-138/Domain: C-type lectin homology <LCH>
F;22-610/Product: endothelial leukocyte adhesion molecule 1 #status pred:
F;143-174/Domain: EGF homology <EGF>
F;180-237/Domain: complement factor H repeat homology <FH01>
F;242-299/Domain: complement factor H repeat homology <FH02>
F;304-362/Domain: complement factor H repeat homology <FH04>
F;367-425/Domain: complement factor H repeat homology <FH04>
F;367-425/Domain: complement factor H repeat homology <FH06>
F;430-488/Domain: complement factor H repeat homology <FH06>
F;430-488/Domain: complement factor H repeat homology <FH06>
F;430-488/Domain: complement factor H repeat homology <FH06>
F;457-578/Domain: complement factor H repeat homology <FH06>
F;457-578/Domain: transmembrane #status predicted <TMM>
F;25,145,160,179,199,203,265,312,332,503,527/Binding site: carbohydrate
                          C;Accession: JN0473
R;Strubel, N.A.; Nguyen, M.; Kansas, G.S.; Tedder, T.F.; Bischoff, J.
Biochem. Biophys. Res. Commun. 192, 338-344, 1993
A;Title: Isolation and characterization of a bovine cDNA encoding a functional homolog A;Reference number: JN0473; MUID:93249394
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A;Cross references: GB:M61893; GB:M58017; NID:g182043; PIDN:AAA52375.1; PID:g182046
R;Hession, C.; Osborn, L.; Goff, D.; Chi-Rosso, G.; Vassallo, C.; Pasek, M.; Pittack, C.
Proc. Natl. Acad. Sci. U.S.A. 87, 1673-1677, 1990
A;Title: Endothelial leukocyte adhesion molecule 1: direct expression cloning and functi A;Reference number: A35046; MUID:90175359
A;Accession: A35046
                                                                                                                                                                                         P-selectin precursor - bovine
N;Alternate names: granule membrane protein-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
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C;Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement facto
C;Superfamily: unassigned EGF-related protein; tandem repeat; transmembrane protein
C;Keywords: duplication; glycoprotein; tandem repeat; transmembrane protein
E;1-21/Domain: signal sequence #status predicted <SIG>
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JNO473
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A; Cross-references: GDB:120612; OMI
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A; Residues: 1-467,'Y',469-610
A; Cross-references: GB:M24736;
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A;Reference number: A38615; MUID:91115870
A;Accession: A38615
A;Status: preliminary
A; Accession:
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A;Title: Endothelial leukocyte adhesion molecule
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41.3%;
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Pred. No. 5.7e-19;
Pred. No. 5.7e-19;
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F;42-646/Product: F;163-194/Domain: F;200-257/Domain: F;262-319/Domain: CF;262-319/Domain: CF;262-319/Domain
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R;Larigan, J.D.; Tsang, T.C.; Rumberger, J.M.; Burn DNA Cell Biol. 11, 149-162, 1992
A;Title: Characterization of cDNA and genomic seque A;Reference number: 146708; MUID:92189729
A;Accession: 146709
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mesidues: 1-646 <STR>
A;Cross-references: GB:L12041; NID:g304246; PIDN:AAA30743.1; PID:g304247
A;Cross-references: GB:L12041; NID:g304246; PIDN:AAA30743.1; PID:g304247
C;Comment: This protein is a Ca2+ dependent receptor for myeloid cells.
C;Comment: This protein is a Ca2+ dependent receptor factor H repeat
F;182-239/Domain: complement factor H repeat homology <FH1>F;244-301/Domain: complement factor H repeat homology <FH2>F;306-364/Domain: complement factor H repeat homology <FH3>F;306-364/Domain: complement factor H repeat homology <FH3>F;309-427/Domain: complement factor H repeat homology <FH4>F;432-486/Domain: complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,201,314,321,466/Binding site: carbohydrate (Asn) (complement factor H repeat homology <FH5>F;32,45,2
                                                                                                                                                                                                                                                                                                                                   A; Map position: 1922-925
A; Introns: 13/1; 143/1; 179/1; 241/1; 303/1; 366/1; 429
C; Superfamily: unassigned EGF-related proteins; C-type
C; Keywords: duplication; glycoprotein; tandem repeat
F; 14-140/Domain: C-type lectin homology 
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C; Keywords: cell
F;1-41/Domain: s:
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A;Residues: 1-307,'T',309-327,'T',329-490,'A',492-551 <LAR2>
A;Cross-references: GB:M91004; NID:g165004; PIDN:AAA31243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-551 <LAR1>
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F;612-646/Domain:
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16/Product: P-selectin #status predicted <MAT>
194/Domain: EGF homology <EGF>
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48; Conserv
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complement factor H repeat homology <FH2>
complement factor H repeat homology <FH3>
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complement factor H repeat homology <FH4>
complement factor H repeat homology <FH5>
complement factor H repeat homology <FH5>
complement factor H repeat homology <FH5>
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Pred. No. 2.1e-18;
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Nature 365, 267-269, 1993

A;Title: A role for sialyl Lewis-X/A glycoconjugates in capillary morphogenes
A;Reference number: S36772; MUID:93382537

A;Recession: S36772
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <NGU>
A;Cross-references: GB:L12039; NID:9402913; PIDN:AAA02991.1; PID:9402914
C;Superfamily: unassigned EGF-related proteins; C-type lectin homology; compl
F;181-337/Domain: C-type lectin homology <ICH>
F;181-337/Domain: complement factor H repeat homology <FH1>
F;242-299/Domain: complement factor H repeat homology <FH2>
F;304-562/Domain: complement factor H repeat homology <FH4>
F;367-421/Domain: complement factor H repeat homology <FH4>
                                                                                                                 RESULT 16
JC5092
E-selectin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 19-May-2000
C;Accession: JC5092
R;Winkler, H.; Brostjan, C.; Csizmadia, V.; Natarajan, G.; Anrather, J.; Bacane 176, 67-72, 1996
Gene 176, 67-72, 1996
Gene 176, 67-72, 1996

A; Title: The intron-exon structure of the porcine E-selectin-encoding gene. A; Reference number: JC5092; MUID:97075911

A; Accession: JC5092

A; Molecule type: DNA
A; Residues: 1-482 CWIND
A; RCoss-references: GB:U37521; NID:g1052974; PIDN:AAC48680.1; PID:g1052975
C; Comment: This protein is a member of the selectin family of adhesion mole C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
$36772
E-selectin - bovine
C:Species: Bos primigenius taurus (cattle
C:Date: 10-Dec-1993 #sequence_revision 27
C:Accession: $36772
C:Accession: $36772
C:Accession: $36772
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Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 CEAQVQPQHGSLNCTHPLGNFSYNSSCSVSCERGYLPSSTETTWCTSSGEWSAPPATCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 VKCDALSNLDNGVVNCSPNHGSLPWNTTCTFECQEGYKLTGPQHLQCTSSGIWDNKQPTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEPLEAPELGTMDCTHPFGNESFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPAQKHPEHGHLVC-NPLGKFTYNSSCSISCAEGYLPSSTEATRCMSSGEWSTPLPKCNV
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Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271.5;
Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1e-17;
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                                                                                                                                                                                                                     G.; Anrather, J.; Bach,
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A; Note: this is u. p. ...
R; Sim, R.B.; Discipio, R.G.
R; Sime, J. 205, 285-293, 1982
Blochem. J. 205, 285-293 and structure.
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A;Title: Human complement factor H: two factor H proteins A;Reference number: A60238; MUID:91184292
                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 'IL',55-401,'Y',403-449 <SCH>
A;Residues: 'IL',55-401,'Y',403-449 <SCH>
A;Residues: 'IL',55-401,'Y',403-449 <SCH>
A;Residues: 'IL',55-401,'Y',403-499; PIDN:CAB41739.1; PID:g4725976
A;Note: an additional nucleotide present within the codon for Glu-310 was thought to A;Note: an additional nucleotide present within the codon for Glu-310 was thought to R;Schweeble, W.; Zwirner, J.; Schulz, T.F.; Linke, R.P.; Dierich, M.P.; Weiss, E.H.
Eur. J. Immunol. 17,185-1489, 1987
Eur. J. Immunol. 17,185-1489, 1987
A;Title: Human complement factor H: expression of an additional truncated gene production of the product of the codon for the codon for an additional truncated gene production of the codon for additional truncated gene production of the codon for Glu-310 was thought to A;Reference number: A61103; MUID:88055295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-33;434-449 <EST>
A; Note: only portions of this 1.8 kilobase mRNA were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change 08-Dec-2000 C;Accession: S03013; B60238; A27877; A61103; A26505; S10479 R;Ripoche, J; Day, A.J; Harris, T.J.R.; Sim, R.B. Biochem, J. 249, 593-602, 1988 A;Title: The complete amino acid sequence of human complement factor H. A;Reference number: S00254; MUID:88134059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 13/1; 1421; 178/1; 237/1; 300/1; 363/1; 422/1; 459/1; 466/1 C;Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement F;13-139/Domain: C-type lectin homology <LCH> F;181-235/Domain: complement factor H repeat homology <FH1> F;240-298/Domain: complement factor H repeat homology <FH2> F;303-361/Domain: complement factor H repeat homology <FH3> F;366-420/Domain: complement factor H repeat homology <FH4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, Eur. J. Immunol. 16, 1311-1355, 1986 Eur. J. Human complement factor H: isolation of cDNA clones and A;Reference number: A27877; MUID:87054207
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                                                                                                                                A; Molecule type: mRNA
A; Residues: 27-76 <SC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X07523; EMBL:X00716; NID:g32492; PIDN:CAA30403.1; PID:g75807 A;Note: part of this sequence, including the amino end of the mature protein was conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-449 < RIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement factor H precursor, short splice form [validated] - human N; Alternate names: complement factor H-related protein; complement p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                     A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                       A; Accession: A61103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: not compared with conceptual translation
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                                                                                             this is a partial sequence of
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43; Conservative
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Pred. No. 1.
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structural studies

on

the complement-system control protein

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A;Pathway: complement alternate pathway
C;Superfamily: complement factor H; complement factor H repeat homology
C;Keywords: alternative splicing; complement alternate pathway; glycoprotein; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-449/Product: complement factor H, short splice form #status experimental <MAT>
F;21-80/Domain: complement factor H repeat homology <FH01>
F;85-141/Domain: complement factor H repeat homology <FH02>
F;146-205/Domain: complement factor H repeat homology <FH03>
F;210-262/Domain: complement factor H repeat homology <FH04>
F;210-262/Domain: complement factor H repeat homology <FH05>
F;210-263/Domain: complement factor H repeat homology <FH05>
F;210-385/Domain: complement factor H repeat homology <FH06>
F;389-442/Domain: complement factor H repeat homology <FH06>
F;389-442/Domain: complement factor H repeat homology <FH06>
F;389-442/Domain: complement factor H repeat homology <FH06>
F;310-408/Domain: complement factor H repeat homology <FH06>
F;310
complement factor H precursor, recomplement factor H precursor, recomplement factor H precursor. Complement factor H precursor (man) C; Species: Homo sapiens (man) C; Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-2000 C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #text_change 08-Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #text_change 08-Dec-2000 C; Dec-1993 #text_change 08-Dec-1993 #text_change 0
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A;ROlecule type: mRNA
A;RCSidues: 226-401,'Y',403-449 <KRI>
A;Residues: 226-401,'Y',403-449 <KRI>
A;Rcsidues: 226-401,'Y',403-449 <KRI>
A;Rcsidues: 226-401,'Y',403-449 <KRI>
A;Cross-references: GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473
A;Cross-references: GB:M12383; NID:g180473; PIDN:AAA52013.1; PID:g180473;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
NBHUH
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A;Map position: 1q32-1q32
A;Note: the correspondence bet
C;Function:
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C; Genetics: <HF4
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A; Map position: 1q32-1q32
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Biochemistry 31, 3626-3634, 1992
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A; Accession: A26505
A; Molecule type: protein
A; Residues: 19-20,'Q',22
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Immunol. 136, 3407-3411, 1986
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                                                                                                                                                                                     C; Comment: Factor H has also been found bound to cell membranes in an unknown manner. C; Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liv
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A; Molecule type: mRNA
A; Residues: 'DFRN', 579-1231 <DAY>
A; Residues: 'DFRN', 579-1231 <DAY>
A; Residues: 'DFRN', 579-1231 <DAY>
A; Cross-references: GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
A; Note: parts of this sequence were determined by protein sequencing
R; Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbell, R.D.; Sim, R
Blosci. Rep. 6, 65-72, 1986
A; Title: Partial characterization of human complement factor H by protein
A; Reference number: A61565; MUID:86188123
A; Accession: A61565
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A; Title: Sequence analysis of a cDNA clone encoding the C-terminal A; Reference number: A54726; MUID:88025472
A; Accession: A54726
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Three-dimensional structure of a complement control protein module A;Reference number: A49224; MUID:91278097
A;Contents: annotation; NMR structure determination, residues 927-985
R;Estaller, C.; Kolstinen, V.; Schwaeble, W.; Dierich, M.P.; Weiss, E.H.
J. Immunol. 146, 3190-3196, 1991
A;Title: Cloning of the 1.4-kb mRNA species of human complement factor H rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Solution structure of the fifth repeat of factor H: A R;Reference number: A44551; MUID:92332649
A;Reference number: NMR structure determination, residues A;Contents: annotation, NMR structure determination, residues R;Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; J. Mol. Biol. 219, 717-725, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 205, 285-293, 1982
A; Title: Purification and structural studies
A; Reference number: A26505; MUID:83048213
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Eur. J. Immunol. 21, 799-802, 1991
A;Title: Human complement factor H: two factor H
                                                                                          A; Reference number: A; Accession: S66298
                                                                                                                           R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, 7
Biochim. Biophys. Acta 1289, 305-311, 1996
A;Title: Factor H co-purifies with thrombospondin
A;Reference number: S66298; MUID:96205365
                                                                                                                                                                                                            A;Cross-references: GB:m65294; NID:g183766; PIDN:AAA35948.1; PID:g183767 R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon
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A; Residues: 1047-1231 <RES>
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A; Residues: 19-20,'Q',22-29,'V',31-33,'Q',35
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A; Residues: 'METGRNHLNAKI', 1050-1057, 'T', 1059-1102
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A; Residues: 1-56;1177-1231 <EST>
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A;Accession: A60238
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A; Residues: 1-1231 <RIP>
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A; Molecule type: protein
A; Residues: 411-419; 574-578, 580-582 <CAR>
                                                             A; Status: preliminary
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534, 1992
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he alternative complement pathway

A; Pathway: complement alternate pathway
C; Superfamily: complement factor H; complement factor H repeat homolo
C; Reywords: alternative splicing; complement alternate pathway; glyco
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-1229/Product: complement factor H #status experimental <MPT>
F; 19-449/Product: complement factor H, short splice form #status experiments for H repeat homology <FH01>
F; 21-80/Domain: complement factor H repeat homology <FH02>
F; 146-205/Domain: complement factor H repeat homology <FH03>
F; 146-262/Domain: complement factor H repeat homology <FH04>
F; 210-320/Domain: complement factor H repeat homology <FH04>
F; 210-320/Domain: complement factor H repeat homology <FH05>
F; 210-325/Domain: complement factor H repeat homology <FH05>
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F; 210-325/Domain: complement factor H repeat homology <FH05>
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A;Cross-references: GDB:120041;
A;Map position: 1932-1932
C;Genetics: <HF2>
A;Gene: GDB:HF2; HF
A;Cross-references: GDB:129095
A;Map position: 1932-1932
A;Mote: the correspondence betwe
C;Function:
A;Description: a cofactor in the
complement receptor 1 - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Oate: 02-Jul-196 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: 136936; 136937
R;Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P.
J. Immunol. 153, 691-700, 1994
A;Title: Primary sequence of an alternatively spliced form of CR1. Candidate A;Reference number: 136935; MUID:94292799
A;Accession: 136936
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F;1109-1163/Domain: complement factor H repeat homology <FH18>
F;1167-1228/Domain: complement factor H repeat homology <FH19>
F;1167-1228/Domain: complement factor H repeat homology <FH19>
F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F;218-1043,811-853,839-864,870-915,901-926,931-973,959-984,989-1032,1018-1043,1048-1091,1077-
F;217/Binding site: carbohydrate (Asn) (covalent) #status experimental F;718,1029,1095/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;870-926/Domain: complement factor H repeat homology <FH15>
F;870-926/Domain: complement factor H repeat homology <FH15>
F;931-984/Domain: complement factor H repeat homology <FH17>
F;989-1043/Domain: complement factor H repeat homology <FH17>
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F;811-864/Domain:
F;870-926/Domain:
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Pred. No. 1.1e-07;
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                                                                     for the
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-683,'X',685-894,'A',896-1000,1451-1471,'X',1473-2489 <VIK2>
A;Cross-references: GB:L17418; NID:g306678; PIDN:AAB60694.1; PID:g306680
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A;Residues: 1-683,'X',685-1133,'X',1135-1471,'X',1473-2489 <VIK1>
A;Cross-references: GB:L17418; NID:g306678; PIDN:AAB60695.1; PID:g451303
                                                                                                                                                                                                           A;Reference number: 156203; MUID:94065175
A;Accession: 173012
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                   R:Vik, D.P.: Wong, W.W.
J. Immunol. 151, 6214-6224, 1993
A:Title: Structure of the gene for the F allele
A:Reference number: I56203; MUID:94065175
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement C3b/C4b receptor, membrane-bound form precursor - N;Alternate names: complement C3b/C4b receptor; complement rN;Contains: complement C3b/C4b receptor, secreted form C;Species: Homo sapiens (man)
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F:333-991/Domain: complement factor H
F:396-462/Domain: complement factor H
F:470-526/Domain: complement factor H
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F;141-207/Domain: complement factor H repeat homology <FH03>
F;213-268/Domain: complement factor H repeat homology <FH04>
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C; Superfamily: C4b-bindir
C; Keywords: duplication;
F; 18-74/Domain: complement
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-Jul-1996 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000 C;Accession: I73012; I56203; A47602; S03291; S03843; A28507; A24748; B24748;
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F;1296-1362/Domain:
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F;1172-1228/Domain:
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A; Residues: 1-397,1751-2014 <BIR2>
                                                                                                               A; Accession: I56203
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F;1749-1815/Domain:
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A; Cross-references: GB:L24920; NID:g551564; PIDN:AAA51438.1; PID:g557725
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1489 CEIISCEPPPTISNGDF----YSNNRASFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1432 CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COVICEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKDDQVGVWSSPPPRCISTNK 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS----GIWSNPSPICQKLDK 125
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complement factor H repeat homology <FH12>
complement factor H repeat homology <FH13>
complement factor H repeat homology <FH14>
complement factor H repeat homology <FH15>
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complement factor H repeat homology <FH15>
complement factor H repeat homology <FH17>
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complement factor H repeat homology <FH17>
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Pred. No. 5.5e
16; Mismatches
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H repeat homology <FH07>
H repeat homology <FH08>
H repeat homology <FH09>
H repeat homology <FH10>
Trepeat homology <FH10>
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F;688'743/Upumain: complement factor H repeat homology F;747-803/Domain: complement factor H repeat homology <FH13>
F;808-866/Domain: complement factor H repeat homology <FH14>
F;871-937/Domain: complement factor H repeat homology <FH15>
F;943-999/Domain: complement factor H repeat homology <FH15>
F;1004-1061/Domain: complement factor H repeat homology <FH1F;1106-1132/Domain: complement factor H repeat homology <FH1F;1118-1193/Domain: complement factor H repeat homology <FH1F;118-1193/Domain: complement factor H repeat homology <FH1F;118-1193/Domain: complement factor H repeat homology <FH1F;118-1193/Domain: complement factor H repeat homology <FH1F;118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:104-161/Domain: complement factor H repeat homology <FH02>
F:166-232/Domain: complement factor H repeat homology <FH03>
F:266-232/Domain: complement factor H repeat homology <FH04>
F:297-353/Domain: complement factor H repeat homology <FH05>
F:297-353/Domain: complement factor H repeat homology <FH05>
F:358-416/Domain: complement factor H repeat homology <FH06>
F:421-487/Domain: complement factor H repeat homology <FH07>
F:493-549/Domain: complement factor H repeat homology <FH08>
F:554-611/Domain: complement factor H repeat homology <FH10>
F:616-682/Domain: complement factor H repeat homology <FH10>
F:688-743/Domain: complement factor H repeat homology <FH11>
F:688-743/Domain: complement factor H repeat homology <FH11>
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A:Introns: 41/1; 101/1; 134/2; 163/1; 296/1; 355/1; 389/2; 418/1; 491/1; 551/1; 584/2; 1484/2; 1513/1; 1646/1; 1705/1; 1739/2; 1768/1; 1844/1; 1904/1; 1937/2; 1966/1; 2099, C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C:Keywords: duplication; glycoprotein; transmembrane protein C:Keywords: duplication; glycoprotein; transmembrane protein F:11-41/Domain: signal sequence #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor, membrane_bound form #status predicted <- CSTC> F:42-2489/Product: complement C3b/C4b receptor <- CSTC> F:42-2489/Product: complement C3b/C4b 
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A;Molecule type: mRNA
A;Residues: 953-1221, YEV, 1224-2064, 'I', 2066-2276, 'P', 2278-2299, 'H', 2301-2325,
A;Residues: 953-1221, YEV, 15309; NID:g30196; PIDN:CAA28933.1; PID:g809019
A;Wong, W.W.; Klickstein, L.B.; Smith, J.A.; Weis, J.H.; Fearon, D.T.
Proc. Natl. Acad. Sci. U.S.A. 82, 7711-7715, 1985
A;Title: Identification of a partial cDNA clone for the human receptor for compa;Reference number: A94073; MUID:86067975
A;Accession: A24748
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A;Title: Structure of the human CR1 gene. Molecular basis of the A;Reference number: A47602; MUID:89176869
A;Accession: A47602
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A;Residues: 1-894,'A',896-1000,1451-2064,'I',2066-2276,'P',2278-2299,'H',2301-2325,
A;Cross-references: EMBL:Y00816; NID:g30185; PIDN:CAA68755.1; PID:g30186
A;Cross-references: EMBL:Y008, Smith, J.A.; Weis, J.H.; Wilson, J.G.; Fearon, D.T.
J. Exp. Med. 165, 1095-1112, 1987
J. Exp. Med. 165, 1095-1112, 1987
A;Title: Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating d
A;Reference number: A28507; MUID:87168191
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R;Kilckstein, L.B.; Bartow, T.J.; Miletic, V
J. Exp. Med. 168, 1699-1717, 1988
A;Title: Identification of distinct C3b and
A;Reference number: S03843; MUID:89035992
A;Accession: S03843
A;Status: translation not shown
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A; Residues: 311-333;729-745;831-845 <WO2>
A; Cross-references: GB:M11569; NID:g180991;
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A; Residues: 26-584 <HOU>
A; Cross-references: EMBL:X14362; NID:g30197;
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R;Hourcade, D.; Miesner, D.R.;
J. Exp. Med. 168, 1255-1270, 1
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A; Residues: 1-41 <WON>
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A;Mclecule type: mRNA
A;Cross references: EMBL:Z35490
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology <FH1>
F;50-107/Domain: complement factor H repeat homology <FH2>
F;112-169/Domain: complement factor H repeat homology <FH4>
F;234/Domain: complement factor H repeat homology <FH4>
F;239-360/Domain: complement factor H repeat homology <FH5>
F;364-422/Domain: complement factor H repeat homology <FH5>
F;364-422/Domain: complement factor H repeat homology <FH6>
F;464-432/Domain: complement factor H repeat homology <FH7>
F;484-538/Domain: complement factor H repeat homology <FH8>
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F;1846-1902/Domain:
F;1907-1964/Domain:
F;1969-2015/Domain:
F;2041-2096/Domain:
F;2100-2156/Domain:
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F:1321-1387/Domain:
F:1393-1449/Domain:
F:1454-1511/Domain:
F:1454-1511/Domain:
F:1516-1582/Domain:
F:1588-1643/Domain:
F:1547-1703/Domain:
F:1708-1766/Domain:
                                                                                                                                                                                                                                                                                                                                                                                            C4BP alpha chain precursor - rabbit
C;Species: Oryctolagus cuniculus (domes
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: $53711
R;de Frutos, P.G.; Dahlbaeck, B.
                                                                                                                                                                                                                                                                                                                                                            R;de Frutos, P.G.; Dahlbaeck, B.
Biochim. Biophys. Acta 1261, 285-289, 1995
A;Title: cDNA structure of rabbit C4b-binding
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S53711
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F;2298-2354/Domain:
F;2359-2415/Domain:
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                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid
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Best Local
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DFSFGSQIEFSCSEGYILIGSTTSHCDIQEKGVEWSDPLPKCEIVKCEP--PPN--IING
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Oryctolagus cuniculus (domestic rabbit)
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45; Conserv
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SHPLAS---FSFTSACTFICSEGTELIGKKKTIC----ESSGIWSNPSPICQKL

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C;Genvertase) in the alternative complement pathway.
C;Gentetics:
A;Map position: 1
C;Superfamily: complement factor H; complement factor H repeat homology
C;Superfamily: complement alternate pathway; duplication; glycoprotein; plasma
F;1-18/Domain: signal sequence #status predicted <MPT>
F;1-80/Domain: signal sequence #status predicted <MPT>
F;1-80/Domain: complement factor H repeat homology <FH02>
F;16-205/Domain: complement factor H repeat homology <FH03>
F;10-262/Domain: complement factor H repeat homology <FH03>
F;246-248/Region: cell attachment (R-G-D) motif
F;267-320/Domain: complement factor H repeat homology <FH07>
F;389-442/Domain: complement factor H repeat homology <FH08>
F;325-385/Domain: complement factor H repeat homology <FH08>
F;325-544/Domain: complement factor H repeat homology <FH08>
F;369-622/Domain: complement factor H repeat homology <FH08>
F;369-633/Domain: complement factor H repeat homology <FH10>
F;696-622/Domain: complement factor H repeat homology <FH11>
F;697-743/Domain: complement factor H repeat homology <FH11>
F;698-641/Domain: complement factor H repeat homology <FH11>
F;936-989/Domain: complement factor H repeat homology <FH13>
F;936-989/Domain: complement factor H repeat homology <FH15>
F;936-989/Domain: complement factor H repeat homology <FH16>
F;936-989/Domain: complement factor H repeat homology <FH16>
F;936-989/Domain: complement factor H repeat homology <FH18>
F;936-989/D
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A;Reference number: I49711; MUID:90111033

A;Recession: I49711

A;Rectus: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: I-18 <RES>

A;Cross-references: GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729

R;Munoz-Canoves, P.; Tack, B.F.; Vik, D.P.

Biochemistry 28, 9891-9897, 1899

A;Title: Analysis of complement factor H mRNA expression: Dexamethasone and IF

A;Reference number: I49728; MUID:90148935

A;Reference number: I49728; MUID:90148935

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: I-19 <RE2>

A;Cross-references: GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926

C;Comment: Two codominant alleles of factor H are present in mice.

C;Comment: Factor H functions as a cofactor in the inactivation of C3b by seri
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Proc. Natl. Acad. Sci. U.S.A. 83, 3963-3967,
A;Title: Murine protein H is comprised of 20
A;Reference number: A26154; MUID:86233353
A;Accession: A26154
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: Ag-1149711; I49728
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                                                                                                                                                                                                                 1053-1107/Domain: complement factor H repeat homology <FH18>;1114-1168/Domain: complement factor H repeat homology <FH19>;1114-123/Domain: complement factor H repeat homology <FH10>;1172-1233/Domain: complement factor H repeat homology <FH20>;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,35;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,35;21-66,52-80,85-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,1082-802,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-850,808-
    Best Local Similarity
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28.0%;
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    Score
Pred.
    160; DB 1;
No. 1.6e-06;
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A; Residues: 1-1019 <MUT>
A; Cross-references: GB:D'
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                                              223 LRFSCDSPYYLIGQETLTCQGNGQWSGQIPQCKKL
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                                                                                                                                                                                                                                                                                                               29 FSCSEGTNLTGIEETTCGPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSHPLASFSFTSA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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C;Superfamily: coagulation factor C; C-type lectin homology; complement C;Keywords: alternative splicing; glycoprotein; hemolymph coagulation; h F;1-25/Domain: signal saquence #status predicted <SIG>F;26-690/Product: coagulation factor C heavy chain #status experimental F;136-195/Domain: complement factor H repeat homology <FH01>F;199-254/Domain: complement factor H repeat homology <FH02>F;199-254/Domain: complement factor H repeat homology <FH03>F;1960-321/Domain: complement factor H repeat homology <FH03>F;1960-521/Domain: C-type lectin homology <FH03>F;1960-564/Domain: C-type lectin homology <FH03>Financin High <FH03-Financin H
                                                                                                                                                                                                                                                                                                                                                                                       F:576-634/Domain: complement factor H repeat homology <FH04>
F:685-747/Domain: complement factor H repeat homology #status
F:685-747/product: coagulation factor C light chain peptide A
F:763-1019/Product: coagulation factor C light chain peptide E:763-1019/Product: coagulation factor C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Notecute type: protein
A; Molecule type: protein
A; Residues: 'S', 27-39, 'S', 41, 'T', 43-54, 'E'; 691-782; 950-977 <TOK>
C: Superfamily: coagulation factor C; C-type lectin homology; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is a novel type of serine protease.
A; Reference number: S00105; MUID:88004461
A; Accession: S00105
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A; Title: Limulus factor C. An endotoxin-sensitive

A: Peference number: A38738; MUID:91177916
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                                                                                                                                                                                                 F;523,534,624,912/Binding site: carbohydrate (Asn) (covalent) #status predicted F;767/Binding site: carbohydrate (Asn) (covalent) #status experimental F;809,865,966/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor
                                                                                                                                                                                                                                                                                                                                                   F;763-1015/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:D9027
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Score 155.5;
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B #status experimental <
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A;Cross-references: GB:M61132; NID:g192692; PIDN:AAA63295.1; PID:g192693 R;Fingeroth, J.D.; Benedict, M.A.; Levy, D.N.; Strominger, J.L. Proc. Natl. Acad. Sci. U.S.A. 86, 242-246, 1989 A;Title: Identification of murine complement receptor type 2. A;Reference number: A32215; MUID:89098890
  A;Cross-references: GB:J04153 R;Kurtz, C.B.; Paul, M.S.; Ae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A43526; A43538; A32215; A45802; B32215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement C3d/Epstein-Barr virus receptor ?
N;Alternate names: complement receptor type
C;Species: Mus musculus (house mouse)
                                              A; Molecule type: mRNA
A; Residues: 343-401; 991-1025 <FI2>
                                                                                                                                                                                                                                                                                                               R; Molina, H.; Kinoshita, T.; Inol
J. Immunol. 145, 2974-2983, 1990
A; Title: A molecular and immunocl
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A43526
                                                                                            A; Accession: A32215
                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 12-305, T, 307-519, A', 521-1025 < MOL>
                                                                                                                                                                                                                                                                                        A; Title: A molecular and immunochemical characterization A; Reference number: A43538; MUID:91010789
                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M35684; EMBL:J04153; NID:g192687; PIDN:AAA37448.1; R;Molina, H.; Kinoshita, T.; Inoue, K.; Carel, J.C.; Holers, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1025 <FIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A43526;
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A;Map position: X
A;Introns: 14/1; 75/1; 102/3; 128/1; 186/1; 272/
C;Superfamily: C4b-binding protein alpha chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, April A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T07H6.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t C;Accession: T16833 R;Geisel, C.
                                                                                                                                                                                                                                                                       A; Accession: A43538
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A43526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U53344; NID:g1255886; PID:g1255889; PIDN:AAA96225.1; GSPDB:GN00A;Experimental source: strain Bristol N2; clone T07H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-560 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T16833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 ATECSRPSSPLHGKVVGS----SLTYQSVVTYSCDHGYRLVGQVQRICLAEGIWGGNEPR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CEEI 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEPLEAPELGTMDCTHPFGN-FSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKARACPDPGDIENGLREGDTFEYPHHVKYSCNPGFLLVGSTSRQCSSNGEWTNEPANCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.D.
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  Aegerter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 150.5;
Pred. No. 5.2e
24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-Sep-1999 #text_change 17-Mar-2000
Weis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996
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ain; complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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J.J.;
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  Weis,
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C4b-binding protein alpha chain precursor - human N;Alternate names: C4BP; proline-rich protein C;Species: Homo sapiens (man) C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Accession: A33568; S02372; A90236; A24182; A93134; S29492; A31785; I52244; R;Matsuguchi, T:; Okamura, S20, T:; Sata, T:; Niho, Y. Biochem. Biophys. Res. Commun. 165, 138-144, 1989 A;Title: Molecular cloning of the cDNA coding for proline-rich protein (PRP) A;Reference number: A33568; MUID: 90073699
                       A;Cross-references: GB:M31452; NID:g190501; PIDN:AAA36507.1; A;Note: the authors translated the codon GGA for residue 492 R;Lintin, S.J.; Lewin, A.R.; Reid, K.B.M.
                                                                                              A; Molecule type: mRNA
A; Residues: 1-597 <MA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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                                                                                                                                              A; Accession: A33568
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F;778-833/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-11/Domain: signal sequence #status predicted <SIG F;12-1025/Product: complement C3d/Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: the authors translated the codon CAC for residue 727 as Asn C;Superfamily: complement C3d/Epstein-Barr virus receptor; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 'E', 100-101,292-961,964-1025 <KUR>
A; Cross-references: GB:M29281; NID:g192685; PIDN:AAA37447.1; PID:g387131
                                                                                                                                                                                                                                                                                                                                                                                                              NBHUC4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;902-958/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;594-649/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;402-458/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;146-202/Domain:
F;207-263/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;82-138/Domain: complement factor H repeat homology <FH02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;12-973/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: alternative splicing; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 VIPTCKEAQCEHPGKFPNGQVKEPLSLQVGTTVYFSCNEGYQLQGQPSSQCVIVEQKAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 PEPTCQVIQC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTGSQKTGIWSGPAPYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C----ESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKKPVCKEILCPPPPPVRNGSH-TGSFSENVPYGSTVTYTCDPSPEKGVSFTLIGEKTIN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CESDFPLECPSLPTIHNGHHTGQHVDQFVAGLSVTYSCEPGYLLTGKKTIKCLSSGDWDG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE---PLEAPELGTMDCTHPFG----NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----APDLGIMNCSHPLASFS----FTSACTFICSEGTE-----LIGKKKTI 106
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complement factor H repeat homology <FH07>
complement factor H repeat homology <FH08>
complement factor H repeat homology <FH09>
complement factor H repeat homology <FH10>
complement factor H repeat homology <FH112>
complement factor H repeat homology <FH12>
complement factor H repeat homology <FH13>
complement factor H repeat homology <FH13>
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complement factor H repeat homology <FH04>
complement factor H repeat homology <FH05>
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1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 150.5; DB : Pred. No. 9.4e-06, 2; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status predicted
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                                                                                                                                                                                                   proline-rich protein (PRP): identit
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                                                                    PID: 9190502
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R.Suzuki, K.; Nishioka, J.
J. Biol. Chem. 263, 17034-17039, 1988
A;Title: Binding site for vitamin K-dependent protein A;Reference number: A31785; MUID:89034204
A;Accession: A31785
                  A;Cross-references: GB:M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500 C;Comment: C4BP controls the classical pathway of complement activation. It binds as a the degradation of the C4BC2a complex (C3 convertase) by dissociating the complement C;Comment: C4BP occurs in plasma in two forms, both of which bind complement fragment isulfide bonds. The beta chain binds the vitamin K-dependent plasma protein S. A minor
                                                                                                                                                                                                                          A;Contents: annotation; electron microscopy; three-dimensional structure; R;ASO, T.; Okamura, S.; Matsuguchi, T.; Sakamoto, N.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. 174, 222-227, 1991
A;Title: Genomic organization of the alpha chain of the human C4b-binding A;Reference number: I52244; MUID:91113199
A;Accession: I52244
                                                                                                                                                                                                                                                                                                                                                                                 A; Note: this peptide appears to bind protein S R; Dahlback, B.; Smith, C.A.; Muller-Eberhard, H.J. Proc. Natl. Acad. Sci. U.S.A. 80, 3461-3465, 1983 A; Title: Visualization of human C4b-binding protein A; Reference number: A93950; MUID:83221615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The region Ser(333)-Arg(356) of the alpha-chain of A;Reference number: S29492; MUID:93146164 A;Accession: S29492
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A; Reference number: A93134; MUID:85296001
A; Accession: A93134
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Mol. Immunol. 22, 427-435, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Studies on the structure of the human A;Reference number: A24182; MUID:86301119 A;Accession: A24182 BNA A;Residues: 203-288 <LIN>A;Cross-references: EMBL:X04284; EMBL:X04296
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                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-597 < ASO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 495-505, 'X',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 381-404 < HES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: this paper reports amino-terminal sequences of the intact R;Hessing, M.; Kanters, D.; Takeya, H.; van't Veer, C.; Hackeng, TFEBS Lett. 317, 228-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 49-81 <CH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Amino acid sequence studies of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rodriguez de Cordoba, S.; J. Exp. Med. 173, 1073-1082,
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A; Cross-references: GB: X02865; NID: g29564;
A; Note: 92-Thr and 37-His were also found
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A; Residues: 17-81 <LI2>
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J. 230, 133-141,
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204, 77-81, 1986
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C;Comment: The molecule has C;Genetics:
A;Gene: GDB:C4BPA
A;Cross-references: GDB:120
A;Map position: 1932-1932
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C;Complex: octamer of seven alpha chains and one beta chain
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
C;Superfamily: C4b-binding protein alpha chain; complement gathway; duplication; glycoprotein;
F;1-48/Domain: signal sequence #status predicted <SIG>
F;1-48/Domain: signal sequence #status predicted <SIG>
F;1-59-7/Product: C4b-binding protein alpha chain #status predicted <MAT>
F;13-10/Domain: complement factor H repeat homology <FH1>
F;13-170/Domain: complement factor H repeat homology <FH3>
F;239-294/Domain: complement factor H repeat homology <FH5>
F;393-360/Domain: complement factor H repeat homology <FH5>
F;364-422/Domain: complement factor H repeat homology <FH6>
F;468-538/Domain: complement factor H repeat homology <FH8>
F;468-538/Domain: complement factor H repeat ho
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PPTCEKI 237
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                                                                                                                                                                                               VKCKP--PPDIRNGRHSGEENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPS
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Pred. No. 6.
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A;Reference number: A45900; MUID:90229754

A;Recession: B45900

A;Status: preliminary; nucleic acid sequence not shown; not com A;Molecule type: mRNA
A;Residues: 1-363 KUR>
A;Residues: 1-363 KUR>
A;Residues: 1-19, fe', 84-363 KU2>
C;Superfamily: complement C3d/Epstein-Barr virus receptor; comp A;Residues: 1-19, fe', 84-363 KU2>
C;Superfamily: complement factor H repeat homology <FH1>
F;23-81/Domain: complement factor H repeat homology <FH3>
F;154-210/Domain: complement factor H repeat homology <FH3>
F;154-210/Domain: complement factor H repeat homology <FH3>
F;218-274/Domain: complement factor H repeat homology <FH4>
F;279-335/Domain: complement factor H repeat homology <FH4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement C3d/Epstein-Barr virus receptor precursor alternative splice form C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999 C;Accession: B45900; C45900
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R; Kurtz, C.B.; O'Toole,
  Query Match
Best Local Similarity
Matches 43; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement receptor gene A45900; MUID:90229754
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                         20.2%;
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     17;
Score 148; DB 2;
Pred. No. 5.7e-06;
7; Mismatches 58
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                                             Length 363
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     16;
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mouse

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210

CESDFPLECPSLPTIHNGHHTGQHVDQFVAGLSVTYSCEPGYLLTGKKTIKCLSSGDWDG 269 CE---PLEAPELGTMDCTHPFG----NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSS 53

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C;Superfamily: complement factor H repeat numurary;
F;22-78/Domain: complement factor H repeat homology <FH01>
F;83-140/Domain: complement factor H repeat homology <FH09>
F;145-211/Domain: complement factor H repeat homology <FH09>
F;217-272/Domain: complement factor H repeat homology <FH04>
F;217-31/Domain: complement factor H repeat homology <FH05>
F;217-331/Domain: complement factor H repeat homology <FH06>
F;336-394/Domain: complement factor H repeat homology <FH06>
F;399-488/Domain: complement factor H repeat homology <FH08>
F;467-523/Domain: complement factor H repeat homology <FH08>
F;531-587/Domain: complement factor H repeat homology <FH08>
F;531-587/Domain: complement factor H repeat homology <FH10>
F;592-648/Domain: complement factor H repeat homology <FH10>
complement C3b/C4b receptor-like protein precursor
C;Species: Homo sapiens (man)
C;Date: 27-Jul-1990 #sequence_revision 11-Apr-1997
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A;Title: Mouse complement regulatory protein Crry/p65 uses A;Reference number: 148306; MUID:95105691
A;Accession: 148306
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
                                                                                A34924
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A; Residues: 21-367 < RES>
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A; Residues: 1-676 < KUI
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                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 80/1; 113/2; 142/1; 275/1; 333/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:U17128; NID:g595980; PIDN:AAA78271.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB.
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A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A45900; I48306
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                                                                                                                                                                                   370
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                                                                                                                                                                                                                                                                                    319 TSLGTWSNTVPTCEVKSCDAIP-----NHLLHGRVFLPPNLQLGAEVSFVCDLGFQ
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                                                                                                                                                                                                                                 99 LIGKKKTICESSG---IWSNPSPICQKL 123
                                                                                                                                                                                                                                                                                                                                    46 GPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSHPL-----ASFSFTSACTFICSEGTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                   LKGKPSSQCIPEGETVIWNNKFPVCEQI 397
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39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 148; Db ., pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.M.; Weis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family. IV. Alternative splicing
  #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 676;
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C;Date: 17 .... S65551 C;Accession: S65551 R;Soames, C.J.; Day, A.J.; Sim, R.B. R;Soames, C.J.; Day, A.J.; Sim, R;Soames, C.J.; Day, A.J.; Sim, R;Soames, C.J.; Day, A.J.; Day, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:X98697; NID:g1419423; PIDN:CAA67257. C;Superfamily: complement factor H; complement factor H repet homology <FHRI>F;55-114/Domain: complement factor H repeat homology <FHRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 315, 523-531, 1996
A; Title: Prediction from sequence comparisons
A; Reference number: S65551; MUID:96202005
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                                                                                                                                                                                                                                                                  F;296-349/Domain: complement factor H repeat F;355-412/Domain: complement factor H repeat F;416-471/Domain: complement factor H repeat F;476-530/Domain: complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar_1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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R;Hourcade, D.; Miesner, D.R.;
J. Biol. Chem. 265, 974-980, 1:
A;Title: Duplication and divers
                                                                                                                                                                                              F;538-592/Domain:
F;599-651/Domain:
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R;Hourcade, D.; Miesner, D.R.; Atkinson, J.P.;
J. Exp. Med. 168, 1255-1270, 1988
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A; Residues: 1-479 <HOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-669 < SOA >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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Matches 32; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 NESESSOCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQVIQCEPLSAPDLGIMNCSHP 79
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       Conservative
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27.5%;
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       26;
Score 147.5; | Pred. No. 1.2e
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Pred. No. 8.4e-06;
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homology <FHR3>
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                                           .2e-05;
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19 GN-FSFSSQCAFSCSEGTNLTG-IEETTCGPFGNWSSPEPTCQVIQCEPLSAPDLG--IM 74

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A; Introns: 66/2; 221/1; 282/1; 404/1; 500/1; 649/3; 750/1; 997/2; 1152/3; 1279/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1827 AWUR>
A;Cross-references: EMBL:U61946; PIDN:AAC24388.1; GSPDB:GN00022; CESP:F47C12.1
A;Experimental source: strain Bristol N2; clone F47C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T34288
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A; Introns: 189/2; 254/2; 291/3; 339/1; 380/2; 536/1; 562/3; 661/1; 756/3; 829/1
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A;Experimental source: clone C54G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-868 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Wilkinson, J. Submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C54G4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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A; Accession: T20239
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Matches 33
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      53
                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 31.4
les 33; Conservative
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                                                                                                                             1 CEPL---EAPEL--GTMDCTHPFGNFSFSSQCAFSCSEG---TNLTGIEETTCGPFGNWS 52
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                                                                 COPIYCGAVPQIANGFVDSA---TNVSFGGQVKYSCHKGFFFASGKDVETVYCGELGKWG 336
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   SPEPTCQVIQCEPLSAPDLGIMNCSHPLASES---
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31.4%; Pred. No. 1.5e-05;
tive 14; Mismatches 47
                                                                                                                                                                                            20.1%; Score 147.5; DB 2; 27.1%; Pred. No. 3.1e-05; tive 18; Mismatches 48;
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      -FTSACTFICSEGTEL 99
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A; Accession: S57953
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A; Residues: 1-610 <HIL>
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A; Residues: 1-558 <HIL>
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C4BP protein alpha chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C;Accession: S57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross references: EMBL:Z50051; NID:g899379; PIDN:CAA90391.1; PID:g899380
C;Superfamily: C4b-binding protein alpha chair; complement factor H repeat homology F;15-72/Domain: complement factor H repeat homology <FH1>
F;77-134/Domain: complement factor H repeat homology <FH2>
F;139-199/Domain: complement factor H repeat homology <FH3>
F;204-258/Domain: complement factor H repeat homology <FH5>
F;264-258/Domain: complement factor H repeat homology <FH5>
F;363-324/Domain: complement factor H repeat homology <FH5>
F;363-324/Domain: complement factor H repeat homology <FH5>
F;363-324/Domain: complement factor H repeat homology <FH5>
F;390-443/Domain: complement factor H repeat homology <FH7>
F;390-447-501/Domain: complement factor H repeat homology <FH8>
A;Cross*references: EMBL:Z31693; NID:g469117; PIDN:CAA83498.1; PID:g469118 C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology <FH2> F;50-107/Domain: complement factor H repeat homology <FH2> F;112-169/Domain: complement factor H repeat homology <FH2> F;114-234/Domain: complement factor H repeat homology <FH3> F;239-324/Domain: complement factor H repeat homology <FH4> F;239-362/Domain: complement factor H repeat homology <FH5> F;366-425/Domain: complement factor H repeat homology <FH5> F;366-425/Domain: complement factor H repeat homology <FH6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Hillarp, A.; Thern, A.; Dahlback, B.
J. Immunol. 153, 4190-4199, 1994
A;Title: Bovine C4b binding protein. Molecular cloning of the A;Reference number: I46001; MUID:95015909
A;Accession: I46001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4b-binding protein alpha chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB
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RESULT 36
S57960
C4BP protein beta chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1996 #sequence_revision 19-
C;Accession: S57960
R;Hillarp, A.; Thern, A.; Dahlback, B.
submitted to the EMBL Data Library, July 1
A;Description: Molecular cloning of rat C4
A;Reference number: S57953
A;Accession: S57960
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-469 <KRI>
A;Note: the authors translated the codon GCT for residue 25 as Val
C;Comment: C4BP controls the classical nathway of comments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:120-176/Domain: complement factor H repeat homology <FH2>F:181-240/Domain: complement factor H repeat homology <FH3>F:245-299/Domain: complement factor H repeat homology <FH4>F:303-355/Domain: complement factor H repeat homology <FH5>F:359-413/Domain: complement factor H repeat homology <FH6>F:359-413/Domain: complement factor H repeat homology <FH6>F:74,227,275,292,366,381,428/Binding site: carbohydrate (Asr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein; F;1-56/Domain: signal sequence #status predicted <SIG> F;57-469/Product: C4b-binding protein alpha chain *status predicted <MAT> F;58-115/Domain: complement factor H repeat homology <FH1> F;58-115/Domain: complement factor H repeat homology <FH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: C4BP controls the classical pathway of complement activation. It binds as a the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement C;Comment: In mouse, C4BP is a multimeric protein of noncovalently associated chains. C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C;Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein; pC;Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: cDNA structure of murine C4b-binding protéin, a regulatory component of A;Reference number: A27117; MUID:88024997
A;Accession: A27117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4b-binding protein alpha chain precursor - mc N;Alternate names: C4BP; proline-rich protein C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #sequence_revision 30-Jun-1993 #sequence_revision 30-Jun-1993 #sequence_revision 30-Jun-1994 #sequence_revision 30-Jun-1994 #sequence_revision 30-Jun-1995 #seq
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPTCQVIQCEPLSAPDLGIMNCSH 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFGSQIEFSCQEGFILVGSSTSSCEVRGKGVAWSNPFPECVIVKCGP--PPDISNGKHSG
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29.4%;
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Pred. No. 1.8e-05;
8; Mismatches 47;
                                                                                                                               July 1995
rat C4b-binding
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                                                                                                                                                                                                                                                                                                      #text_change
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    C;Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL lase activity, and binds heparin. It may prevent activation of the intrinsic blood c C;Superfamily: apolipoprotein H; complement factor H repeat homology
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A; Molecule type: protein A; Residues: 20-22, 'X', 24-41 <LIQ>
                                             A;Title: Isolation from fetal bovine serum of A;Reference number: S09032; MUID:90226328 A;Accession: S09032
                                                                                                                 A; Molecule type: protein
A; Residues: 20-301, 'N', 303-345 < KAT>
R; Li, Q; Blacher, R; Esch, F; Con
Biochem. J. 267, 261-264, 1990
                                                                                                                                                                                                                                       A; Title: Amino acid
A; Reference number:
                                                                                                                                                                                                                                                                                                                A; Note: 186-Glu was also found R; Kato, H.; Enjyoji, K.
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 4-345 <BE2>
A;Cross-references: EMBL:X60065; NID:g5; PIDN:CAA42669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S23597; MUID:92232647 A; Accession: S23597
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A; Residues: 20.49 < CAL>
R; Bendixen, E.; Halkier, T.; Magnusson,
Biochemistry 31, 3611-3617, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-100,'G',102-107,'S',109-176,'R',178-193,'C',195-258,'N',260-301,'N',303
A;Cross-references: GB:L07303; NID:g162679; PIDN:AAA30382.1; PID:g162680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 126, 287-288, 1993
A; Title: Sequence of a cDNA encoding bovine apolipoprotein A; Reference number: JN0502; MUID:93246260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1993 #sequence_revision 19-May-1995 #text_change
C;Accession: JN0502; PN0465; S2397; A43209; A39300; S09032
C;Accession: JN0502; PN0465; S2397; A43209; A39300; S08032
R;Gao, B.; Virmani, M.; Romm, E.; Lazar-Wesley, E.; Sakaguchi, F
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A; Residues: 1-258 <HILD
A; Residues: 1-258 <HILD
A; Cross-references: EMBL: 250052; NID: 9899381; PIDN: CAA90392
C; Superfamily: complement factor H repeat homology
F; 20-73/Domain: complement factor H repeat homology <FH01>
F; 78-131/Domain: complement factor H repeat homology <FH02>
                                                                                                                                                                                                                   A; Accession: A39300
                                                                                                                                                                                                                                                                                            Biochemistry 30,
                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A43209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Complete primary structure of bovine beta(2)-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: A; Accession: PN0465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JN0502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apolipoprotein H precursor - bovine
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 PICQKLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 CRSRDCEPPETPVHGYFEGE----TFTSGSVVTYYCEDGYHLVGTQKVQC-SDGEWSPSY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PECLLGHCPDPVLENGKINSSGPVNISGKIMFECNDGYILKGSNWSQCLEDHTWAPPLPI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTCESIQE
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                                                                                                                                                                                                                                                                                                                                                                  20-58;63-100;108-110;124-145;150-163;174-201;203-217;228-253,'X',255-256
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                                                                                                                                          F.; Congote,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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Pred. No. 9.4e-06;
6; Mismatches 62;
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                                                                                                                                                                                                                                                                     of
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                                                                                               apolipoprotein-H-like
                                                                                                                                                                                                                                                                     disulfide
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CO L a

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N;Alternate names: complement receptor 2; CR2/CD21
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C;Accession: JL0028; A39958; A32036; A24319; B24319; C24319; D24319; E24319;
R;Mels, J.J; Toothaker, L.E.; Smith, J.A.; Weis, J.H.; Fearon, D.T.
J. Exp. Med. 167, 1047-1066, 1988
A;Title: Structure of the human B lymphocyte receptor for C3d and the Epstei A;Reference number: JL0028; MUID:88171282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Rosidues: 1-456, 'G', 457-644, 'R', 646-669, 'R', 671-816, 'NCSAEVILKAWILERAF', 835-840,
A;Cross references: GB:J03565; NID:g181919; PIDN:AAA35784.1; PID:g181920
R;FUJISAKU, A.; Harley, J.B.; Frank, M.B.; Gruner, B.A.; Frazier, B.; Holers, V.M.
J. Biol. Chem. 264, 2118-2125, 1989
A;Title: Genomic organization and polymorphisms of the human C3d/Epstein-Barr viru.
A;Reference number: A32036; MUID:89123277
A;Accession: A32036
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F;205-260/Domain: complement factor H repeat homology <FH4>
F;205-260/Domain: complement factor H repeat homology <FH4>
F;264-315/Domain: complement factor H repeat homology <FH5>
F;264-315/Domain: complement factor H repeat homology <FH5>
F;23-66,51-79,84-124,110-137,142-188,174-200,205-248,234-260,264-315,300-325,307-345/Dis
F;92,162,183,193,253/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                        A;ACCESSION......A;ACCESSION.......A;Molecule type: protein
A;Molecule: 226-230, 'XIIQ';257-267;332-341;583-591,'Q'
A;Residues: 226-230, 'XIIQ';257-267;332-341;583-591,'Q'
A;Porcerimental source: B-Lymphoblastoid cell lines SB
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A; Note: nucleotides 1566-1625 are missing from Figur A; Note: nucleotides 1566-1625 are missing from Figur R; Moore, M.D.; Cooper, N.R.; Tack, B.F.; Nemerow, G. Proc. Natl. Acad. Sci. U.S.A. 84, 9194-9198, 1987 A; Title: Molecular cloning of the cDNA encoding the A; Reference number: A39958; MUID:88097454 A; Accession: A39958
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A;Gene: GDB:CR2
A;Cross-references:
A;Map position: 1q3;
                                                                                                                                                                                                                                                                                                                                                                                                             A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Weis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-456,'G',457-658,718-1050,'I',1052-1060,'E',1062-1091
A;Cross-references: GB:J04463
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                         A; Accession: A24319
                                                                                                                                                                                                                                                                                                                          A; Reference number: A94114;
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Best Local s
Matches 39
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                                                                                                                                                                                                                                                                                                                                                                complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ls, J.J.; Fea
Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                         Identification of a partial cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVRCPFPSRPDNGFVN--HPANPVLYYKDTATFGCHETYSLDGPEEVECSKFGNWS-AQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Fearon, D.T.; Klickstein, L.B.; Wong, cad. Sci. U.S.A. 83, 5639-5643, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                             GDB:119802;
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Pred. No. 2.1e
15; Mismatches
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Nemerow, G.R.
9198, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.A.;
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F;777-837/Domain:
F;846-901/Domain:
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                                                                                                                                                                                                                                                                                                              F;154-210/Domain:
                                                                                                                                                                                                                                                                                                                                                  F;23-82/Domain: complement factor H repeat homology <FH01>
                                                                                                                                                                                                                                                                                                                                                                  F;21-658,718-1091/Product: complement receptor 2
     F;121,127,294,372,622,698,858,
                   F; 1034-1056/Domain: F; 1057-1091/Domain:
                                                                                                                                      F;720-772/Domain:
                                                                                                                                                                                                                 F;470-521/Domain:
                                                                                                                                                                                                                                 F;410-465/Domain:
                                                                                                                                                                                                                                                   F;351-406/Domain:
                                                           F;970-1026/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                       1-20/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: complement C3d/Epstein-Barr virus receptor; complement factor H repeat; Keywords: alternative splicing; duplication; glycoprotein; transmembrane protein
                                                                                                                                                                                           526-592/Domain:
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                                                           complement factor H repeat homology <FH16>
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transmembrane #status predicted <TMM>
intracellular #status predicted <INT>
22,698,858,881,919/Binding site: carbol
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homology <FH13>
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homology <FH07>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
                                                                                                                                A; Molecule type: mRNA
A; Residues: 467-546; 550-595;752-764 <WOO>
A; Cross-references: GB:J00185; GB:J00186
A; Note: the authors translated the codon TAC
R; Mole, J.E.; Anderson, J.K.; Davison, E.A.;
J. Biol. Chem. 259, 3407-3412, 1984
A; Title: Complete primary structure for the 2
A; Reference number: A20751; MUID:84161997
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X72875; NID:g297568; PIDN:CAA51389.1; PID:
R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten,
Proc. Natl. Acad. Sci. U.S.A. 79; 561-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein 1
A;Reference number: A44622; MUID:83039428
A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement factor B precursor [validated] - human N;Alternate names: C3 convertase; C3 proactivator; glycine-rich N;Contains: alternative-complement-pathway C3/C5 convertase (EC
                                                                       A; Molecule type: protein A; Residues: 26-764 < MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-764 < MEJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, A; Reference number: S34075 A; Accession: S34075
                                             A; Cross-references: GB: K01566
                                                                                                                  A; Accession: A00934
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nucleic acid translation 736-Ser was also found
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A;Cross-references: GDB:119726; OMIM:138470

A;Map position: 6p21.3-6p21.3

A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A;Introns: c1/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A;Note: the list of introns may be incomplete

A;Note: gene is located in the major histocompatibility complex, class III region

C;Complex: complement factor B initially forms an inactive complex with complement factor B initially forms an inactive complex with complement factor B initially forms an inactive complex with complement factor B initially forms an inactive complex with complement factor B initially forms an inactive complex with complement factor B initially forms an inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complement factor B initially forms and inactive complex with complex 
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R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties A;Reference number: I54409; MUID:94041399
A;Accession: I54409
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A;Title: The principal site of glycation of A;Reference number: S14339; MUID:91174758
A;Accession: S14339
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A; Residues: 339-509 <CAl>
A; Cross-references: GB.J00126; NID:9187723; PIDN:AAA36226.1;
A; Cross-references: GB.J00126; NID:9187723; PIDN:AAA36226.1;
R; Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
Cell 48, 331-342, 1987
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A;Residues: 270-329 <KUIE>
A;Note: binding site for carbohydrate to lysine under
R;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
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Biochem. J. 209, 61-70, 1983
A;Title: Amino acid sequence of the Bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, Mol. Immunol. 30, 1587-1592, 1993
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A; Residues: 1-764 < RE:
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A; Residues: 1-99 <WUL>
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A; Residues: 346-764 < CAM>
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Acad. Sci. U.S.A. 80, 4464-4468,
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A;Pathway: complement alternate pathway
C;Superfamily: complement C2; complement factor H repeat homology; trypsin homology;
C;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hyd
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-764/Product: complement factor B #status experimental <MAT>
F;26-259/Product: complement factor Ba fragment #status experimental <BAF>
F;37-98/Domain: complement factor H repeat homology cFH1>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;268-458/Domain: von Willebrand factor type A repeat homology <FH3>
F;388-458/Domain: trypsin homology #status atypical <TRY>
F;388-752/Domain: trypsin homology #status atypical <TRY>
F;39-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725
F;312-316,285-378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
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A; Note:
C; Date:
C; Access
A;Contents: annotation; possible protein-coding frames A;Note: neither amino acid nor nucleotide sequence is given C;Superfamily: herpesvirus complement control protein; comp. C;Keywords: duplication; extracellular protein F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                      R:Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S
Virology 179, 247-266, 1990
A;Title: The complete DNA sequence of vaccinia virus.
A;Reference number: A42531; MUID:91021027
                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-263 <GOE>
A; Cross-references: GB:M35027; NID:g335317;
A; Experimental source: strain Copenhagen
                                                                                                                                                                                                                                                                                                                  Virology 179, 517-563, 1990
A;Title: Appendix to "The complete
A;Reference number: A42501
A;Accession: B42504
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A;Experimental source: strain WR
R;Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
A; Residues: 1-26
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A; Reference number: A31005;
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Accession: A31005; B42504
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176-178, 1988
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| cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
| cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
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APPLICANT: Darbe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 15305
SOFTWARE: Patentin version 3.0
SEQ ID NO 152667
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KFY: misc feature
RESULT 2
US-10-212-054-1437
; Sequence 1437, Application US/10212054
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ12C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: X is
US-09-791-537-152667
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Pred. No. 2.5e-57;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22816
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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          Sequence 42657, Application GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22816
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Best Local Similarity
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Prior application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1437
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APPLICANT:
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CURRENT FILING DATE: 2002-08-06
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Pred. No. 4.1e-57;
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PAtentin version 3.0
SEQ ID NO 42657
LENGTH: 372
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 84593
LENGTH: 372
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josepl
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                                                                                                                                                                              Local Similarity
nes 131; Conserv
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nes 131; Conserv
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QKLDKSFSMIKE
                                                                                    IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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                                                         IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
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328
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99.2%;
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METHODS OF USE THEREOF
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Pred. No. 8.6e-57;
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Pred. No. 8.6e-57;
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US-09-791-537-51391 ; Sequence 51391, Application US/09791537

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US-09-791-537-42659
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PROTEIN VERSION 3.0
SEQ ID NO 42659
LENGTH: 372
TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 51391
LENGTH: 385
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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330 QKLDKSFSMIKE 341
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QKLDKSFSMIKE 328
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Pred. No. 1.6e-56;
1; Mismatches 1
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Pred. No. 8.9e-57;
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 113060
LENGTH: 385
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 58446
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Best Local S
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Best Local Similarity
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121 QKLDKSFSMIKE 132
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nes 130; Conserv
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98.5%;
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Pred. No. 4.6e-56;
0; Mismatches 2
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Pred. No. 4.3e-56;
0; Mismatches 2
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330 QKLDKSFSMIKE

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-53844
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US-09-791-537-53844
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; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-69658
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                                                                                                                                    Matches
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Best Local S
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILINGATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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210
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Local Similarity 97.0%;
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97.0%;
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Pred. No. 1.5e-55;
Prematches 2;
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                                                                            Query Match
Best Local Similarity
Matches 122; Conserv
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42658
LENGTH: 372
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Best Local Similarity 92.4%;
Matches 122; Conservative
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LENGTH: 372
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SOFTWARE: Patentin version 3.0
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
121 QKLDKSFSMIKE 132
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                                                                                       Conservative
                                                                                94.1%; Score 690; DB 5; 192.4%; Pred. No. 1.7e-53; tive 7; Mismatches 3;
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Pred. No. 1.7e-53;
                                                                                                                          Length 372;
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RESULT 15
US-10-212-054-1328
; Sequence 1328, Application US/10212054
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/215,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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Best Local Similarity
Matches 120; Conser
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NUMBER OF SEQ ID NOS: 1778
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1171
LENGTH: 341
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
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PRIOR FILING DATE: 2001-01-16
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CURRENT FILING DATE: 2002-08-05
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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99.2%;
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; LCCATION: (215)
; OTHER INFORMATION: Xaa equals any
US-10-212-054-1328
                             В
                                                                                                                                                                       ; NAME/KEY: misc_feature ; LOCATION: (215) ; LOCATION: (215) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-212-778-1158
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PRIOR APPLICATION NUMBER: 09/758,449
PRIOR TELING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEO ID NOS: 1478
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
SEQ ID NO 1158
LENGTH: 341
                                                                                            Matches
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Best Local Similarity
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Best Local :
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LENGTH: 341
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CURRENT FILING DATE: 2002-08-06
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                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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                             CEPLEAPELGTMDCTHPLGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                             Conservative
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Pred. No. 4.1e-52;
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Pred. No. 4.1e-52;
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APPLICANT: Biolomix, Inc.

APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION UNUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTMARE: Patentin version 3.0
SEQ ID NO 132144
LENGTH: 376
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
                   Qy
                                                                                                                                 ; ORGANISM: Bos taurus US-09-791-537-50403
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US-09-791-537-50403
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US-09-791-537-132144
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                                                                     Query Match
Best Local
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Best Local Similarity
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317 QKVDRSFSMIKE 328
                                                   Local Similarity hes 91; Conserv
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                                                     Conservative
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                                                 73.3%; Score 537; DB 5; L 68.9%; Pred. No. 6.7e-40; Live 19; Mismatches 22;
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Pred. No. 2.1e-45;
8; Mismatches 18; Indels
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Query Match
Best Local Similarity
Thes 93; Conserve
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US-09-791-537-6693
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6693
LENGTH: 372
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 81233
LENGTH: 372
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                        72.0%;
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                                      Score 528; DB 5; Length 372; Pred. No. 4.2e-39;
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US-09-791-537-60503
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US-09-791-537-53485
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 53485
LENGTH: 323
TYPE: PRT
                                                                                                                     APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILIG DATE: 201-01-02-22
RUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 60503
LENGTH: 360
TYPE: PRT
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 Query Match 70.7
Best Local Similarity 68.7
Matches 90; Conservative
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Best Local Similarity
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70.7%; Score 518; DI
68.2%; Pred. No. 3.20
tive 13; Mismatches
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                  .2e-38;
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US-09-791-537-37750
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37750
LENGTH: 372
TYPE: PRT
                                                   SOFTWARE: PatentIn version
SEQ ID NO 18300
LENGTH: 646
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Best Local S
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                                                                                                      FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                      APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Query Match

43.48;

Score 318;

DB 5;

Length 646;

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; ORGANISM: Homo sapiens US-09-791-537-22819
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                                                                   APPLICANT: Blonomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HETHOE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 22819
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 32024
                                                                                                                                                                                                                                                                                                                    Sequence 22819,
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                                         TYPE: PRT
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TYPE: PRT
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                                                         LENGTH: 830
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2; Mismatches
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION MUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 86038
LENGTH: 768
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US-09-791-537-86038
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Best Local Similarity
Matches 54; Conserv
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35618
LENGTH: 830
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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Pred. No. 8.5e
21; Mismatches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32025
LENGTH: 616
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
APPLICANT: INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                           Sequence 32023, Application US/09791537 GENERAL INFORMATION:
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Best Local 9
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Best Local Similarity
                                                  APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                         APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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41.5%; Pred. No. 2.1e-19;
ative 23; Mismatches 49;
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Pred. No. 1.2e-19;
7; Mismatches 52
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US-09-791-537-73416; Sequence 73416, Application; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14651
LENGTH: 754
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.7
Best Local Similarity 40.5
Matches 49; Conservative
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Best Local Similarity
Matches 50; Conserv
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APPLICANT: Danzer, Joseph TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME TITLE OF INVENTION: METHODS OF USE THEREOF
                                                      APPLICANT: Debe, Derek
                                                                                        APPLICANT: Bionomix, Inc.
                                             APPLICANT:
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TYPE: PRT
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40.7%; Pred. No. 3.9e-19;
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red. No. 4.8e-19;
Mismatches 48;
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RESULT 34
US-09-791-537-37749
Sequence 37749, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
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US-09-791-537-73416
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US-09-791-537-81892
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATCHTIN VERSION 3.0
SEQ ID NO 73416
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LENGTH: 618
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Best Local
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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CK 301
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                                                                                                                                                                                                                                                                                                                                                                                   41.7%; Score 305.5; DB 5; 42.6%; Pred. No. 4.3e-19;
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Pred. No. 4.3e-19;
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FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37749
LENGTH: 619
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-37749
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RESULT 36
US-09-791-537-20989
; Sequence 20989, Application US/09791537
; GENERAL INFORMATION:
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Matches
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 118878
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Best Local Similarity
Matches 52; Conserv
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TYPE: PRT
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nes 52; Conserv
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43.0%; Pred. No. 1.3e-18;
rative 18; Mismatches 51
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42.6%; Pred. No. 4.4e-19;
70. Mismatches 47;
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37753
LENGTH: 768
TYPE: PAT
ORGANISM: Mus musculus
US-09-791-537-37753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 20989
LENGTH: 768
TYPE: PRT
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bionomix, Inc.
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320
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                                                                                                                     61 IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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                                                                                                                                                                                                                                                                                          Length 768;
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Qy Db

240 VVECKALTQPAHGVRKCSSNPGSYPWNTTCTFDCEEGYRRVGAQNLQCTSSGVWDNEKPS

299

120 CQ 121 |: 300 CK 301

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APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50409
LENGTH: 769
TYPE: PRT
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
SEQ ID NO 50406
LENGTH: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50406, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.9%; Score 300; DB 5; Best Local Similarity 39.8%; Pred. No. 1.7e-18; Matches 49; Conservative 24; Mismatches 50
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 153055
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                                               180 CQEQEYPDHGSLNCTHPFGLFSYNSSCSFSCERGYVPSSMETTVRCTSSGEWSAPAPACH 239
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60 VIQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                         1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETT-CGPFGNWSSPEPTCQ 59
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                                                                                                                                      Conservative
                                                                                                                                    40.9%; Score 299.5; DB 5;
41.0%; Pred. No. 1.3e-18;
tive 23; Mismatches 48;
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RESULT 40

PCT-US02-23913-357

Sequence 357, Application PC/TUS0223913

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc. et al.

APPLICANT: Millennium Pharmaceuticals, Inc. et al.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044PC

CURRENT APPLICATION NUMBER: PCT/US02/23913

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR APPLICATION NUMBER: 60/314,746

PRIOR APPLICATION NUMBER: 60/341,746

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-05

NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-05
Search completed: September Job time: 559 sec
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-23913-357
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.4%; Score 296; DB 1; Length 610; Best Local Similarity 41.3%; Pred. No. 3e-18; Matches 50; Conservative 21; Mismatches 50; Indels 0;
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Maximum Match 100%
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Maximum DB
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                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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[2602_6/ptodatta/2/paa/PCTUS_COMB.pep:*

cgn2_6/ptodatta/2/paa/US06_COMB.pep:*

cgn2_6/ptodatta/2/paa/US07_COMB.pep:*

cgn2_6/ptodatta/2/paa/US080_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    /cgn2_6/ptodata/2/paa//ISO86_COMB.pep: *
    /cgn2_6/ptodata/2/paa//ISO86_COMB.pep: *
    /cgn2_6/ptodata/2/paa//ISO86_COMB.pep: *
    /cgn2_6/ptodata/2/paa//ISO90_COMB.pep: *
    /cgn2_6/ptodata/2/paa//ISO00_COMB.pep: *
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727	727	727	727		Score
99.2	99.2	99.2	99.2	100.0 372	% Query Match Length DB
1078	382	184	184	372	Length :
26	2 L	21	21	15	DB
US-60-212-659-523	PCT-USU1-26675-3 L US-09-760-475-2123 L HS-60-207-315-428	US-09-760-475-3252	US-09-760-443-1437	US-09-119-209-2	ID
Sequence 523, App	Sequence 3, Appli Sequence 2123, Ap	Sequence 3252, Ap	Sequence 1437. Ap	Sequence 2, Appli	Description

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G-01/-	-60-196-7	-US01-03800A-	-09-764-902-1	-09-764-875-9	PCT-US01-01332-938	PCT-US01-01239-1688	-760-498-9	-09-760-475-325	-09-760-443-	-09-760-475-212	-60-196-718-448	4-875-6	-US01-01332-6	-09-764-902-114	-US01-01239	-10-021-660-1	-09-857-670-1	US-09-802-640-36	US-09-784-356-122	US-09-266-091A-2	US-09-266-091-2	US-08-770-435-3	US-08-657-753-2	PCT-US99-28965-19	US-60-207-315-467	-020-141-1			US-09-119-209-4	US-09-760-443-1328	115	-08-410-569	-08-340-539-	8-008-459-	T-US94-0090	-US92-03970-	ω
Sequence 5336, Ap	e 5358,	1802, 7	e 1688,	e 938,	938, 1	1688,	e 920, A	3255,	132	2126,	4486,	e 615,	615,	e 1145	1145,	122,	æ	equence 36,	e 122,	2, Appl	'n	ω ,	e 2,	19, 1	467,	e 1	4		4	е !:	e ∷	N	ν	ν,	'n	2, Appl	Sequence 1751, Ap

ALIGNMENTS

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RESULT 1
US-09-119-209-2
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GENERAL INFORMATION:
APPLICANT: LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
                                                                                                                            ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
                                                                                       APPLICATION NUMBER: US/09/119,209 FILING DATE: 20-Jul-1998
                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                       STREET:
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER:

FILING DATE:

6-MAY-1993

08/059027

FILING DATE: APPLICATION NUMBER:

31-OCT-1991

07/786149

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US-09-760-443-1437
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins,

FILE REFERENCE: PJZ12
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CURRENT FILING DATE: 2001-01-16

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2164

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1437
                                                                                                                                                                                    Query Match
Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                       LENGTH: 184
TYPE: PRT
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NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
 121 QKLDKSFSMIKE 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 100.0%; Score 733; DB 15; Local Similarity 100.0%; Pred. No. 6.6e-63; hes 132; Conservative 0; Mismatches 0;
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                  1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                             IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                    131; Conservative
                                                                                               CEPLEAPELGTMDCTHPLGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 68
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                              IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 128
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650/952-9881
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                                                                                                                                                                  Score 727; DB 21;
Pred. No. 1.2e-62;
0; Mismatches 1;
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                                                                                                                                                                                                  Length 184;
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APPLICANT: Genalssance Pharmaceuticals,
APPLICANT: Ansatasio, Alison E
APPLICANT: Bieglecki, Karyn M
                                                                           Matches
                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3252
LENGTH: 184
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Best Local Similarity
                                                                                                                                                                                                                                                                                            FILE REFERENCE: SELL MWH1116-PCT
CURRENT APPLICATION NUMBER: PCT/US01/26675
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/228,262
PRIOR EILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KOShy, Beena
APPLICANT: Kumar, Anant Madan
TITLE OF INVENTION: HAPLOTYPES OF THE SELL GENE
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APPLICANT:
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CURRENT FILING DATE: 2001-01-16
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ49
FILE REFERENCE: TTZ49
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 101
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197 CEPLEAPELGTMDCTHPLGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 256
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                                                                                          Local Similarity
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                 1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                                                                        99.2%;
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                                                                   Score 727; DB 1; Pred. No. 2.5e-62; 0; Mismatches 1;
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                                                                                                        Length 372;
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US-09-760-475-2123
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Best Local S
Matches 131
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2123
LENGTH: 382
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 428
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 428, Application US/60207315 GENERAL INFORMATION:
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING H TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL000601
CURRENT APPLICATION NUMBER: US/60/207,315
CURRENT FILING DATE: 2000-05-30
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ49
CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                  LENGTH: 10
TYPE: PRT
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TYPE: PRT
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CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                                                                                                                                                                                 1078
                                                                               Similarity
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                                                                                 99.2%;
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                                                                Score 727; DB 26; Pred. No. 8.1e-62; 0; Mismatches 1
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Pred. No. 2.6e-62;
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                                                                                               Length 1078;
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; SOFTWARE: FastSEG; SEQ ID NO 1751; LENGTH: 1078; LENGTH: PRT; ORGANISM: HUMAN US-60-230-435-1751
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; TYPE: PRT
; ORGANISM: HUMAN
US-60-212-659-523
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                                                             Query Match
Best Local Similarity
Matches 131; Conser
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Best Local Similarity
Matches 131; Conservat
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SEQ ID NO 523
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/230,435
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 2991
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CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 879
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TITLE OF INVENTION: NUCL
TITLE OF INVENTION: USES
FILE REFERENCE: CL000674
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                                                            Score 727; DB 26; Pred. No. 8.1e-62; 0; Mismatches 1;
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                                                                                           Length 1078;
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TELLX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
               Sequence 2, Application PC/TUS9400909 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.0
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/US92/03970
FILING DATE: 19920513
CLASSIFICATION:
                                                                                                                                                                                                                                           210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Helne, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFO
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ADDRESSEE: Weingarten, STREET: Ten Post Office
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TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
TITLE OF INVENTION: PROTEIN
                                                                                                               330
                                                                                                                                                                               270
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                                                                                                                                            121 QKLDKSFSMIKE 132
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                                                                                                            QKLDKSFSMIKE 341
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e Square
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Pred. No. 6.1e-61;
2; Mismatches 2
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Best Local S
Matches 128
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                     APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEC
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SI
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
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APPLICATION NUMBER: 1
FILING DATE: 03-OCT-
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STREET:
CITY: I
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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             Ten Post Office Square
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                                                                                  Geoffrey S.
CHIMERIC SELECTINS AS SIMULTANEOUS
BLOCKING AGENTS FOR COMPONENT SELEC
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97.0%;
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Pred. No. 6.1e-61;
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COMPUTER READABLE FORM:

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MEDIUM TYPE:

Floppy disk

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Sequence 2, Application US/08340539
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 07/770,608
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APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
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LENGTH: 385 amino acids
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REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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NAME: Heine, Holliday C.
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CLASSIFICATION:
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Pred. No. 6.1e-61;
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IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC CEPLEAPELGTMDCTHPLGNFNFNSQCAFSCSEGTNLTGIEETTCEPFGNWSSPEPTCQV

IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC

329 120 269 60 Matches

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Conservative

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Indels

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; MOLECULE TYPE: protein US-08-340-539-2
                 Query Match
Best Local Similarity
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: DFO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
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APPLICATION NUMBER: (
FILING DATE: 29-JUL-
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-NOV-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                  LENGTH:
TYPE: a
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                                                                                                                                                                                                                  TELEFAX:
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                                                                                                                      TOPOLOGY:
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SYSTEM: PC-DOS/MS-DOS
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97.0%;
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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Score 713; DB 7;
Pred. No. 6.1e-61;
2; Mismatches 2
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                                 Length 385;
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US-09-758-449-1158
; Sequence 1158, Application US/09758449
; GENERAL INFORMATION:
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Best Local Similarity
Matches 128; Conserva
APPLICANT:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
TYPOLOGY: line?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGINSTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEPAX: (617) 451-0313
TRELEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07/770,608
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spertini, Olivier G.
TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
TITLE OF INVENTION: AND LIGAND THEREOF
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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ZIP: 02109
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                                                                                                                 QKLDKSFSMIKE
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Rosen et al
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97.0%;
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Pred. No. 6.1e-61;
""matches 2;
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RESULT 15
US-09-760-443-1328
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; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals
US-09-760-443-1328
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
SEQ ID NO 1328
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                 Matches
                                                                                                                                            Query Match
Best Local Similarity
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SEQ ID NO 1158
LENGTH: 341
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                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2164
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PJZ12
CURRENT APPLICATION NUMBER: US/09/760,443
CURRENT FILING DATE: 2001-01-16
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TYPE: PRT
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1478
                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PM026
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LOCATION: (215)
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             61 IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
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99.2%;
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.5e-57;
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.5e-57;
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Best Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993
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                 121
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                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 23-FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/786149 FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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QKLDKSFSMIKE 132
                                              VQCEPLEAPELGTMDCTHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPIC
                                                                                                          CEPLEAPELGTMDCIHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPICQV
                                                              IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                        CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
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Amino Acid
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSEN, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                       Richard B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     JMBER: 07/315015
23-FEB-1989
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                                                                                                                                                                    Score 518; DB 15;
Pred. No. 6.6e-42;
3; Mismatches 29;
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                                                                                                                                                                                                 Length 372;
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US-08-449-687B-4
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                                                                                                                                Sequence 4, Application US/08449687B GENERAL INFORMATION:
APPLICANT: MCEVEY, Rodger P.
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GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: Expression Control Sequences of the P-Selectin Gene
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: PABSE, PALTEA L.
REGISTRATION UNMBER: 31,284
TELECOMMUNICATION INFORMATION:
                                                                              APPLICANT: Pan, Junliang
TITLE OF INVENTION: Expression Control Sequences of the
TITLE OF INVENTION: P-Selectin Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L.
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                                                                NUMBER OF SEQUENCES:
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CTTY: Atlanta
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                                                                                                                                                                                                                                                                                                                             384 ISCEPLESPVHGSMDCSPSLRAFQYDTNCSFRCAEGFMLRGADIVRCDNLGQWTAPAPVC 443
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STREET:
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1201 West Peachtree Street
                2800 One Atlantic Center
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43.9%;
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Pred. No. 1.1e-21;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: USA ZIP: 30309-3450

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; ORGANISM: Homo sapiens US-10-020-141-10
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GENERAL INFORMATION:

APPLICANT: MCCATTHY, Jeanette

APPLICANT: Ableson, Allen

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE

FILE REFERENCE: MMI-002

CURRENT APPLICATION NUMBER: US/10/020,141

CURRENT FILING DATE: 2001-12-14
                                                                                SEQ ID NO 10
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                                                                                             PRIOR APPLICATION NUMBER: US 60/327,485
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/313,097 PRIOR FILING DATE: 2001-08-16
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                                        LENGTH: 830
TYPE: PRT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,158
FILING DATE: 20-AUG-1993
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APPLICATION NUMBER: US/01
FILING DATE: 24-MAY-1995
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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APPLICATION NUMBER: 1
FILING DATE: 08-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
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(404)873-8795
'OR SEQ ID NO: 4:
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08-MAR-1989
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; FEATURE:

NAME/KEY: VARIANT

; LOCATION: (1)...(700)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-60-207-315-467
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Sequence 467, Application US/60207315

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN I

TITLE OF INVENTION: NUCLEIC ACID MOI

TITLE OF INVENTION: USES THEREOF
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Sequence 19, Application PC/TUS9928965
GENERAL INFORMATION:
APPLICANT: Wonia, Brett P.
APPLICANT: Xi, Xiaoxing S.
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: ISIS PHARMACEUTICALS, Inc.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0424
CURRENT APPLICATION NUMBER: PCT/US99/28965
CURRENT FILING DATE: 1999-12-08
EARLIER APPLICATION NUMBER: US 09/209,668
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SEQ ID NO 467
LENGTH: 700
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Best Local Similarity
Matches 54; Conserv
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CURRENT FILING DATE: 2000-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 CGELELPQHYLMNCSHPLGNESENSQCSFHCTDGYQVNGPSKLECLASGIWINKPPQCLA 251
                                                                                                                                                                                                                                                                                                                                       312 K 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 CQHLEAPSEGIMDCVHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDSGHWSAPLPTCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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43.9%; Pred. No. 1.1e-21;
tive 21; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.7%; Score 306; DB 26;
41.3%; Pred. No. 6.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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AND

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NUMBER OF SEQ ID NOS: 25 SOFTWARE: PatentIn Ver. SEQ ID NO 19

2.0

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-657-753-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-28965-19
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Best Local Similarity
                                 Matches
                                                              Query Match
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                                                                                                                                                                               TELEFAX: (415) 576-USU
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
510 amino acid
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                          610 amino acids
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                                                                                                                                                                                                                         (415) 576-0300
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Hope, Michael J.
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                                 Conservative
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DN: 514
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                                              40.48;
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41.3%; Pred. No. 5.5e-20;
                                                                                                                                                                                                                                                                                                                                                                      US/08/657,753
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                               Score 296; DB
Pred. No. 5.5e-
21; Mismatches
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                               DB 10;
5.5e-20;
nes 50;
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                                                           Length 610;
                               Indels
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US-08-770-435-3
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                                                                                                                                 Matches
                                                                                                                                                                 Query Match
                                                                                                                                                     Best
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/102,510
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/850,802
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERRE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-DEC-1994
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gimbrone, Jr., Michael A. APPLICANT: Bevilacqua, Michael P.
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                   61 IQCEPLSAPDLGIMNCSHPLASFSTTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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                                                                                                                                 Local Similarity 41.3 tes 50; Conservative
                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Markowicz, Kai
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: herew
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                                                                                1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                                                                                                                     LENGTH:
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VECDAVTNPANGFVECFQNPGSFPWNTTCTFDCEEGFELMGAQSLQCTSSGNWDNEKPTC
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                                                                                                                                Score 296; DB 11;
Pred. No. 5.5e-20;
1; Mismatches 50;
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                                                                                                                                                                   Length 610;
                                                                                                                                 Indels
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RESULT 25
US-09-266-091A-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-266-091-2
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CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 08/657,753
PRIOR FILING DATE: 1996-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scherrer, Peter
APPLICANT: Hope, Michael J.
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: ENHANCED EFFICACY OF LIPOSOMAL ANTISENSE THERAPY
FILE REFERENCE: ISPH-0342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 Q 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 CTALESPEHGSLVCSHPLGNFSYNSSCSISCDRGYLPSSMETMQCMSSGEWSAPIPACNV 239
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                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PB Telentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   NUMBER OF ENQUENCES: 10
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend Center, Eighth Floor
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enhanced Efficacy of Liposomal Antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Klimuk, Sandra K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
              APPLICATION NUMBER: US/09/266,091A FILING DATE: 10-Mar-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Semple, Sean
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Hope, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                         Semple, Sean C.
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41.3%;
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Pred. No. 5.5e-20;
21; Mismatches 50;
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SOFTWARE: FastSEQ f
SEQ ID NO 122
LENGTH: 610
TYPE: PRT
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US-09-784-356-122
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                                                                                                                                                                        Best
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Best Local Similarity 41.3
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 122,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/09/784,356
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/148,425 PRIOR FILING DATE: 1999-08-11
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/637,977 PRIOR FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                              180 CTALESPEHGSLVCSHPLGNFSYNSSCSISCDRGYLPSSMETMQCMSSGEWSAPIPACNV 239
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                                                                                                     1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Kezer, William B
                                                                                                                                                  Similarity
50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 610 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
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                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                   ID NOS: 135
SEQ for Windows Version 3.0
                                                                                                                                              40.4%; Score 296; DB 21;
41.3%; Pred. No. 5.5e-20;
tive 21; Mismatches 50;
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Pred. No. 5.5e-20;
1; Mismatches 50;
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Sequence 36, Application US, GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bonsal Aruna
APPLICANT: Kleyn Patrick
APPLICANT: Kleyn Patrick
                                                                                                                                               ; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-857-670-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 610
TYPE: PRT
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                                            Matches
                                                           Query Match
Best Local S
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Isis Pharmaceuticals, Inc.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-04.24
CURRENT APPLICATION NUMBER: US/09/857,670
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE FILE REFERENCE: 24736-2048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/802,640 CURRENT FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/209,668 PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Xiaoxing S APPLICANT: Isis Pharmaceut
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  1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                         1 Similarity
50; Conserv
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41.3%; Pred. No. 5.5e-20;
ative 21; Mismatches 50;
                                         40.4%; Score 296; DB 22;
41.3%; Pred. No. 5.5e-20;
htive 21; Mismatches 50;
                                                                               Length 610;
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PCT-US01-01239-1145
; Sequence 1145, Application PC/TUS0101239
; GENERAL INFORMATION:
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US-10-021-660-122
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                                                               Prior application data removed - refer to PALM
NUMBER OF SEQ ID NOS: 2318
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1145
LENGTH: 355
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LENGTH: 610
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Best Local Similarity
                                                                                                                                                                                                                         APPLICANT: Human Genome Sciences, Inc., et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ13PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: EOS Biotechnology, Inc.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Anglogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Anglogenesis
TITLE OF INVENTION: Modulators
TITLE REFERENCE: 018501-000710US
                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US01/01239
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/021,660 CURRENT FILING DATE: 2001-12-06 PRIOR APPLICATION NUMBER: US/09/784,356 PRIOR FILING DATE: 2001-02-14 PRIOR APPLICATION NUMBER: US 09/637,977 PRIOR FILING DATE: 2000-08-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Murray, Richard
ORGANISM: Homo sapiens FEATURE:
                                            TYPE: PRT
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41.3%; Pred. No. 5.5e-20;
7ative 21; Mismatches 50;
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; LOCATION: (193)
; OTHER INFORMATION:
US-09-764-902-1145
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US-09-764-902-1145
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 Query Match
Best Local Similarity
Matches 48; Conserv
Matches
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                                                                                                                                                                                                                                                                                                                                    Prior application data removed
NUMBER OF SEQ ID NOS: 2318
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1145
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ13
CURRENT APPLICATION NUMBER: US/09/764,902
CURRENT FILING DATE: 2001-01-17
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Best Local Similarity
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LOCATION: (150/
OTHER INFORMATION: )
                                                                                                                    NAME/KEY: SITE LOCATION: (151) OTHER INFORMATION:
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                                                                                                                                                            LOCATION: (150)
OTHER INFORMATION:
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                                                                                                         NAME/KEY: SITE
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OTHER INFORMATION:
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; Score 268; DB 21;
; Pred. No. 1.6e-17;
17; Mismatches 56;
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Pred. No. 1.6e-17;
7; Mismatches 56
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Query Match
Best Local Similarity
"---hes 47; Conserve
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US-09-764-875-615
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Sequence 615, Application PC/TUS0101332
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
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SEQ ID NO 615
LENGTH: 309
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
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SEQ ID NO 615
LENGTH: 309
TYPE: PRT
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Best Local Similarity 38.8
Matches 47; Conservative
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                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,875 CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-05-09
                                                                                                                                   TYPE: PRT
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                              Score 255;
Pred. No. 2.
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Pred. No. 2.6e-16;
6; Mismatches 58;
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Conservative

16;

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US-60-196-718-4486; Sequence 4486; Application US/60196718; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 4486
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CL00
                                                                                                                                                                                                                                                                                                                                  Sequence 2126, Application US/09760475 GENERAL INFORMATION:
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILLING DATE: 2001-01-16
Prior application data removed - consult |
NUMBER OF SEQ ID NOS: 4122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2126
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Best Local Similarity
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                            LOCATION: (143)
OTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (157)
OTHER INFORMATION: >
NAME/KEY: SITE
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CURRENT FILING DATE: 2000-04-13
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ49
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NAME/KEY: SITE
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 LOCATION: (161)
OTHER INFORMATION:
                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                    TYPE: PRT
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CEPLEAPELGTMDCTH-PFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59

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Conservative

CDAVHQPPKGLVRCAHSPIGEFTYKSSCAFSCEEGFELHGSTQLECTSQGQWTEEVPSCQ 82

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; LOCATION: (198)
; OTHER INFORMATION:
US-09-760-443-1321
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1321
LENGTH: 207
TYPE: 707
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Query Match
Best Local Similarity
Matches 46; Conserv
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Best Local
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LOCATION: (195)
OTHER INFORMATION:
NAME/KEY: SITE
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CURRENT FILING DATE: 2001-01-16
                                                                                                 OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                         NAME/KEY: SITE LOCATION: (194)
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OTHER INFORMATION:
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OTHER INFORMATION:
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US-09-760-498-920; Sequence 920, Applic.; GENERAL INFORMATION:
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Matches 46
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CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 4122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3255
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CURRENT APPLICATION NUMBER: US/09/760,498
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult I
NUMBER OF SEQ ID NOS: 930
                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC017
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ49
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LOCATION: (198)
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PCT-US01-01239-1688
                                                                                                                                                                                                                                                                                                                   RESULT 39
PCT-US01-01239-1688
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                                                                                                                                                                             SOFTWARE: PatentIn
SEQ ID NO 1688
LENGTH: 138
                                                                                                                                                                                                                                                                      Sequence 1688, Application PC/TUS0101239
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Nucleic Acids, Prot
                                                                                                                     NAME/KEY: SITE
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                                                                                                                                                                                                                                     FILE REFERENCE: PTZ13PCT
CURRENT APPLICATION NUMBER: PCT/US01/01239
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                 Prior application data removed - NUMBER OF SEQ ID NOS: 2318
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OTHER INFORMATION: NAME/KEY: SITE LOCATION: (198)
                                                                                                                                                                     TYPE: PRT
        LOCATION: (135)
OTHER INFORMATION:
                                         LOCATION: (127)
OTHER INFORMATION:
                                NAME/KEY: SITE
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LOCATION:
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ORGANISM: Homo
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RESULT 40

PCT-USO1-01332-938

Sequence 938, Application PC/TUSO101332

Sequence 938, Application PC/TUSO101332

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc., et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PJZ02PCT

CURRENT APPLICATION NUMBER: PCT/US01/01332

CURRENT FILING DATE: 2001-05-09

PRIOR APPLICATION DATE: TOTOLOGY OF PALM OF file wrapper

NUMBER OF SEQ ID NOS: 1249

SEQ ID NO 938

LENGTH: 138

TYPE: PRT

TYPE: PRT
Search completed: September Job time: 488 sec
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Best Local Similarity 42.6
Matches 40; Conservative
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Best Local Similarity
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FEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (135)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (135)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
     Score
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2: /cgn2_6/ptodata/2,

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Listing first 45 summaries
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/AB_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
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US-08-252-493C-9
US-08-276-197-9
US-08-824-692-23
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(without alignments)
112.615 Million cell updates/sec
Sequence 2, Appli patent No. 5514582 Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli Patent No. 5378464 Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 9, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequenc
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| US-08-513-278-2 28 162 22.1 128 6 5514582-33 29 153 20.9 62 1 US-08-202-047 30 152.5 20.9 62 3 US-08-964-690 31 152.5 20.9 36.3 US-08-981-234 32 149 20.3 216 3 US-08-981-234 32 149 20.3 216 5514582-35 34 140.5 19.2 265 2 US-08-6177-109 35 140.5 19.2 265 2 US-08-6177-109 36 140.5 19.2 265 2 US-08-177-109 37 140.5 19.2 265 2 US-08-177-109 38 139 19.0 263 1 US-08-247 39 139 19.0 263 1 US-07-906-983 41 139 19.0 324 2 US-08-435-4361 42 139 19.0 324 2 US-08-435-446 43 139 19.0 577 2 US-08-435-446 44 139 19.0 577 2 US-08-435-460 45 138 18.8 197 2 US-08-356-361 |
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| eCEPTORS | Patent No. 5514582 -047-20 Sequence 20, Appl 2348-2 Sequence 24, Appl 692-24 Sequence 24, Appl 692-24 Sequence 27, Appl 706-57 Sequence 57, Appl 706-57 Sequence 57, Appl 109A-2 Sequence 57, Appl 1109A-2 Sequence 2, Appl 1209A-2 Sequence 3, Appl 1209A-3 Sequence 3, Appl |

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                                                                                                                         Sequence 2, Application US/08340539A Patent No. 5808025
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 132; Conserv
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Best Local :
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                                       GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIONS OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
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APPLICATION NUMBER: US,
                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                         121 QKLDKSFSMIKE 132
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ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 372
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Pred. No. 4.1e-71;
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Pred. No. 4.1e-71;
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Best Local
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TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,592B
                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Tedder, Thomas F. APPLICANT: Kansas, Geoffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                COUNTRY: US
ZIP: 02109
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                                                                                                                                                                       STATE:
                                                                                                                                                                                                        STREET:
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Local Similarity 97.0%;
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
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Pred. No. 6e-69;
2; Mismatches
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FILING DATE: CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 2:
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FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
             APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 385 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270
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                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 97.0%;
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKLDKSFSMIKE 341
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                                                                                                                                                                                                                          94080
                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                STACHELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LASKY, LAURENCE A. STACHELL, SCOTT E.
06-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/008,459
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                                                                                                                                                                                   360 Kb floppy disk
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Pred. No. 6e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Patent No.
                                                                                                                                                                                                                                                        FILING DATE:
SEQ ID NO:4:
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                                                                                                                                      Matches
                                                                                                                                                    Query Match
Best Local
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Best Local Similarity
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/3:
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 43
                                                              197 CEPLEAPELGTMDCIHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPICQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 QETNRSFSKIKE 328
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257 VQCEPLEAPELGTMDCIHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 VQCEPLEAPELGTMDCIHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 CEPLEAPELGTMDCIHPLGNFSFQSKCAFNCSEGRELLGTAETQCGASGNWSSPEPICQV 256
                APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 986,931 FILING DATE: 08-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                        LENGTH: 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                  1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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                                                                                                                                                    Similarity
                                                                                                                                      Conservative
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                                                                                                                                  70.7%; Score 518; DB 6; 68.2%; Pred. No. 5.4e-48; vative 13; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.7%;
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Pred. No. 5.4e-48;
Pred. No. 5.4e-29;
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                                                                                                                                                                  Length 372;
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                                                                                                                                    Indels
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QKLDKSFSMIKE 132

317 QETNRSFSKIKE 328

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RESULT 8
US-08-110-158-4
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5514582-31
5PATENT NO. 5514582
FAPPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5514582-31
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/18
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
EILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,158
FILING DATE: 19930820
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                    APPLICANT: McEver, Rodger P.
APPLICANT: Pan, Junliang
TITLE OF INVENTION: Expression Control Sequences of the
TITLE OF INVENTION: P-Selectin Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QKLDKS 126
                                                                                                                                                                            COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                       ADDRESSEE: Patrea L. rausc
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CEPLEAPELGIMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
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GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: PABSE, PATREA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 08-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 17-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (404)-815-655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rela
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
FILING DATE: 19910717
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Regents of the Board of the, University of APPLICANT: Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-MAR-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 30303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgia
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100 Peachtree Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 amino acids
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                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                           OMRF110CIP
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TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear

<u>ب</u>

LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:

Disulfide-bond 131..150

Disulfide-bond 60..158

LOCATION: FEATURE: NAME/KEY:

LOCATION: FEATURE: NAME/KEY:

Disulfide-bond 168..183

Disulfide-bond 163..174

LOCATION: FEATURE: NAME/KEY:

Disulfide-bond 200..244

Disulfide-bond 185..194

LOCATION: FEATURE: NAME/KEY:

CELL TYPE:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:

Disulfide-bond 4..25

FRAGMENT TYPE: NORIGINAL SOURCE:
ORGANISM: Homo
TISSUE TYPE: B

Homo sapien E: Blood

Endothelial

MOLECULE TYPE: peptide HYPOTHETICAL: YES

ss: single linear

ANTI-SENSE:

YES /PE: N-terminal

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FEATURE:

NAME/KEY: Binding-site
LOCATION: 411
OTHER INFORMATION: /note
OTHER INFORMATION: glyce
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LOCATION:
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                                                                                                                                                                                                                   NAME/KEY: Binding-site LOCATION: 180
OTHER INFORMATION: /not OTHER INFORMATION: glyc
                                                                                                                                                                                                                                                                                                                                          LOCATION: 54
OTHER INFORMATION: /note= "Potential asparagine-linked OTHER INFORMATION: glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                   NAME/KEY: Binding-site LOCATION: 219
OTHER INFORMATION: /not OTHER INFORMATION: 91yr
                                                                                                                                                   NAME/KEY: Binding-site LOCATION: 212 /not OTHER INFORMATION: /not OTHER INFORMATION: 91y
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717..730
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585..616
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572..616
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glycosylation site"
                                                                                      /note= "Potential asparagine-linked
glycosylation site"
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glycosylation site"
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glycosylation site"
                       /note= "Potential asparagine-linked
glycosylation site"
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LOCATION:
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NAME/KEY:
LOCATION:
FEATURE:

Disulfide-bond 354..381

Disulfide-bond 337..350

Disulfide-bond 324..368

Disulfide-bond 292..319

NAME/KEY: LOCATION:

Disulfide-bond 448..492

Disulfide-bond 416..443

Disulfide-bond 399..412

Disulfide-bond 386..430

NAME/KEY: LOCATION: FEATURE: NAME/KEY:

Disulfide-bond 262..306

LOCATION: FEATURE: LOCATION: FEATURE: NAME/KEY:

Disulfide-bond 230..257

Disulfide-bond 213..226

LOCATION: FEATURE: NAME/KEY:

Disulfide-bond 275..288

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RESULT 11
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;Patent No. 5378464
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; APPLICANT: MCEVER, RODGER P.
TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES; BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION NAMBER: US/07/320,408
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5378464-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 QKL 123
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) NO:3:
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                                                                                                                                                                                                                                                                           Similarity 41.3 50; Conservative
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53; Conservative
MCEVER,
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518
RODGER
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glycosylation site"
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glycosylation site"
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glycosylation site"
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glycosylation site"
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                                                                                                                                                                                                                                                                          Score 305; DB 6;
Pred. No. 7.5e-25;
3; Mismatches 48;
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SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES; BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140; NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08365470 Patent No. 5632991
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                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/850,802
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,510
FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gimbrone, TITLE OF INVENTION: 7
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                                                                                                                                                NAME: Markowicz, Karen R. REGISTRATION NUMBER: 36,3 REFERENCE/DOCKET NUMBER:
                 TOPOLOGY:
                                 TYPE:
                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: U. FILING DATE: herewith
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                                             LENGTH:
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53; Conserv
                               amino acid
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                                           610 amino acids
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42.7%; Pred. No. 1.7e-24;
7ative 22; Mismatches 48;
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Antibodies Specific For E-selectin
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MEDIUM TYPE:

DISKETTE,

3.5 INCH,

1.44 Mb · STORAGE

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US-09-009-490A-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-209-668-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 19
LENGTH: 610
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09209668A Patent No. 6114517
GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Sequence 89, Application US/09009490A Patent No. 6300491
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF LAVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Bennet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/209,668A CURRENT FILING DATE: 1998-12-10
                                                                                                                        APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonuclectide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                      STREET: 66 Eas
CITY: Marlton
STATE: NJ
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                                  COUNTRY:
                                                                                                                ADDRESSEE:
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                                                                                                                Law Office of Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.4%; Score 296; DB 3; 41.3%; Pred. No. 7.5e-24;
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RESULT 15
5217870-2
5217870
PATENT NO. 5217870
APPLICANT: HESSION, CATHERINE A.;LOBB, ROY R.;GOELZ, SUSAN E.;
ITILE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/345,151
FILING DATE: 28-APR-1989
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; ANTI-SENSE:
US-09-009-490A-89
5217870-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: IS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER
FILING DATE: September 2, 1992
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 567, FILING DATE: August 14, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 440,740
FILING DATE: May 12, 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
063,167
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 063,10 FILING DATE: May 17, 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                  LENGTH: 610
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SOFTWARE: WORDPERFECT 6.0
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US-08-252-493C-9
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 776-1790 TELEFAX: (203) 772-3655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: June 1, 1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                            DESCRIPTION:
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                        NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: AL
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
1 CEPLEAPELGTMDCTH-PFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59
                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New Haven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                            ENGTH:
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NO. 5891645
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                                                                                                                                                                                                            484 amino acids
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matis, Louis A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rother, Russell P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rollins, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC compatible
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                                                                                                                            cDNA to mRNA
predicted amino acid sequence
Porcine E-selectin
                                                                                                                                                                                 Single
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                                                          33.4%;
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                                         Score 245; DB 2; I
Pred. No. 1.7e-18;
22; Mismatches 56;
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Pred.
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No. 7.5e-24;
                                                                    Length 484;
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                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (203) 772-365
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Matis, Louis A. TITLE OF INVENTION: PORCINE E-SELECTIN NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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 119 ICQ 121
                            300 AVKCPAVSQPKNGLVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVP 359
                                                                                         240 CDTVGHPQNGDVSCNHSSIGEFAYKSTCHFTCAEGFGLQGPAQIECTAQGQWTQQAPVCK 299
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                                                       60 VIQCEPLSAPDLGIMNCSH-PLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSP 118
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                               DESCRIPTION:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fidel, Seth A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                       1 CEPLEAPELGTMDCTH-PFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                       Conservative
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Porcine E-selectin
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35.0%;
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Pred. No. 1.7e-18;
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                                                                                                                            ;Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.; TITLE OF INVENTION: RECOMBINANT DNA ENCODING F
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                                                                                                                     ; IMMUNOGLOBULINS
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
                                               NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                        GN-FSFSSQCAFSCSEGTNLTG-IEETTCGPFGNWSSPEDTCQVIQCEPLSAPDLG--IM 74
                                                                                                                                                                                                                                                        SAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEI 113
                                                                                                                                                                                                                                                                                                                          GNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVS 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Hass, G. Michael
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08-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                      22.6%; Score 165.5; DB 3; 30.3%; Pred. NO. 2.5e-10; Mismatches 47;
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                                                                 US/08/185,670
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RESULT 21
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; APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG, ;WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN;H.;MAKRIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT;
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LENGTH: 1466
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Best Local Similarity
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Best Local (
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                  1068
                                                                                                                                     1012 CEIISCEPPPTISNGDF----YSNNRTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT 1067
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                                                                                                   109
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                                                                                                                                                                                                          955 CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1011
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                                                                                                                                                                      58 CQVIQCEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 412,745 FILING DATE: 26-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 CTH----PFGNFS------FSSQCAFSCSEGTNLTG-IEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 332,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSE-KP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IQCEPLSAPDLG--IMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 808,122 FILING DATE: 16-DEC-1991
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                                                                                                                                                                                                                            1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSBGTNLTGIEETTCGPFGN---WSSPEPT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEV 60
                                                                  SKDDQVGVWSSPPPRCISTNK 1088
                                                                                                   SS----GIWSNPSPICQKLDK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT (CR1) AND A THROMBOLTIC AGENT, AND THE METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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NUMBER: 315,015
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                                                                                                                                                                                                                                                                           Score 163.5; DB Pred. No. 4e-09; 6; Mismatches
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Pred. No. 1.
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;Patent No.

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TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT;RECEPTOR 1 (CR1) AND A THROMBOLTIC AGENT, AND THE METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 22
5256642-5
;Patent No. 5256642
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; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
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TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
                                                                                     Matches
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Best Local :
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
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FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
955 CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-19AP
NO.E:
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                                                                                                        Local
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                                                                                                                                                                                                             LENGTH: 1537
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FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
                                      1 CEPLEAPELGTMDCTHPFGNESESSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT 57
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 412,745
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FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
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                                                                                   1 Similarity
45; Conserv
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                 26-SEP-1989
                                                                               22.3%; Score 163.5; DB 6; 31.9%; Pred. No. 4.2e-09; tive 16; Mismatches 57;
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RESULT 24
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; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
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5472939-5
;SEQ
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TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT;RECEPTOR 1 (CR1) AND A THROMEOLTIC AGENT, AND THE METHODS OF
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TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
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LENGTH: 1537
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                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
                                                                                                                                                                                                       NUMBER OF SEQUENCES: 30 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                        APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
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                 FILING DATE:
                                       APPLICATION NUMBER: 176,532
                                                                                                                                                             FILING DATE: 24-SEP-1990
                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 CQVIQCEP----LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
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APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
NO:10:
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Pred. No. 4.2e-09;
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RESULT 25
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5256642-2
;Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG, ;WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN ;H.;MAKRIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT;RECEPTOR 1 (CR1) AND A THROMBOLTIC AGENT, AND THE METHODS OF JUSE THEREOF
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; APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B;WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, S';H.;MAKRIDES, SAVVAS;MARSH, HEMRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
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NUMBER OF SEQUENCES: 30
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Best Local S
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FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
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nes 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                    1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN----WSSPEPT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 2006
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                                                                                                                                                                                                                                                           SS----GIWSNPSPICQKLDK 125
                                                                                                                                                                                                                                                                                                   CEIISCEPPPTISNGDF----YSNNRTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDDQVGVWSSPPPRCISTNK 1595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 163.5; DB 6
Pred. No. 5.3e-09;
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Pred. No. 5.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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F.; IP, STEPHEN
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FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:2:
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5472939-2
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;Patent No. 5472939
;APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG, WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN H.;MAKRIDES, SAVVAS;MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
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Matches 45
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APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
                                                                                                                                        1457 CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1513
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 588,128
FILING DATE: 24 - SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26 - SEP-1989
APPLICATION NUMBER: 32,865
FILING DATE: 03 - APR-1989
APPLICATION NUMBER: 176,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                           1514 CEIISCEPPPTISNGDF ---- YSNNRTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCT 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1457 CGPPPEPFNGMV---HINTDTQFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKKAPI 1513
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                                                                                                                                                                                                                    Local Similarity 31.9 nes 45; Conservative
                                                                                                                                                                                                                                                                                                                                          LENGTH: 2039
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                                                                                                                                                                   1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT
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SS----GIWSNPSPICQKLDK 125
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                                                                                                 CQVIQCEP---LSAPDLGIMNCSHPLASFSFTSACTFICSEGT-----ELIGKKKTICE 108
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                                                                                                                                                                                                                  22.3%; Score 163.5; DB
31.9%; Pred. No. 6e-09;
Live 16; Mismatches
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Indels Length 2039;

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1570 SKDDQVGVWSSPPPRCISTNK 1590

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RESULT 28
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; LENGTH: 128
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       applicant: Capon, Daniel J.;Lasky, Laurence TITLE OF INVENTION: RECOMBINANT DNA ENCODING
                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 ICQKL 123
                                                                                                                                                                                         STREET: One .... CITY: San Francisco
                APPLICATION NUMBER: FILING DATE: 25-FEE
CLASSIFICATION:
                                                                                                                MEDIUM TYPE:
                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLWSNEKP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IQCEPLSAPDLG--IMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSP 118
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APPLICATION NUMBER: 808,122
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                                                                                                                                                                                                                        One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                         JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                                            BENDIG, Mary M.
                                                                                                                                                                                                                                                                                                                                                               POLLEY, Margaret PAULSON, James C.
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                                                                                                                  Floppy disk
              25-FEB-1994
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                             US/08/202,047
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                                                                 Version #1.25
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Best Local Similarity
"hes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20,
               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERRNCE/DOCKET NUMBER: 1413
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SALDANHA, APPLICANT: BENDIG, MATITLE OF INVENTION: A NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 25-FE
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                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 20
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 ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CQDLPVPNEARVNCSHPFGAFRYQSVCSFTCNEGLLLVGASVLQCLATGNWNSVPPECQA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
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6033667
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                                                                                                                                                                                                                                                                                                                                                                                          California
62 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENDIG, Mary M.
VENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAULSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLLEY, Margaret J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHESNUT, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-326-2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
                                                                                                                                                                               US/08/202,047
                                                                                                                                                                                                                                           US/08/964,690
                                                                                                 14137-77
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Pred. No. 1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08981234B Patent No. 6270997
                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 363 amino acid
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,234B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURCHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA ENCOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                               108
166 CEKILCKPPGEIPNGKYTNSHK-DVFEYNEVVTYSCLSSTGPDEFSLVGESSLFCIGKDE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                            TYPE: amino acid
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TOPOLOGY: linear
                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 I 61
                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                            1 CEPLEAPELGIMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGN---WSSPEPT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CEPLEAPELGIMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                             COVICCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGT----ELIGKKKTICESSGI 112
                                                               CSNLPDPLNGQV--SYPNGDMLFGSKAQFTCNTGFYIIGAETVYCQVSGNVMAWSEPSPL 165
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                                                                                                                                                                                                                                                                              363 amino acids
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MURAKAMI, HIROSHI
SHIGEHISA, TAMOTSU
VVENTION: DNA ENCODING A PORCINE COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                Conservative
                                                                                                                                                                                                                             protein
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12-DEC-1997
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                                                                                                                                              20.8%; Score 152.5; DB 4 29.5%; Pred. No. 1.1e-08;
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Pred. No. 1e-09;
                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 62
                                                                                                                                                            DB 4;
                                                                                                                              64;
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                                                                                                                                                             Length 363;
                                                                                                                              Indels
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                                                                                                                             11; Gaps
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RESULT 33
5514582-35
;PATENT NO. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID;IMMUNGGLOBULINS
;IMMUNGGLOBULINS
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US-08-824-692-24
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                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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FILING DATE: 08-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: YOLUY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
                                               NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                   30 SCSEGTNLTG-IEETTCGPFGNWSSPEPTCQVIQCEPLSAPDLG--IMNCSHPLASFSFT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                1 TCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                         QAVRFVCNSGYKIEGDEEMHCSDDGFWGKEKPKCVEI 96
                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 amino acids
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Enfield, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hass, G. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHODS AND COMPOSITIONS FOR SCREENING FOR OR MODULATING A TUMOR ASSOCIATED A
                                                                                                                                                                                                                                                                                                                                                                                       20.3%; Score 149; DB 3; Length 216; 29.9%; Pred. No. 1.3e-08; Live 21; Mismatches 43; Indels
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                                    US/08/185,670
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                                      Matches
                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.3
Best Local Similarity 28.4
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                        TELEFAX: (404) 873-879 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                           TYPE:
                                                    Local
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 03-JAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 L--ASFSFTSACTFICSEGTELIGKKKTICESSG---IWSNPSPICQKL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 LFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 NFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQVIQCEPLSAFDLGIMNCSHP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
   1 CEPLEAPELGTMDCTHPFGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 315, FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 808,122 FILING DATE: 16-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 986, FILING DATE: 08-DEC-1992
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                                                   Similarity
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                                                                                                                                                                                       amino acid
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2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                     265 amino acids
                                     Conservative
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                                                                                                                                                                       linear
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NO
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                                                                                                                                                                                                                                                        873-8795

    Hourcade and Teresa J. Oglesby
MODIFIED COMPLEMENT PROTEASES
    62

                               19.2%; Score 140.5; DB 2; 25.2%; Pred. No. 1.4e-07; ive 14; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.3%; Score 148.5; DB 6 28.4%; Pred. No. 7.6e-09;
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   ---FSFSSQCAFSCSEGTNLTGIEETTCGPFGNW 51
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                                 Indels
                                                                   Length 265;
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US-08-687-706-57
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                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (404) 873-8795 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JUL-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PABST, PALTGA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                               103 KKTICESSGIWSNPSPICQ 121
                                                                   127
                                                                                                                                                                                                     Local Similarity hes 35; Conserv
                                                                                                 52 SSPEPTCQVIQCEPLSAPDLGIMNCSHP---
                                                                                                                               73 CRAIHCPR-----PHDFENGEYWPRSPYYNVSDEISFHCYDGYTLRGSANRTCQVNGRW 126
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 QRRTCQEGGSWSGTEPSCQ 194
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STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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                                                                                                                                                                1 CEPLEAPELGTMDCTHPFGN-----FSFSSQCAFSCSEGTNLTGIEETTCGPFGNW 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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QRRTCQEGGSWSGTEPSCQ 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSPEPTCQVIQCEPLSAPDLGIMNCSHP----
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                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                        265 amino acids
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                       Protein
NO
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                                                             -----DNGAGYCSNPGIPIGTRKVGSQYRLEDSVTYHCSRGLTLRGS 175
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25.2%;
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                                                                                                                                                                                                                  Score 140.5; DB 2
Pred. No. 1.4e-07;
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                                                                                               -----LASFSFTSACTFICSEGTELIGK 102
                                                                                                                                                                                                                                    DB 2;
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; HYPOTHETICAL:
US-08-177-109A-2
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US-08-177-109A-2
                                                                                                                 Sequence 2, Application Patent No. 5928892
GENERAL INFORMATION:
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Best Local S
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                 APPLICANT: Dennis E. Hourcade and Teresa J. Ogles TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU
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                                                                                                                                                                                                                                            201 QRRTCQEGGSWSGTEPSCQ 219
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                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                               KKTICESSGIWSNPSPICQ 121
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                                                                                                                                                                                                                                                                                                                                                   SSPEPTCQVIQCEPLSAPDLGIMNCSHP------LASFSFTSACTFICSEGTELIGK 102
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                                                                                                                                                         Application US/08687706
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Pred. No. 5.2e-07;
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5514582-43
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5514582-43
                             SEQ ID NO:43:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                      APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (404) 873-8794
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                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 KKTICESSGIWSNPSPICQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 SGQTAIC------DNGAGYCSNPGIPIGTRKVGSQYRLEDSVTYHCSRGLTLRGS 200
                                                                                                                                                                                                                                                                                                                                                                                                                      201 QRRTCQEGGSWSGTEPSCQ 219
                                                               FILING DATE: APPLICATION
                                                                                 APPLICATION NUMBER: 440, FILING DATE: 22-NOV-1989
                                                                                                                APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
                                                                                                                                                   APPLICATION NUMBER: 9
FILING DATE: 08-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 SSPEPTCQVIQCEPLSAPDLGIMNCSHP-----LASFSFTSACTFICSEGTELIGK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 CRAIHCPR-----PHDFENGEYWPRSPYYNVSDEISFHCYDGYTLRGSANRTCQVNGRW 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                LENGTH: 126
                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CEPLEAPELGIMDCTHPFGN-----FSFSSQCAFSCSEGINLIGIEETTCGPFGNW 51
                                                                                                                                                                                                                                                                                                   5514582
ANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
35; Conserv
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                                                                 NUMBER:
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                                                                                                                                                       986,931
-1992
                                                                                                    440,625
                                                                 315,015
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Sequence 2, Application US/08435149
                        RESULT 40
US-08-435-149-2
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US-07-906-983-2
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Best Local :
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Patent No. 5187268
GENERAL INFORMATION:
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Best Local
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NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kotwal, Girish
APPLICANT: Moss, Bernard
TITLE OF INVENTION: Synthetic, Anti-Complement Protein and
TITLE OF INVENTION: the Gene Encoding Same
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TE //77/GDE GRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415-543-9600
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MEDIUM TYPE: Floppy
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ADDRESSEE: Townsend and Townsend
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                                                                                                                           66 LSAPDLGIMNCSHPLASFSFT--SACTFICSEGTELIGKKKTICESSGIWSNPSPICQ 121
                                                                                                                                                                        95
                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                      10 GTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTC--GPFGN--WSSPEPTCQVIQCEP 65
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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FILING DATE: 19920701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 263 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTC--GPFGN--WSSPEPTCQVIQCEP 65
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                                                                                        -SPP--SISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLC-SGGEWSDP-PTCQ 202
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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33.1%; Pred. No. 8e-08;
ative 17; Mismatches
                                                                                                                                                                                                                                                       19.0%;
33.1%;
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Pred. No. 2e-07;
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Search completed: September Job time: 278 sec

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (-
                                                            204 GERD--HYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECR
                                                                                                                        144 GGILFGATISESCNTGYKLEGSTSSECLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQ 203
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                                                                                         76 CSHPLASFSFTSACTFICSEGTELIGKKKTIC---ESSGIWSNPSPICQ 121
                                                                                                                                                     19 GNFSFSSQCAFSCSEGTNLTGIEETTC---GPFGNWSSPEPTCQVIQCEPLSAPDLGIMN 75
                                                                                                                                                                                        Local Similarity hes 32; Conserv
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                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 09
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INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
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2002, 10:14:45
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Pred. No. 2.6e-07;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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(without alignments)
202.119 Million cell updates/sec
                                                                      Human lymphocyte
Human lymphocyte
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Human

ALIGNMENTS

RESULT AAR98125

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Human

lymphocyte cell surface glycoprotein (HuLHR) variant.

01-NOV-1996 (first entry)

AAR98125;

AAR98125 standard; Protein;

369

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Key
Region
                                                                                                                                                                         Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
US5514582-A.
                        Domain
                                                        Binding-site
                                                                       Binding-site
                                                                                         Domain
                                                                                                         Domain
                                                                                                                                                   Homo sapiens
                                                                                                                                                                   metastasis.
                                        Domain
                                                        /label= C
256..314
                                                                         /label=
194..255
                                                                                        /label Lectin domain.
157..190
              /label= Cytoplasmic domain
                                        330..352
                                                                                                                 /label-
                                                                                                                                  Location/Qualifiers
                               /label=
                                                label-
                               Transmembrane domain.
                                              Complement binding repeat 2.
                                                                Complement binding repeat
                                                                                 EGF domain
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RESULT
AAR98126
ID AAR9
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AC AAR9
DT 01-N
XX
DE Huma
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Best Local S
Matches 132
Human lymphocyte cell surface glycoprotein (HuLHR) variant
                                  01-NOV-1996
                                                             AAR98126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antivirial, neuromodulating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                          AAR98126 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                 facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is a Gly96-Ile97 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                                                                                                314
                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capon
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                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                       132;
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                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            369
                                                                                                                                                                                                                                                                                                                                     Conservative
                               (first entry)
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92US-0986931.
94US-0185670.
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89US-0315015
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                                                                                                                                                                325
                                                                                        Protein; 370
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                                                                                                                                                                                                                                                                                                                               Score 733; DB 1/,
Pred. No. 1.4e-63;
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Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant is an Asn136 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                       immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                              A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-238773/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                                                                                                                                                                                                                                                              fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                  and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lasky LA;
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89US-0315015.
91US-0808122.
92US-0986931.
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331..353
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257..315
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158..191
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                                                                                                                                                                                                                                                                 The receptor is not a member
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RESULT AAR98127
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IDA P8127
IV AAR98127
IV AAR98
XX AAR9
XX ITMM
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                                                                                                                                                                                                                                                                                                                              22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                       Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidingnosis and treatment e.g. of inflammation
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                          Disclosure;
                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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diagnosis; therapy; drug delivery; antiviral; neuromodulator;
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                             Page 19; 41pp;
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92US-0986931
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257..315
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cell adhesion; graft rejection; inflammation;
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; Mismatches 0;
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Best Local S
Matches 132
                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lymphocyte cell surface glycoprotein (HuLHR) variant.
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                                                                                                                                                                                                                                                                                 /label= Signal region 38..154
                             /label- Transmembrane domain 355..371
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                                                                                                                                                                                                                                 /label= Lectin domain 159..192
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                         /label= EGF domain.
                                                                                                    'label - Complement binding repeat
                                                                                                                                                          /label=
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Pred. No. 1.4e-63;
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Best Local
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                                                                         AAR98110 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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les 132; Conserv
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91US-0808122.
92US-0986931.
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Mismatches 0;
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immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin constant region. The adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in control of LBP and their targets; or therapeutically to deliver vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region improved the province of the transmembrane region improved the province of the transmembrane region in the province of the province of the transmembrane region in the province of the transmembrane region in the province of the province 
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                                                                   cell surface glycoprotein AAR98109-R98135. This var
                                                                              facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in the control of the control
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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159..192
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cell adhesion; graft rejection; inflammation;
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Best Local Similarity
Matches 132; Conser
                                                                                                                                                 22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful fidiagnosis and treatment e.g. of inflammation
                                                                                                                      (GETH ) GENENTECH INC
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89US-0315015.
91US-0808122.
92US-0986931.
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196..257
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/label= Lectin domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                              abel- Complement binding repeat 1.
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Pred. No. 1.
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.4e-63;
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                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
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                                                                                                                                                                                                                                                                                                                                  (first entry)
 /label= |
332..354
                                                            196..
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1..37
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inflammation

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CC a single transmembrane receptor without an active transmembrane concerns to the constant region. The N-terminus of an continuous of the N-terminus of an continuous of the continuous of the immunoglobulin constant region. The receptor is not a member of the continuous of the continuous of the continuous of the continuous of the immunoglobulin chain combines continuous of the provided the adhesion/targetting of a ligand binding partner (LBP) with the continuous of immunoglobulin and can bind to and/or activate continuous of the partner transmembrane recurs to continuous of the partner transmembrane continuous of the partner transmembrane tells.

CC Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in continuous of the process of the immunoglobulin component increases plasma half life and continuous partners continuous of the immunoglobulin component increases plasma half life and continuous partners purification while deletion of the transmembrane region contentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Lys78Gin substitution.
                                                                                                                                                                                                               1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                       cepleapelgtmdcthpfgnfsfssqcafscsegtnltg1eettcgpfgnwsspeptcqv
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Pred. No. 1.4e-63;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery improves anneous solubility and removes
               AAR98113 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                  facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Aspl16Glu substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis
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                                                                                                                                                iqcepl sap dlgimncs hplasfs ft sact fic seg teligk kktices sgiwsnpspic \\
                                                                                                                                                                                                                                                                             132;
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding hybrid immunoglobulin comprising site of a receptor fused to Ig constant region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lasky LA;
                                                                                                                                                                                                                                                                                                                                                      371
                                                                                                                                                                                                                                                                             Conservative
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89US-0315015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Cytoplasmic domain
                                                                                                                       132
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                                                                                                                                                                                                                                                                                         .0%;
              371 AA
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                                                                                                                                                                                                                                                                        Score 733; DB 17;
Pred. No. 1.4e-63;
); Mismatches 0;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                        371;
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useful fo
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the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
              facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                     A hybrid immunoglobulin chain comprising the ligand binding a single transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                         immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain com
cell surface glycoprotein
AAR98109-R98135. This va:
                                                                                                                                                                                                                                                     a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1989;
23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1989;
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diagnosis; therapy; drug deliver
                                                                                                                                                                                                                                         immunoglobulin constant region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Lasky LA;
                                                                                                                                                                                                                                                                                                                  Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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89US-0315015.

91US-0808122.

92US-0986931.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane receptor; adhesion; targetting; apy; drug delivery; antiviral; neuromodulator; cell adhesion; graft rejection; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=332..354
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258..316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF domain.
            described in AAR98106 are given
                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                         The receptor is not a member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HuLHR) variant.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                 23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation;
Nucleic acid encoding hybrid immunoglobulin comprising the ligand
                                                                                         Capon
                                                                                                                                      (GETH
                                                                                                                                                                                                                                                                             22-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR98114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR98114 standard; Protein;
                                            WPI; 1996-238773/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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|||||||||||
|qkldksfsmike 327
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                                                                                         ď,
                                                                                                                                      ) GENENTECH INC
                                                                                       Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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196..257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- Complement binding repeat 1.
258..316
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355..371
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159..192
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Pred. No. 1.4e-63;
Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver the purchase account of the control of 
                                                                                                                                                                                            Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc. The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
  Binding-site
                                            Binding-site
                                                                                                                                                Domain
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                 metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98115 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
  /label = 1
196..257
/label = (
258..316
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38..154
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                        Complement binding repeat
                                                                          EGF domain.
                                                                                                                       Lectin
                                                                                                                                                                   Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 733; DB 17;
Pred. No. 1.4e-63;
                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
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RESULT 11
AAR98116
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 132
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                           Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitcopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin super family nor a multiple subunit polypeptide encoded by discrete genes. The hydrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver vitro assay of LBP and to act to the superficiency and the superficiency to deliver the such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A hybrid immunoglobulin chain comprising the ligand binding sit a single transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                  cell surface glycoprotein
AAR98109-R98135. This var
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5514582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                            316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                          121
                                                                                                                         256
                                                                                                                                                                                  196
                                                                                                                                                    61
                                                                                                                                                                                                                                             Local Similarity
les 132; Conserv
                                                                                                                                                                                                                ш
                                                                                                                                                                          qkldksfsmike
                                                                                       QKLDKSFSMIKE 132
                                                                                                                 IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DJ, Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fused at its C-terminus with the N-terminus of lobulin constant region. The receptor is not a
                                                                                                                                                                                                                                                                                                                      371 AA
                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Complement binding repeat 2. 332...354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Transmembrane 355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                     variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic domain
                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                          Score 733; DB 17; Pred. No. 1.4e-63;
                                                                                                                                                                                                                                                                                                                                                     contains
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                                                                                                                  Ile174Leu substitution
                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                       Length 371;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               member of the
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
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facilitates potentially

immunogenic recovery,

improves aqueous solubility

and removes

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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                        immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                      Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. treating graft rejection; inflammation; metastasis of lymphoma et The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane regificallitates.
                                                                                                                                                                                                       A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane a single transmembrane receptor, fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                        Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for
                                                                                                                                                                                                                                                                   Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-238773/24
                                                                                                                                                                                                                                                                                                                                                                                Capon
                                                                                                                                                                                                                                                                                                                                                                                                            (GETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5514582-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator; ce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98116 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin; transmembrane receptor; adhesion;
                                                                                                                                                                                                                                                                                                                                                                                DJ,
                                                                                                                                                                                                                                                                                                                                                                                                            ) GENENTECH INC.
                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                              Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                            treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
332..354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oy; drug delivery; antiviral; neuromodulator;
cell adhesion; graft rejection; inflammation;
                                                                                                                                                                                                                                                                41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                       of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      targetting;
                                                                                                                                                                                                                                                                                                         - useful for
                                                    etc.)
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RESULT 1
AAR12469
ID AAR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 132
                 The gene product may be used as a ligand binding partner in combination with a stable plasma protein eg. IgGl-IgG4, IgA, IgE, IgD or IgM. The fusion product is joined by N- or C-terminal groups, preferably the N-terminal of the Fc region of the spp is linked to the C-terminal of lbp. They may be used to provide antiviral, immunomodulatory and neuromodulatory treatment as well as in treatment of receptor
                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
         mediated
                                                                                             Disclosure; Fig 1; 67pp; English.
                                                                                                                          New hybrid immunoglobulin(s) ligand binding molecules and
                                                                                                                                                                                           Capon
                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                    22-NOV-1989;
                                                                                                                                                                                                                                                        21-NOV-1990;
                                                                                                                                                                                                                                                                              13-JUN-1991
                                                                                                                                                                                                                                                                                                  WO9108298-A.
                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                    Ligand binding partner; lbp; stable plasma protein; spp; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lyphocyte cell surface glycoprotein (LHR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR12469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR12469 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Asn181Gln substitution.
                                                                                                                                                                                                                                                                                                                                                                                                           1mmunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                  inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1991-193202/26.
DB; AAQ12118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                          Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 100.0%; al Similarity 100.0%; 132; Conservative (
         abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                          Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                    89US-0444625
                                                                                                                                                                                                                                                        90WO-US06849
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 20..32
                                                                                                                                                                                                                                                                                                                                 /label- signal peptide
38..372
                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
                                                                                                                                                                                                                                                                                                                                                                                                           neuromodulatory;
                                                                                                                                                                                                                                                                                                                      probable mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                            б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 733; DB 17;
Pred. No. 1.4e-63;
); Mismatches 0;
                                                                                                                           for use as diagnostic reagents for treat organ and graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                          receptor mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                           abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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RESULT 13
AAR24026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 132;
                                                                                                                                                                                                                                                                                                                                            AAR24026;
                                                                                                                                                                                                                                                                                                                                                         AAR24026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Nucleic acid encoding polypeptide fusions - comprising ligand
              WPI; 1992-199589/24.
N-PSDB; AAQ24987.
                                  Capon
                                                              23-FEB-1989;
22-NOV-1989;
                                                                                    22-NOV-1989;
                                                                                                  26-MAY-1992
                                                                                                               US5116964-A
                                                                                                                                   Region
                                                                                                                                                  Modified-site
                                                                                                                                                               Modified-site
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                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                           Lyphocyte cell
                                                                                                                                                                                                                                                                                                               Sequence of
                                                                                                                                                                                                                                                                                                                              22-NOV-1992
                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                         (HuLHR)
                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                           qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                                   QKLDKSFSMIKE
                                  Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                  Lasky LA;
                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                             89US-0315015
89US-0440625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                                                           surface glycoprotein; ligand binding protein.
                                                                                   89US-0440625
                                                                                                                                                  /label=
311..313
                                                                                                                                                                                            216..
                                                                                                                                                                                                         /label= see above 177..179
                                                                                                                                                                                                                                    /label= signal 60..62
                                                                                                                                                                                                                      104..106
                                                                                                                            /label=
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                          /label= see above
                                                                                                                                                                     /label= see above
                                                                                                                                                                                    /label=
                                                                                                                                                                                                  'label=
                                                                                                                                                                                                                             'label-
                                                                                                                                                                                                                                                                                                                                                                                                         132
                                                                                                                                                                                                                                                                                                               lymphocyte
                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                              234
                                                                                                                                     355
5
                                                                                                                                                  313
                                                                                                                                                                                            218
                                                                                                                             stop transfer sequence
                                                                                                                                                        see
                                                                                                                                                                                    see above
                                                                                                                                                                                                  see above
                                                                                                                                                                                                                             potential N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                          372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 733; DB 12;
Pred. No. 1.4e-63;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                surface
                                                                                                                                                                                                                                                                                                               glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
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site"

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RESULT 1
AAR37960
ID AAR37960
ID AAR37960
ID AAR3
XX AAR3
AC AAR3
AC Huma
XX HuLE
KW HuLE
KW Cran
XX Homc
XX Homc
YFT Prot
FT Prot
FT Prot
FT Modi
FT Modi
FT Modi
FT Modi
FT Regi
FT Modi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHR mediates the binding of lymphocytes to the endothelium of lymphoid tissue. Full length cDNA clones and DNA encoding the human and the murine LHR (HuLHR and MLHR, respectively) have been identified and isolated (see AAQ24987 and AAQ24988). LHR is a glycoprotein which contains the following protein domains: a signal sequence, a carbohydrate binding domain, and epidermal growth factor-like (egf) domain, at least one and preferably two complement binding domain repeat, a transmembrane binding domain (TMD), and a charged intracellular or cytoplasmic domain. LHR is used as the ligand-binding partner in fusion polypeptides with an immunoglobulin,
              Modified-site
                                                                                                                 Domain
                                                                                                                                           Modified-site
                                                                                                                                                                    Modified-site
                                                                                                                                                                                               Domain
                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                               HulhR; lymphocyte binding inhibition; lymphoma metastasis;
transplant rejection; inflammation.
                                                                                                                                                                                                                                                                                                                                                    Human .Lymphocyte Homing
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR37960 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding partner protein diagnosis and therapy
                                                                                         Modified-site
                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                         AAR37960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for use in diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
            /note= "!
232..234
                                                                                        /label= F
177..179
                                                                                                                                                                    /label= Lectin_domain
60..62
                                                                                                                                                                                             /note=
39..155
                                                                                                                                                                                                                      /label= signal_sequence
39..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-1 - 1-3;
                                                               /note=
197..25
                                                                                                                 /note=
160..19
                                   216..218
                                                                                                                                          /note= "potential N-glycosylation
104..106
                                                                                                                                                                                                                                                             Location/Qualifiers
/note=
                                                /label= Complement_Binding_Repeat_1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                               . 258
                                                                                                                e= "potential N-glycosylation
.193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 733; DB 13; 100.0%; Pred. No. 1.4e-63; tive 0; Mismatches 0;
                                                                          "potential N-glycosylation
                                                                                                                                                                                                          "Trp39 is probable N-terminus of mature
"potential N-glycosylation site"
                        "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                     Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                     EGF_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                           site"
                                                                                                                              site"
                                                                                                                                                       site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                            LHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 1
AAR38908
ID AAR3
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                                                                                                                                                                                В
                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 132; Conserv
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                      A human peripheral blood lymphocyte cDNA library in lambda gt10 was screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was isolated and sequenced. The ORF codes for 372 amino acids with a mol. wt. of approximately 42.200. Comparison of the HuLHR amino acid sequence with the murine LHR sequence (AAR37951) showed a high degree of amino acid conservation in each of the LHR domains, e.g. 96% in the transmembrane domain and 83% in the carbohydrate binding of lymphocytes to lymphoid tissue to treat inflammation or graft rejection. They could also be used to control lymphoma metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human and murine lymphocyte homing receptors to treat graft rejection and inflammation - comprise carbohydrate binding, epidermal growth factor and complement binding domains
             AAR38908
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-188588/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1989;
31-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                     121 QKLDKSFSMIKE 132
                                                                                                                               257
                                                                                                                                                                                 197
                                                                                                                                                      61
                                                                                                                                                                                            1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                                                                                                                                                                          to treat conditions involving lymphocyte accumulation.
                                                                          IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                                {\tt cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv}
                                                                                                                              iqceplsapdlgimncshplasfsftsactficsegteligkkkticessgiwsnpspic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĽĀ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ43154.
            standard; Protein; 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0315015
91US-0786149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Trans
/note= "stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "potential N-glycosylation site"
311..313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Complement_Binding_Repeat_2
271..273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "potential N-glycosylation site"
259..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246..248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane_Domain
stop transfer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic_Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32pp; English.
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                               Score 733;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,SW
             ΑA
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                   > 733; DB 14;
. No. 1.4e-63;
smatches 0;
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Length Indels

372; 0;

Gaps

0;

256

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Query Match
Best Local Similarity
                                                      The sequences given in AAR38908-09 represent human and murine lymphocyte cell surface glycoprotein (LHR) respectively. These proteins mediate the binding of lymphocytes to the endothelium of lymphoid tissue. LHR is a glycoprotein which contains a signal domain, a carbohydrate binding domain, an epidermal growth factor-like (egf) domain, at least one complement binding domain repeat, a transmembrane binding domain (YMD) and a charged intracellular or cytoplasmic domain. The murine and human amino acid sequences show a high degree of overall homology (83%), however degrees of homology between the various domains is variable. These proteins may be fused to a ligand binding partner protein (LBPP) which causes an increase in the half life of the LHR. The fusions may be used therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue. They may be used in organ or graft rejection and for the treatment of inflammation.
                                                                                                                                                                                                                                                                                                                                23-FEB-1989;
22-NOV-1989;
16-DEC-1991;
                                                                                                                                                                                                     Disclosure; Fig 1; 44pp; English.
                                                                                                                                                                                                                       New lymphocyte homing receptor immunoglobulin fusion polypeptide(s) - used to inhibit binding of lymphocytes therapeutic and diagnostic uses
                                                                                                                                                                                                                                                                                          Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; murine; lymphocyte; cell surface glycoprotein; homing receptor; LHR; endothelium; lymphoid tissue; signal; domain; complement binding; carbohydrate binding; epidermal growth factor-like; egf; intracellular; transmembrane binding; cytoplasmic; ligand binding partner protein;
                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38908
                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-1994
                                                                                                                                                                                                                                                                       1993-226664/28.
                                                                                                                                                                                                                                                                                           Ę,
                                      372
                                                                                                                                                                                                                                                                                          Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                               89US-0315015.
89US-0440625.
91US-0808122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 355
100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Lectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complement factor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                             "Cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Transmembrane binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "egf domain"
.0%;
Score 733; DB 14;
Pred. No. 1.4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                domain"
          Length
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RESULT 1
AAR76506
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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphocyte homing receptor; lymphocyte cell surface glycoprotein; LHR; ligand binding partner; immunoglobulin; constant region; antibody engineering; immunomodulator.
                                                                                      27-JUN-1995
                                                                                                             US5428130-A
                                                                                                                                                  Region
                                                                                                                                                                                        Domain
                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human LHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR76506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
                                                              89US-0315015
                                                                                                                                                                                                                                                                                                                                             /label-
177..179
                                                                                                                                                                                                                                                                                                                                                                   /label=
104..106
                                                                                                                                                                                                                                                                                                                    /label-
216..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
/note= "hydrophobic domain, may act as signification into the endoplasmic reticulum lumen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 20..32
                                                                                                                                                                                                                                                                                                                                                                                                        /note-
                                                                                                                                                                                                                           'label=
                                                                                                                                                                                                  'label=
                                                                                                                                                                                                                                                                             label-
                                                                                                                                                                                                                                                                                                   label.
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                                                                                                                                                                                                                                                    label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mat_protein
                                                                                                                                      "putative
                                                                                                                                                                           "putative
                                                                                                                                                                                                                                                                                                                                                                                                        "putative extracellular domain"
                                                                                                                                                                                                  N-glycosylation_site
                                                                                                                                                                                                                           N-glycosylation_site
                                                                                                                                                                                                                                                    N-glycosylation_site
                                                                                                                                                                                                                                                                            N-glycosylation_site
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                                                                                                                                                                                                                                                                                                                             N-glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                               N-glycosylation-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                        intracellular
                                                                                                                                                                           stop
                                                                                                                                                                           transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                may act as signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                      region"
                                                                                                                                                                            membrane anchor
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RESULT 1
AAAR83050
ID AAAR8
XX AAR8
XX AAR8
AC AAR8
XX Lymp
KW Lymp
KW Lymp
KW Lymp
KW Vect
XX Homc
XX Homc
FF Pept
FT Doma
FT Doma
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Best Local Similarity
Matches 132; Conserv
      Modified-site
                         Modified-site
                                                                           Domain
                                             Modified-site
                                                                                                                  Domain
                                                                                              Domain
                                                                                                                                      Domain
                                                                                                                                                       Domain
                                                                                                                                                                           Peptide
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                          vector; plasma-life.
                                                                                                                                                                                                                                  Lymphocyte cell surface glycoprotein; LHR; transmembrane immunoglobulin; IgG; constant region; receptor-mediated (
                                                                                                                                                                                                                                                                   Human LHR
                                                                                                                                                                                                                                                                                      31-JAN-1996
                                                                                                                                                                                                                                                                                                          AAR83050
                                                                                                                                                                                                                                                                                                                             AAR83050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A murine Mel 14 antigen cDNA clone was used to screen a lambda gtl cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells. A cDNA clone encoding LHR was isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library derives ...... obtd. from primary cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig.la-lc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid ligand binding constant region sequences half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ92802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-240086/31.
                                                                                                                                                                                                                                                                                                                                                                           121 QKLDKSFSMIKE 132
|||||||||||
| 317 qkldksfsmike 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      iqceplsapdlgimncshplasfsftsactficsegteligkkkticessgiwsnpspic
                                                                                                                                                                                                                                                                                                                                                                                                                         IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNDSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Д,
                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                      (first
                                                                          /label=
356..372
                                                                                                                                                       /label= Sig_peptide 39..155
     /label= N-glycosylation_site
177..179
                         /label= N-glycosylation_site
104..106
                                                                                                                                                                          Location/Qualifiers 20..32
                                                     /label= Cytoplasmic_domain
/note= "potential stop tra
                                                                                                   /label=_Complement_factor_binding_domain
                                                                                                                       /label=_Epidermal_growth_factor_domain
                                                                                                                                          /label= Carbohydrate_binding_domain
                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                    entry)
                                                                                                                  317
                                                                                              355
                                                                                Transmembrane_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partner molecules - futo increase stability
                                                                                                                                                                                                                                                                                                                            372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 733; DB 16;
Pred. No. 1.4e-63;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                            AA.
                                                    stop transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fused
ty and
                                                    sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin
vivo plasma
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AAR98106
ID AAR9
XX
AC AAR9
XX
DT 31-0
XX
DE Huma
                                                                                                                             Qγ
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                                                                                                                                                                     Qγ
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RESULT
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Best Local
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AAR98106;
                      AAR98106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                      A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used to screen an oligo-dT primed lambda gt10 cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells. A 2.2 kb clone (sequence given in AATOS869) was isolated that encoded the human LHR protein (AAR83050). LHR-IgG hybrids were constructed for use in the targeting of therapeutic moieties to lymphoid tissue.
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Expression vector encoding fusion protein to increase plasma life comprises receptor ligand binding site and Ig constant region, for
                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of receptor mediated disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT05869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                 317
                                                                                                       121
                                                                                                                               257
                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capon DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1989;
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                                                                                                                                                      61
                                              18
                                                                               qkldksfsmike
                                                                                             QKLDKSFSMIKE 132
                                                                                                                         IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                   CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                                                        cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995-350776/45
                                                                                                                                                                                                                          132;
                                                                                                                                                                                                                         Similarity 100.
32; Conservative
                   standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                    372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lasky LA;
                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-0440625.
89US-0315015.
91US-0808122.
92US-0986931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0185669
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271..273
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/label= N
248..248
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216..218
/label= N-glycosylation_site
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311..313
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                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycosylation_site
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                      Score 733; DB 16;
Pred. No. 1.4e-63;
); Mismatches 0;
                                                                                                                                                                                                                                              Length 372;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                      Gaps
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Human lymphocyte cell surface glycoprotein (HuLHR).

31-OCT-1996

(first entry)

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                         immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery immoves
                                                                                                                                                                                                                                                                                                                                                                  a single
                                                                                                                                                                                                                                                                                                                                                                                    A hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment {\rm e.g.} of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation;
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                      region;
                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastasis.
                                                                                                 potentially
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                                                                                                                 facilitates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                 d immunoglobulin chain comprising the ligand binding site transmembrane receptor without an active transmembrane fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98106
                                                                                                                                                                                                                                                                                                                                                                                                                       Figure 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasky LA;
                                                                  372
                                                                                               recovery, in immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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333..355
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259..317
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197..258
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160..193
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39..155
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                                                                                                                                                                                                                                                                                                                                                                                                                       41pp; English.
100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                             improves aqueous solubility ic epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
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.0%;
Score
Pred.
733;
No. 1
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DB 17;
.4e-63;
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               Length
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RESULUTANAW ACK AAW ACK AAW ACK AAW ACK AAW ACK ACK AW CIPE FOR REGETT R
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                                                                                                               22-NOV-1989;
23-FEB-1989;
19-DEC-1991;
08-DEC-1992;
21-JAN-1994;
26-MAY-1995;
WPI; 1998-129805/12
N-PSDB; AAV19012.
                                                Capon
                                                                                                                                                                                                                                                                   03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accumulation.
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                                                                                                                                                                                                                                   23-FEB-1989;
                                                                                                                                                                                                                                                                                                    US5714147-A.
                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                                 (GETH
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lymphocyte homing receptor; LHR; HuLHR; organ; graft; retreatment; inflammatory disorders; rheumatoid arthritis; autoimmune diseases; lymphoma metastasis; control; lymph
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                      ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
Lasky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocyte homing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                              92US-0986931.
94US-0185670.
95US-0451848.
                                                                                 89US-0440625.
89US-0315015.
91US-0808122.
                                                                                                                                  89US-0315015
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                                                                                                                                                                                                                                                                   /note= "|
271..273
                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
60..62
                                                                                                                                                                                                                    /note=
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177..1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 20..33
                                                                                                                                                                                                                                                                                                                     232..234
                                                                                                                                                                                                                                                                                                                                             216..218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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                                                                                                                                                                                                                   te= "potential .
.357
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                                                                                                                                                                                                                                                                                                                                                                                "potential
                                                                                                                                                                                                                                                                                                                                                                                                      potential
                                                                                                                                                                                                                                                                                                                                                                                                                              "potential signal sequence
                                                                                                                                                                                                        "membrane anchoring
                                                                                                                                                                                                                                                       "potential
                                                                                                                                                                                                                                                                                "potential
                                                                                                                                                                                                                                                                                                        "potential
                                                                                                                                                                                                                                                                                                                               "potential
                                                                                                                                                                                                                                                                                                                                                        "potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor (LHR).
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                                                                                                                                                                                                                                                                                                                                                                                                     N-linked glycosylation
                                                                                                                                                                                                                               N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                N-linked
                                                                                                                                                                                                                                                                                                                                                                             N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                        N-linked
                                                                                                                                                                                                                                                                                                                              glycosylation
                                                                                                                                                                                                         domain/stop transfer*
                                                                                                                                                                                                                                                                                                        glycosylation
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                                                                                                                                                                                                                                                                               glycosylation
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                                                                                                                                                                                                                                                        site"
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RESULT 2
AAW73264
ID AAW73267
XX AAW7
XX AAW7
AX AAW7
AX AAW7
AX Lymp
XX Lymp
KW Lymp
KW 1ymp
XX 1ymp
XX 1ymp
XX 1ymp
XX 21-h
XX 22-F
PR 23-F
PR 31-C
PR 31-C
PR 31-C
PR 31-C
PR 31-C
PR 10-A
XX 10-A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1989;
31-OCT-1991;
06-MAY-1993;
10-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 132; Conserv
N-PSDB; AAV08321
                                                                Lasky LA, Rosen SD,
                                                                                                             (REGC ) UNIV CALIFORNI
                                                                                                                                                                                                                                                                                                             10-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                            24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                         US5840844-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein; lymphocyte binding; endothelium; graft rejection; inflammation; therapy; arthritis; autoimmune disease; lymphoma metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte accumulation; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lymphocyte homing receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW73264 standard; Protein; 372 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a human lymphocyte homing receptor (LHR) which may be used in the construction of a chimeric molecule comprising an LHR fused at its C terminus to the N terminus of an of lymphocyte attachment to endothelial cells. Such a method may inflammatory disorders, e.g. rheumatoid arthritis or other autoimmune diseases, for controlling lymphoma metastasis and for treating and incommune diseases, for controlling lymphoma metastasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 QKLDKSFSMIKE 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prevention of lymphocyte attachment to endothelial cells - using chimeric molecule comprising lymphocyte homing receptor and
                   1999-034122/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin constant region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating conditions in which there is an accumulation of
                                                                                                                CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                              89US-0315015.
91US-0786149.
93US-0059029.
95US-0513278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                     95US-0513278.
                                                           Singer
                                                              , SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 733; DB 19;
Pred. No. 1.4e-63;
Mismatches 0;
                                                    Stachel SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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This sequence is the human lymphocyte homing receptor (LHR) of the CC invention. LHR is a lymphocyte cell-surface glycoprotein that mediates CC the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble CC LHR polypeptides, lacking signal peptide (amino acids 1-38), acids 356-372), can be used therapeutically to compete with the normal CC organ or graft rejection treatment protocols, for treating inflammations CC such as arthritis and other autoimmune diseases, for control of lymphoma CC interesting the autoimmune diseases, for control of lymphoma CC interesting conditions involving lymphocyte accumulation. CC orcompetitive inhibitors of LHR activity, and for purifying anti-LHR antibodies or antibodies, and as immunogens for raising anti-LHR antibodies.
Sequence
                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Lymphocyte homing receptor polypeptides - useful for inhibiting lymphocyte binding to lymphoid endothelium
372 AA;
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RESULT 21
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Best Local
                                                                                                                                             Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                             Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                     01-NOV-1996
                                                                                                                                                                                                                                AAR98131 standard; Protein;
                                                                                                                                                                                                                                                                         317 qkldksfsmike
                                                                                                                                                                                                                                                                                 121 QKLDKSFSMIKE
                                                                                                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                      IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                              {\tt iqceplsapdlgimncshplasfsftsactficsegteligkkkticessgiwsnpspic}
                                                                                                                                                                                                                                                                                                                                                                       132;
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                         328
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 733; DB 20; 100.0%; Pred. No. 1.4e-63;
                                                                                                                                                                                                                                 374
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                              rejection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                 0;
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Domain Binding-site Binding-site Domain Domain Region

199.

/label= EGF domain. /label=_Lectin /label= Signal region 38..157 Location/Qualifiers 1..37

. 195 260

Homo sapiens

Domain

335...357 // Label = Transmembrane domain 358...374

Cytoplasmic domain

/label= Complement binding repeat 1. 251..319 /label= Complement binding repeat 2.

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RESULT 2
AAR98132
ID AAR9
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AC AAR9
AC AAR9
XX
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A hybrid immunoglobulin chain comprising the ligand binding sit a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                 AAR98132 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 67-Glu-Ser-Ala insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
               01-NOV-1996
                                          AAR98132;
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding
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                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                            22
                                                                                                                                      qkldksfsmike
                                                                                                                                                    QKLDKSFSMIKE
                                                                                                                                                                                         IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996-238773/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding hybrid immunoglobulin comprising site of a receptor fused to Ig constant region
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                          374
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 19; 41pp; English.
               (first entry)
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                 132
                                                                                                                                        330
                                                                     Protein;
                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                     374
                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                     Score 733; DB 17;
Pred. No. 1.4e-63;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the ligand - useful for
                                                                                                                                                                                                                                                                                                                               374;
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site
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                                                                                                                                                                                                                     120
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immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are glven in AAR98105. This variant contains a 83-Gly-Thr-Thr insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                              a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                               A hybrid
                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lymphocyte cell surface glycoprotein (HuLHR)
                                                                                                                                                                                                                                                                  immunoglobulin constant region. The receptor is not a member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ďď,
                                                                                                                                                                                                                                                                                              immunoglobulin chain comprising the ligand binding site transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lasky
                                                                                                                                                                                                                                                                                                                                            Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
335..357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
38..157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
358..374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261..319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
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                                                                                                                                                                                                                                                                                                                                           41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complement binding repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region.
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of

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RESULT 2
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          Disclosure; Page 19; 41pp; English.
                                   Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                              23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                              WPI; 1996-238773/24.
                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                              22-NOV-1989;
                                                                                                                                                                                                                                                                                                               23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                             07-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lymphocyte cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR98122 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV 60
                                                                                                                                              DJ, Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qkldksfsmike 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132;
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                                                                                                                                                                                                           89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                         89US-0315015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal region 38..154
                                                                                                                                                                                                                                                                                                                                                                                                             'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /labe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= EGF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .59..192
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                                                                                                                                                                                                                                                                                                                                                                                                                             .371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l= Complement binding repeat 1.
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                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 733; DB 17;
; Pred. No. 1.4e-63;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 374;
                                                    the ligand - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
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RESULT 24
AAR98124
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Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin constant region. The receptor is not a member of the cenceded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the ceffector functions of immunoglobulin and can bind to and/or activate concern than one ligand. It can be used diagnostically for the in combines concern than one ligand. It can be used diagnostically to deliver control assay of LBP and their targets; or therapeutically to deliver constant applications are as antiviral, neuromodulating and control assay of the control as antiviral, neuromodulating and control applications are as antiviral, neuromodulating and control immunomodulating agents, or as modulators of cell adhesion (e.g. in control control component increases plasma half life and control contro
          Domain
                                                                                                                 Domain
                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                   Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98124 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QKLDKSFSMIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Ile288Val substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an incomprising the ligand binding site of region; fused at its C-terminus with the N-terminus of an incomprising the ligand binding site of the site of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               /label= Lectin domain 159..192
                                                                                                                                                                                                  258..316
                                                                                                                                                                                                                                                                                                        /label= EGF domain
196..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal region 38..154
/label= Transmembrane
355..371
                                                                                                 332..354
                                                                                                                 /label= Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                             /label=
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                                                                                                                                                                                                                       Complement binding repeat
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Pred. No. 1.8e-63;
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                                domain
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains an Ile302Leu substitution.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          Matches
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a single transmembrane receptor without an active trans
region; fused at its C-terminus with the N-terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 19;
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               AAR98119;
                                          AAR98119 standard;
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                                                                                                                                                                                                                                              1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                      IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                QKLDKSFSMIKE 132
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                                                                                                                                                                                                                                                                                          Conservative
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91US-0808122.
92US-0986931.
94US-0185670.
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                                            Protein; 371
                                                                                                                                                                                                                                                                                                      99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41pp; English.
                                                                                                                                                                                                                                                                                       Score 731; DB 17;
Pred. No. 2.2e-63;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                  Length
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                        Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc. The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Ser226Thr substitution.
                                                                                                                                                           immunoglobulin super family nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                  region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a men
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capon DJ, Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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diagnosis; therapy; drug deliv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (first entry)
Sequence
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                                                                                                                                                                                                                                                                                                single transmembrane receptor without an active transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                   1996-238773/24.
                                                                                                                                                                                                                                                                                                              immunoglobulin chain comprising the ligand binding site
371
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92US-0986931
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89US-0315015
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332..35
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1..37
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355..371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein (HuLHR)
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graft rejection; inflamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat 1.
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RESULT 26
AAR99117
ID AAR9911
XX AAR991
XX AAR981
XX VX
DE Human
XX Immunc
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K
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Best Local S
Matches 131
Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
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16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                   WPI; 1996-238773/24.
                                                                                                                                                                                     (GETH ) GENENTECH INC
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89US-0315015.
91US-0808122.
92US-0986931.
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                                                                                                                                            LA;
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355..371
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196..257
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99.2%;
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2.8e-63;
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RESULT
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cc encoded by discrete genes. The hybrid immunoglobulin chain combines
cc effector functions of immunoglobulin and can bind to and/or activate
cc effector functions of immunoglobulin and can bind to and/or activate
cc effector functions of immunoglobulin and can bind to and/or activate
cc vitro assay of LBP and their targets; or therapeutically for the in
cc LBP such as toxins, enzymes growth factors to particular cells.
cr Typical applications are as antiviral, neuromodulating and
creating graft rejection; inflammation; metastasis of lymphoma etc.)
cr The immunoglobulin component increases plasma half life and
cf facilitates purification while deletion of the transmembrane region
contentially immunogenic epitopes. Variants of the human lymphocyte
cell surface glycoprotein described in AAR98106 are diven in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 131;
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Best Local
                           Binding-site
                                                      Binding-site
                                                                                      Domain
                                                                                                                                                          Key
                                                                                                                  Domain
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                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                         diagnosis; therapy;
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                                                                                                                                                                                                                                            Immunoglobulin; transmembrane receptor; adhesion; targetting;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
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                                                                                                                                                                                                                                                                                                                                                                                                  27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA;
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
/label= (
332..354
                    /label= Complement binding repeat 1. 258..316
                                                                                     159.
                                                       196..257
                                                                                                            38..154
                                                                      /label=
                                                                                                                                             Location/Qualifiers
1..37
                                                                                            /label= Lectin domain
                                                                                                                        /label= Signal region
                                                                                                                                                                                                                     by; drug delivery; antiviral; neuromodul cell adhesion; graft rejection; inflamm
                                                                                   .192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%;
       Complement binding repeat 2.
                                                                  EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 729; DB 17;
Pred. No. 3.5e-63;
1; Mismatches 0
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                                                                                                                                                                                                                     inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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RESULT 2
AAR22802
ID AAR2
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                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation, metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
               AAR22802 standard;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                   facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Thr282Ser substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5514582-A
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                                                                                       316
                                                                                                                  121
                                                                                                                                                 256
                                                                                                                                                                                                          196
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                                                                                                                  OKLDKSFSMIKE 132
                                                                                                                                                               IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
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                                                                                                                                               iqceplsapdlgimncshplasfsfssactficsegteligkkkticessgiwsnpspic
                                                                                                                                                                                                                                                                  131;
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lasky LA;
                                                                                                                                                                                                                                                                                                                                          371
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0315015.
91US-0808122.
92US-0986931.
94US-0185670.
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355..371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
               Protein; 372 AA
                                                                                                                                                                                                                                                                             99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic domain
                                                                                                                                                                                                                                                                               Score 729; DB 17;
Pred. No. 3.5e-63;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                            Length 371;
                                                                                                                                                                                                                                                                 Indels
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    useful for

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The protein sequence was deduced from the DNA sequence obtd. by screening an oligo dT primed lambda gt10 cDNA library derived from human peripheral blood lymphocyte mRNA obtd. from primary cells, with a 2.2 kb EcoRI insert of the murine Mel 14 antigen cDNA clone. The protein contains regions encoding a carbohydrate binding domain, an EGF-like domain, a complement binding domain and a transmembrane domain. The protein contains 26 cystein residues. Cells transformed by the hLHR DNA are used to produce LHR (which mediates binding of lymphocytes to the endothelium of lymphold tissue). LHR or its variants are useful as reagents for assaying LHR or anti-LHR anti-bodies, to purify the antibodies, as immunogens, and therapeutically to compete with normal binding of lymphocytes (to prevent graft/organ rejection; to treat inflammation (such as rheumatod arthritis or
                                     other autoimmune diseases); for control of lymphocyte metastasis, and to treat conditions associated with accumulation of lymphocytes). Derivs. and variants of LHR may be produced having modified properties, e.g. increased activity, longer plasma half-life, reduced side effects and better aq. solubility.
                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1;
                                                                                                                                                                                                                                                                                                                                         New DNA encoding at least one domain of lymphocyte homing receptor - useful for treating graft rejection, inflammat
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-123385/15
                                                                                                                                                                                                                                                                                                                                                                                                                            Lasky LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HuLHR; LHR; binding; endothelium; immunogens; graft; organ;
rejection; inflammation; rheumatoid arthritis; lymphoma met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphocyte homing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA.
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216..218
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311..3
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177..179
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104..106
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                                                                                                                                                                                                                                                                                                 32pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Stachel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "potential signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "stop transfer or membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "N-glycosylation
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                                                                                                                                                                                                                                                                                                   English
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                                                                                                                                                                                                                                                                                                                                                                                                                            Singer MS,
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                                                                                                                                                                                                                                                                                                                                             inflammation,
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Sequence

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RESULT 29
AAR98118
AXY
AAR9811
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AAR9811
XX

AAR9811
XX

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O1-NOV
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HUMMAN
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                                                                                                                                                                                                                                      22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 131;
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                                                                                                       WPI; 1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1996
                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                              23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5514582-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin;
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||||||||||
317 qkldksfsmike 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
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                                                                                                                                                 Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulin; transmembrane receptor; adhesion; targetting; therapy; drug delivery; antiviral; neuromodulator; lator; cell adhesion; graft rejection; inflammation
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Complement binding repeat 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= EGF domain
196..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Lectin domain.
159..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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4.4e-63;
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AAR98120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A hybrid immunoglobulin chain comprising the ligand binding site of a single transmembrane receptor without an active transmembrane as a single transmembrane receptor without an active transmembrane creation; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide cencoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the creation of limmunoglobulin and can bind to and/or activate center than one ligand. It can be used diagnostically for the in creation of LBP such as toxins, enzymes, growth factors to particular cells. The such as toxins, enzymes, growth factors to particular cells. Immunomodulating agents, or as modulators of cell adhesion (e.g. in creating graft rejection; inflammation; metastasis of lymphoma etc.) and creating graft rejection; inflammation; metastasis of lymphoma etc.) and creatilitates purification while deletion of the transmembrane region cellitates recovery, improves aqueous solubility and removes cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Phe214Leu substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 131; Conserv
    Domain
                                Binding-site
                                                            Binding-site
                                                                                            Domain
                                                                                                                                                                                                                                       Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                                                                                                                          Domain
                                                                                                                                                                       Key
                                                                                                                                                       Region
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                  metastasis.
                                                                                                                                                                                                                                                                                                   Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
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                                                            /label=
196..257
                              /label= Complement binding repeat 1. 258..316
                                                                                                                          /label= Signal region 38..154
/label= Complement binding repeat 2.
332..354
                                                                                         /label= Lectin domain
159..192
                                                                                                                                                                    Location/Qualifiers
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                                                        el≡ EGF domain.
.257
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99.2%;
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Pred. No. 5.5e-63;
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                     Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a Phe244Met substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin super family nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A hybrid immunoglobulir a single transmembrane
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hes 131;
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                                                                                                                                                                                                                                                                                Similarity
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               standard;
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                                                                                                                                                                                                                                                                    Conservative
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89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                Protein;
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                371
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Pred. No. 5.5e-63;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                            Length 371;
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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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92US-0986931.
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89US-0315015
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258..316
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159..192
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Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation the ligand - useful for

Disclosure; Page 19; 41pp; English.

immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are glven in AAR98109-R98135. This variant contains a Lys298-Lys299; Arg-Arg A hybrid immunoglobulin chain comprising the ligand binding situating situations as single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an site of

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Best Local Similarity
Matches 130; Conserv
     The specification describes a product which antagonizes binding respiratory synctial virus (RSV) G-protein to annexin II or L-selectin, or causes a decrease in cell surface levels of annex II or L-selectin. Such products are used in the manufacture of a
                                   Disclosure;
                                              Treatment of respiratory synctial virus infection (RSV) using Annexin II or L-selectin derivatives
                                                                WPI;
                                                                            Malhotra
                                                                                       (GLAX ) GLAXO GROUP LTD.
                                                                                                  21-OCT-1999;
                                                                                                              23-OCT-2000;
                                                                                                                          26-APR-2001
                                                                                                                                      WO200129054-A2
                                                                                                                                                       Domain
                                                                                                                                                                  Region
                                                                                                                                                                             Region
                                                                                                                                                                                         Domain
                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                 Respiratory synctial virus; RSV infection.
                                                                                                                                                                                                                                                  Amino acid
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                                  Page 67-69; 74pp;
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in prevention
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99
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                                                                                                                                                           "cytoplasmic
                                                                                                                                                                       "transmembrane region"
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5.5e-63;
hes 0;
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RESULT 33
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23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
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Lasky LA;
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therapy; drug delivery; antiviral; neuromodulator;
lator; cell adhesion; graft rejection; inflammation;
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159..192
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38..154
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356..372
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                                                                                                                                                                 Cytoplasmic
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
.5e-63;
                                                                                                                                                                                                       repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372;
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RESULT 3
AAR98134
IID AARK
XX AAR
AC AAR
XX Imm
DE Huma
XX Imm
KW Imm
KW Imm
KW Imm
KW Imm
KW Imm
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Best Local
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binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 209-Asn insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells.
                                                                                                                                                                                                         Immunoglobulin; transmembrane receptor; adhesion; targetting; diagnosis; therapy; drug delivery; antiviral; neuromodulator; immunomodulator; cell adhesion; graft rejection; inflammation
                  Binding-site
                                                  Domain
                                                                                Domain
                                                                                                                                                              Homo
                                                                                                                                                                                              metastasis
                                                                                                                                                                                                                                                                          Human lymphocyte cell surface glycoprotein (HuLHR) variant.
                                                                                                                                                                                                                                                                                                          01-NOV-1996
                                                                                                                                                                                                                                                                                                                                            AAR98134;
                                                                                                                                                                                                                                                                                                                                                                          AAR98134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and treatment e.g. of inflammation
                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lmmunoglobulin constant region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CEPLEAPELGTM-DCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQ
                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cepleapelgtmndcthpfgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d immunoglobulin chain comprising the ligand binding site of e transmembrane receptor without an active transmembrane fused at its C-terminus with the N-terminus of an lobulin constant region. The receptor is not a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding hybrid immunoglobulin comprising the ligand site of a receptor fused to Ig constant region - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                              /label=
38..154
                                                  /label= I
159..192
                  196..
                                                                                                               Location/Qualifiers
1..37
                              /label- EGF domain
                                                                                                                                                                                                                                                                                                                                                                        Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                        328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%;
99.2%;
                  260
                                                                 Lectin domain
                                                                                               Signal
Complement binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Score 722.5; DB 17
Pred. No. 1.5e-62;
0; Mismatches 0;
                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                              inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255
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Ωy
                                                              В
                                                                                          Qγ
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                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                          immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targettling of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region facilitates recovery, improves aqueous solubility and removes potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR88106 are given in
                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A hybrid immunoglobulin chain comprising the ligand binding site a single transmembrane receptor without an active transmembrane region; fused at its C-terminus with the N-terminus of an immunoglobulin constant region. The receptor is not a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding hybrid immunoglobulin comprising the ligand binding site of a receptor fused to Ig constant region - useful for diagnosis and treatment e.g. of inflammation {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                      cell surface glycoprotein AAR98109-R98135. This va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH
   316
                                 118
                                                                256
                                                                                                                             196
                                                                                                                                                                                          Local Similarity 97.1 hes 132; Conservative
                                                                                              58
                                                                                                                                                           \vdash
PICQKLDKSFSMIKE 132
                                                                                                                                            CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETT----CGPFGNWSSPEPT
                                                             CQVIQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPS
                                                                                                                            cepleapelgtmdcthpfgnfsfssqcafscsegtnltgieettvencgpfgnwsspept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996-238773/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lasky LA;
                                                                                                                                                                                                                                                                           374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0315015.
91US-0808122.
92US-0986931.
94US-0185670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0440625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261..319
/label= Complement binding repeat 335..357
/label= Transmembrane domain. 358..374
                                                                                                                                                                                                                                                                                                       This variant contains a 241-Val-Glu-Asn insertion
                                                                                                                                                                                                         98.4%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic domain
                                                                                                                                                                                          0;
                                                                                                                                                                                       Score 721.5; DB 1/;
Pred. No. 1.9e-62;
                                                                                                                                                                                                                          17;
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              member of the
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of.

57

1;

117 255

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22-NOV-1989;
23-FEB-1989;
16-DEC-1991;
08-DEC-1992;
21-JAN-1994;
                                                                                                                                                                                 A hybrid
a single
          immunoglobulin constant region. The receptor is not a member of the immunoglobulin super family, nor a multiple subunit polypeptide encoded by discrete genes. The hybrid immunoglobulin chain combines the adhesion/targetting of a ligand binding partner (LBP) with the effector functions of immunoglobulin and can bind to and/or activate more than one ligand. It can be used diagnostically for the in vitro assay of LBP and their targets; or therapeutically to deliver LBP such as toxins, enzymes, growth factors to particular cells. Typical applications are as antiviral, neuromodulating and immunomodulating agents, or as modulators of cell adhesion (e.g. in treating graft rejection; inflammation; metastasis of lymphoma etc.) The immunoglobulin component increases plasma half life and facilitates purification while deletion of the transmembrane region
                                                                                                                                                                                                                                           Nucleic acid encoding hybrid immunoglobulin comprising binding site of a receptor fused to Ig constant region diagnosis and treatment e.g. of inflammation
                                                                                                                                                                                                                                                                                                                                            (GETH
                                                                                                                                                                      region;
                                                                                                                                                                                                                    Disclosure; Page 19;
                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                    Capon
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis;
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                                                                                                                                                                                                                                                                                              1996-238773/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                     ДJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -site
                                                                                                                                                                                                                                                                                                                                             GENENTECH
                                                                                                                                                                    immunoglobulin chain comprising the ligand binding site
transmembrane receptor without an active transmembrane
fused at its C-terminus with the N-terminus of an
                                                                                                                                                                                                                                                                                                                `Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; drug deliver lator; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                  89US-0440625.

89US-0315015.

91US-0808122.

92US-0986931.

94US-0185670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane receptor; adhesion;
apy; drug delivery; antiviral; neu
; cell adhesion; graft rejection;
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358..374
/label=
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258..319
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196..257
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159..192
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38..154
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                                                                                                                                                                                                                    41pp; English.
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  improves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement binding repeat 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lectin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein (HuLHR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
  aqueous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
  solubility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuromodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variant.
                                                                                                                                                                                                                                                         the ligand - useful for
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RESULT
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Best Local
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Seed
                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                        T lymphocyte-specific Leu8 Antigen minor form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potentially immunogenic epitopes. Variants of the human lymphocyte cell surface glycoprotein described in AAR98106 are given in AAR98109-R98135. This variant contains a 292-Tyr-Tyr-Tyr insertion
                                                               23-JAN-1992
                                                                                                                                     Modified-site
                                                                                                                                                             Modified-site
                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                  Нопо
                                                                                                                                                                                                                                                                                                          Rapid immunoselection cloning technique;
                                                                                                                                                                                                                                                                                                                                         21-MAY-1992
                                                                                                                                                                                                                                                                                                                                                         AAR22551;
                                                                                                                                                                                                                                                                                                                                                                       AAR22551 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
               (GEHO-)
                               13-JUL-1990;
                                               15-JUL-1990;
                                                                               WO9201049-A
                                                                                                              Modified-site
                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                 receptor;
                GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
Aruffo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 AA;
                HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
P,
                               90US-0553759
                                               90WO-US04986
                                                                                                                                                          /label= N-linked_glycosylation
/note= "putative"
285..287
                                                                                                                                                                                    /note= "
269..271
                                                                                                             /note=
324..32
                                                                                                                                                                                                            /label= N-linked_glycosylation
/note= "putative"
230...232
                                                                                                                                                                                                                                   /note=
157..15
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                      299..301
                                                                                                                                                                                           /label= N-linked_glycosylation
/note= "putative"
                                                                                                                                            /label= N-linked_glycosylation
/note= "putative"
                                                                                              'note=
                                                                                                      /label=
                                                                                                                     /label= N-linked_glycosylation
/note= "putative"
                                                                                                                                                                                                                                           /label= N-linked_glycosylation
/note= "putative"
                                                                                                                                                                                                                                                                                                 antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                       Protein; 363
                                                                                                                                                                                                                                    . . 159
Amiot M;
                CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.4%;
97.8%;
                                                                                                              326
                                                                                                                                                                                                                                                                                                                                                                                                                             132
                                                                                             "Putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 721.5;
pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                  cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e-62;
                                                                                                                                                                                                                                                                                                          cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               315
                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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useful for isolation

were

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ARESULT 3
AARP1443
AAR AARS
XX 10
DT 31-C
XX CCLL
XX C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.3
Best Local Similarity 98.3
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Two cDNA clones encoding Leu8 determinants were isolated from a human T cell library using the rapid immunoselection cloning method (see e.g. AAQ21164 for description of method). This protein sequence was deduced from the shorter insert. The weakly hydrophobic C-terminal domain is characteristic of surface proteins that are
                                                                                                                                                                                                                                                                                                                                                                                                               therapy; diagnosi antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attached to the cell membrane by covalent linkage to a phosphatidylinositol-substituted glycan. See AAQ21184 for the larger insert and AAR20815 for the major form
                    US5506126-A
                                                                             Modified-site
                                                                                                                  Modified-site
                                                                                                                                                        Modified-site
                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Leu8 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR91443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91443 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New CD53 cell surface antigen and DNA encoding it - for immuno-therapy and diagnosis of haematopoietic neoplasms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leu8 antigen that it encodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1992-056864/07.
                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cepleapelgtmdcthslgnfsfssqcafscsegtnltgleettcgpfgnwsspeptcqv 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Page 106; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                               /label= Glycosylation_site
269..271
                                                                                                                                                                                                                                                                          /label= Glycosylation_site
156..158
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                           /label-
                                                                                                                                                                                                                                                    'label Glycosylation_site
                                                                                                                                  'label Glycosylation_site
                                                                                               label- Glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.1%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                             cloning; immunoselection; immunotherapy;
ector; Leu8 antigen; T-lymphocyte;
                                                                                                                                                                         _Glycosylation_site
                                                         Glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 719; DB 13;
Pred. No. 3.2e-62;
D; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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AAY96184
ID AAY
XX
AC AAY
AC AAY
AC Hum
DE Hum
XX
KW Leu
KW Leu
KW Lim
KW imm
KW amy
XX
AX
OS Hom
XX
PN US6
                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 cDNA clones encoding Leu8 determinants (AAR91442 and AAR91443) were isolated from a human T-cell library using a novel immunoselection cloning method. The longer insert (AAR14723) contained 2,350 residues, while the shorter lacked 436 internal residues. A major transcript of 2.4 kb was present in peripheral blood mononuclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukaemic T-cell lines. Leu8 antigens can be obtd. for diagnostic and therapeutic use. The presence or absence of Leu8 on CD4+ T-cell subsets. Soluble forms of Leu8 can act as antiinflammatory agents by reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning of cDNA encoding cell surface antigen of diagnostic and therapeutic proteins
US6111093-A
                                    Homo sapiens
                                                                         amyloidosis;
                                                                                             immunodiagnosis;
immune disorder;
                                                                                                                                                                             Human
                                                                                                                                                                                                               19-DEC-2000
                                                                                                                                                                                                                                                      AAY96184;
                                                                                                                                                                                                                                                                                             AAY96184 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Column 71-74; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aruffo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1996
                                                                                                                                      Leu8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sin
                                                                                                                                                                                                                                                                                                                                                                                            330
                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996-200279/20
DB; AAT14723.
                                                                                                                                                                                                                                                                                                                                                                                                               QKLDKSFSMIKE 132
                                                                                                                                                                                                                                                                                                                                                                                          qkldksfsmike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cepleapelgtmdcthslgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv
                                                                                         cell surface antigen; human; immunoselection; panning odiagnosis; diagnosis; immunotherapy; gene therapy; e disorder; infection; asthma; immune complex disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC
                                                                                                                                                                           T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                         specific Leu8
                                                                         multiple sclerosis; inflammation;
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0983647.

88US-0160416.

89US-0379076.

89US-0553759.

93US-0139273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0160416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP
                                                                                                                                                                         antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 719; DB 17;
Pred. No. 3.2e-62;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                             B
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Length

0

Gaps

0

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DЬ
                                           Q
                                                                                                   Дb
                                                                                                                                                 Qy
                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992;
25-FEB-1988;
13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leu8- T-cells to antigen presenting cells, or the ability to cause such binding to occur on surfaces other than lymphocyte cells, can be useful in diagnostics and therapy. The level of activated Leu8-T-cells relative to resting Leu8+ cells could serve as a measure of immune response to a particular antigen. Modification of the specificity of the extracellular domain of Leu8, which mediates adhesion to specific endothelial cells of lymph nodes, could serve to regulate the homing potential of resting T cells. Soluble forms of Leu8 could act as antiinflammatory agents by reducing lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen is given in AAY96138. The method, designed to isolate cell surface antigen (CSA) cDNAs, is based upon transient expression of a CSA in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to (panning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the disonosis and treatment of immune-mediated infections, diseases, and disorders in animals, including humans. These disorders include asthmatic applications in the contraction of the contractio
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis.
Leu8- T-cells +0 ~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a T-cell specific Leu8 ant predicted from 1 of 2 clones (see AAA50632) isolated from T-cell library by the method of the invention. A longer I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Column 69-72; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stamenkovic
330
                                             121
                                                                                                   270
                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000
                                                                                                                                                    61
                                                                                                                                                                                                                                                          \vdash
                  QKLDKSFSMIKE 132
                                                                                                                                                                                                                            CEPLEAPELGIMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
                                                                                           {\tt cepleapelgtmdcthslgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv}
                                                                                                                                                                                                                                                                                                             130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune-complex disease, amyloidosis, parasitic diseases or e sclerosis. The ability to interfere with the binding of
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0160416.
89US-0379076.
90US-0498809.
90US-0553759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9205-0983647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0181612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seed
                                                                                                                                                                                                                                                                                                                                   98.1%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                Score 719;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                DB 21;
.2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A longer Leu8
                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen,
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                 269
                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                        0;
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RESULT 3
AAR20815
TD AAR2

39

AAR20815 standard;

Protein;

385

AA

Query Match
Best Local Similarity
Matches 130; Conser

Conservative

0; Mismatches Score 719; DB 13; Pred. No. 3.5e-62; 0; Mismatches 2;

98.1%; 98.5%;

Length 385;

0;

Gaps

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human T cell library using the rapid immunoselection cloning method (see e.g. AAQ21164 for description of method). This protein sequence was deduced from the larger insert. The hydrophobic putative membrane-spanning domain is followed by several positively charged residues resembling a cytoplasmic anchor sequence. The protein is closely related to the murine Mel-14 homing receptor. See AAQ22500 for the shorter insert and AAR22551 for the phospholinia anchored form of Leu8 antigen.
Sequence
                                                                                                                       Example 14; Page 106; 160pp; English
                                                                                                                                                    New CD53 cell surface antigen and DNA encoding
                                                                                                                                                                                                                                               13-JUL-1990;
                                                                                                                                                                                                                                                                   15-JUL-1990;
                                                                                                                                                                                                                                                                                       23-JAN-1992
                                                                                                                                                                                                                                                                                                          WO9201049-A
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid immunoselection cloning technique; cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocyte-specific Leu8 Antigen major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mel-14;
                                                                                                                                                                                                                          GEN HOSPITAL CORP
                                                                                                                                                                                                      Aruffo A,
 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                           and
AA;
                                                                                                                                                                                                                                               90US-0553759
                                                                                                                                                                                                                                                                   90WO-US04986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homing receptor; antigen-presenting cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,_auel= N-linked_glycosylation

note= "putative"

157..159
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230..232
                                                                                                                                                                                                                                                                                                                                       324..326
/label= 1
                                                                                                                                                                                                                                                                                                                                                                               /label= N-linked_glycosylation
/note= "putative"
299.301
                                                                                                                                                                                                                                                                                                                                                                                                              /label= N-linked_glycosylation
/note= "putative"
285..287
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= N-linked_glycosylation
/note= "putative"
269...271
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                                                                                                                                                                                                                                                                                                                                                           /note= "putative'
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/note= "putative"
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"putative"
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                                                                                                                                           neoplasms,
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330 121 270

OKLDKSFSMIKE 132

341

40

210 61

269 60

IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120

31-OCT-1996 AAR91442;

(first

entry)

AAR91442 standard; Protein; 385 AA.

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25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                           Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; Leu8 antigen; T-lymphocyte; antiinflammatory.
                                Cloning of cDNA encoding cell surface antigen of diagnostic and therapeutic proteins
                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                    Modified-site
                Example 14; Column 71-74; 79pp; English
                                                                                   Aruffo A, Seed B;
                                                                                                    (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                      01-DEC-1992;
                                                                                                                                                                      25-FEB-1988;
                                                                                                                                                                                       09-APR-1996
                                                                                                                                                                                                        US5506126-A
                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Human Leu8 antigen
                                                          1996-200279/20
DB; AAT14723.
                                                                                                                   88US-0160416.
89US-0379076.
90US-0553759.
93US-0139273.
                                                                                                                                                      92US-0983647
                                                                                                                                                                      88US-0160416
                                                                                                                                                                                                                                                                  /label- Glycosylation_site 299..301
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 113..115
                                                                                                                                                                                                                                 /label= Glycosylation_site
347..368
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324 . 326
                                                                                                                                                                                                                                                                                                    269..271
                                                                                                                                                                                                                                                                                                       229 .231
/label=_Glycosylation_site
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156..158
                                                                                                                                                                                                                        /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                         label Glycosylation_site
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                                                                                                                                                                                                                                                                                   . . 287
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                                          useful
                                          for isolation
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2 cDNA clones encoding Leu8 determinants (AAR91442 and

AAR91443) were

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Best Local Sim
Matches 130;
                                                                                                                                                                                                                                                                                                                    isolated from a human T-cell library using a novel immunoselection cloning method. The longer insert (AAT1473) contained 2,350 residues, while the shorter lacked 436 internal residues. A major transcript of 2.4 kb was present in peripheral blood mononuclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukaemic T-cell lines. Leu8 antigens can be obtd. for diagnostic and therapeutic use. The presence or absence of Leu8 on CD4+ T-cells subsets. Soluble forms of Leu8 can act as antiinflammatory agents by reducing
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                         lymphocyte migration.
   330
                121 QKLDKSFSMIKE 132
                                                                  270
                                                                                                                           210 cepleapelgtmdcthslgnfsfssqcafscsegtnltgieettcgpfgnwsspeptcqv 269
                                                                                               65
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                                                                                                                                             CEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLTGIEETTCGPFGNWSSPEPTCQV
qkldksfsmike
                                                             IQCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGTELIGKKKTICESSGIWSNPSPIC 120
                                                                                                                                                                                            Similarity 98.5
30; Conservative
                                                                                                                                                                                                                                                                         385 AA;
                                                                                                                                                                                                          98.1%;
98.5%;
                                                                                                                                                                                          Score 719; DB Pred. No. 3.5e 0; Mismatches
                                                                                                                                                                                            0;
                                                                                                                                                                                          DB 17;
3.5e-62;
nes 2;
                                                                                                                                                                                                                      Length
                                                                                                                                                                                            Indels
                                                                                                                                                                                            0:
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Search completed: Job time: 267 sec September 7, 2002, 10:14:09

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